

Sn. 08/401, 881



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re the Application of:

**William A. HASELTINE, Craig A. ROSEN, Steven M. RUBIN, Patrick J. DILLON,  
Haodong LI, and Julie EARLE-HUGHES**

Serial No.: Unassigned

Filed: Unassigned

For: HUMAN GENES, SEQUENCES AND EXPRESSION PRODUCTS-17

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### SEQUENCE LISTING

SECTION 1 of 2 SECTIONS,

PAGES 116 TO 459

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Haseltine, William  
Rosen, Craig  
Ruben, Steve  
Dillon, Patrick  
Li, Haodong  
Earle-Hughes, Julie

(ii) TITLE OF INVENTION: Human Genes, Sequences, and Expression  
Products

(iii) NUMBER OF SEQUENCES: 1767

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart, &  
Olstein

(B) STREET: 6 Becker Farm Road

(C) CITY: Roseland

(D) STATE: New Jersey

(E) COUNTRY: USA

(F) ZIP: 07068

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

(B) COMPUTER: HP Vectra 486/33

(C) OPERATING SYSTEM: MSDOS version 5.0

(D) SOFTWARE: ASCII Text

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/401,881

(B) FILING DATE: March 10, 1995

(C) CLASSIFICATION:



(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Olstein, Elliot

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(C) REFERENCE/DOCKET NUMBER: 325800-306

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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 272 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGNANAAAGG AGGAGCACGA GGTGGCTGTC CTGGGGGCGC CCCAAAACCC TGCTCCCCCA	60
ANGTCCACCG TGAATCCAAA TCCGCAGCGA GAACCTCCGT GCCCAACCAT GTGNTGCTGG	120
TCCCTGTTC AANACCCTCTT AATGAACCCC TGNTGCCTGG GNCTTAANAG CATTGCGCTA	180
CTCCGTGAAA GTNTAGGGNC AGGAAAGATG GTTGGCGACG TGAACCGGGG CCCAGGNNTA	240
TGCTTCCACC GNCAAGTGCC TGAAAATTTG GG	272

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 136 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGAANACCAG CTCTGGGGGC ACGGCCANC TTCCTTAAAA ATGTCTACTG TTCCANAAAA	60
TCCTGTNCAA GCCCAGCTTG AGGGGTAATC ACTCTANACC CCCAAGTCCA TATGGNTCTT	120
TAAAAGCCTA TNCTAA	136

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 68 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGCANAGNAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	60
AAAAAANN	68

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATCCCCAACG TGNCCGGCCG ACACCAAGCT CTCCAAGATC AAGACTCTGC GCCTAGCCAC	60
CAGCTNACAT CGCCTGACCT GAATGGACGT GCTGGGCCAA GGGATGCACA GTCTGGGCGA	120
TNCCAAGGGC CTT	133

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 316 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GACTCAATCA TGGNTTGTGG TCTGGTCGCC AGCAACCTGT AATCTCAAAC CTGGAGAGTG	60
CCTTCGAGTG CNAGGCGAGG TGGCTCCTGC ACGCTAAGAG CTTCGTGCCT GNAACCTGGG	120
CAAAGACAGC AACANCCTGT NCCTGNACTT ACAACCCTNG CTTCAACGTC NACGAGAACG	180
CCAACACCAT CGTGTGCAAC AGACAAAGGT ACGGCGGGGC CTGGGGGGAC CGAGCAGCGG	240
GAGGCTGTCT TTCCTTCCC AGNCTGGAAG TTTTTCGAGG GTGTGCATCA CCTTTGGACC	300
AGGNCCAACC GCCCTA	316

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 333 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGCAGAGCCT GTCGGCCACC AAGGTAGTGC ACNGACCCAT GGGNCACCCG CAAGCACCTG	60
GTGCCCAAGG NACCTGGATA TNCGGCCTGT GAAAGACTCG GAACTCGTCT ATCTGCAGAG	120
CTGCACCTGA ACTTCTGCAT GAAGNAATGA GAAAGGTGNG CTCCCACGGG ANCACAAGAC	180
AGGNCAGTGC AACAAGGACA TCCAACGGAA AGCGAACATT GCGAGACCTT GATGTGCCTG	240
CGGGCGTGGG TGACAACCCC TACACAGGAC CGCNTGGTGC AGCGGTGCCA TGTNAGTTAC	300

333

CATGGTGCTG TTACGTTCAA NNGCCGCAGT NTG

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 84 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGCACGAGCC TATCGGCCAC CAAGGTAGTA CACNGACCCA TNGNCACCCG CAAGCACCNN 60  
 GTGCCCAAGG ACCTGGATAT CCGG 84

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 220 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GNAGGCAAGG CCAGGGATAA GGNGTGGATG CCGTCACCAA GTTGGGCGCG TTNGTCAAGG 60  
 ACATGAAGAT CAAGTCCNGG AGGAGATCNT TCTCTTCTCC TGCCCATTA A GGGTTCAANG 120  
 ATCATTGATT TCTTCCTGGG GGCCCTCTCA NGGATGAGGT TTTGAAGATT ATGCCGTNCA 180  
 GAAGNAGACC CTGCCGGCCA GNGAACCGGT TNAAGGCTTT 220

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 330 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGCCCCTTTG GGCATGGCTA TGGGGAGGGG GCTGGAGANG GTATCGATGA TGCTGAGTGG 60  
 GTGGTGGCCA GGGACAAGCC CATGTACGAC GAGATCTTCT ACACCCTGTC ACCGGTTGNT 120  
 GGCAAGATCA CAGGCGCTAA TNCCAAGANG GAGATGGTGC GCTCCAAGCT GCCCAACAGT 180  
 GTGCTGGGCA AGATCTGGAA GCTGGCCGAC ATTGAACAAG GATGGCATGC TGGTACGACG 240  
 AACGAGTTTG GCACTGGNCC AACCACCTAC ATNCAAAGTT CAAGCTGGGA GGGGGCACGA 300

GCTNACCCAA CNAGCTGGCC TNACCCACCT

330

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTCCAAGAAC GTCATGATGA TCCAGTCCTG CAAATGCAAC TACAACTGCC CGCATGCCAA 60

TGANGCAGCG TTTCCNTCT ACAGNNTGTT CAATGACATT CACAAATTNA GGG 113

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGCANAGNAG AACGCAGAGT ACAAGCAATT GCTGGGACAT CAAGACACGC CTGGNGGTGG 60

AGATCNNGAC CTACCGCCGC CTGCTCGATG GAGAGGGAGG TGGTTCTAGT TTTGCAGAAT 120

TTGGTGGTAG AAACCTCAGGA TCTGTAAAC ATGGGATCCA GGGATCTGGT NATCCNGGTG 180

ACTCAAGATC TGGAAGCTGT TCTGGTCAAG GACGAGATTC AAGCAAGACT AGAGTGNACT 240

AAGAACTATN GTTAGAGGNG TTGGTGGATG GCAAGGTTGT CTCGTTCTCC AAGTCCAGCA 300

GTATTTCTGA GGGTNGAAAG TTAAATAAG GGACCTTNCC AGTTCAACAA AAGTGTCTT 360

TTNCAAGGGN ANAAAAATTC CAGG 384

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGCAGAGCCC AGAAGAACCA CATCCCTNTT TTAGTCCCG CACTTACAGA CGGNTCGCTG 60

GGCGACATGA TCTTTTCCA TTCCTACAAG AACCCGGGCC TGGTCCTGGA CATCGTTGAG 120

GACCTGAAGG CTCATCAACA CACAGGCCAT CTTNCCAAG TGCCTGGGN ATGATCATTC	180
TGGGCGGGG CGTGGTCAAG CACCACATTG CCAATGCCAA CCTCATGCGG AANGGGGCCG	240
ACTTACGCTG TTTACATCAA CACAGCCCAG GAGTTTGATG GCTCTGAACT CAGGTGCCCCG	300
ACCAGACGAG GCTGTTNTCC TGGGGCAAGA TNCGGGTGGA TGCACAGNCC GTCAAGGTTT	360
ATGCTGGAGG CNTNCCTGGG TCTTTCCCCC TGGTT	395

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 439 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGCACGAGGC CTTACAGAGA GGTACAGATGC AGAAGCCATT TGAAGACGCC TCGTTTGCGC	60
TGCGGACGGG GGAGATGAGC GGGCCCGTGT TCACGGATTC CGGCATCCAC ATCATCCTCC	120
GCACTGAGTG AGGGTGGGGA GCCCAGGCCT GGCCTCGGGG CAGGGCAGGG CGGCTAGGCC	180
NNCCAGCTCC CCCTTGCCCG CCAGCCAGTG GCCGAACCCC CCACTCCCTG CCACCGTTCA	240
CACAGTGATT TTATTGTTCC CACAATGGCT GGAAGGGGG CCCTTTCCAG ATTGGGGGCC	300
CTGGGGTCCC CACTCCCTGT NCCATNCCCC AGTTGGGGCT GNGAACCGCC AATTTTTCCT	360
TTAAGTATTG NATTTTCAGNA NGGGTGGGAG GTTCCCAAAC CCAGGCATNT GGTGGGAGGG	420
GTGTTTCCAA AGAGAAAGG	439

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 317 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGCAGAGNAC AAGGGCCGTG GCCGCTTCGC CCTCATCATC TATGAGAACA TCCTCAAGTA	60
TGTCAACCTG GACGCCTGGN AACCGGGAGC TGCTGGGACA AGTACTGTGT GGCCTACGGC	120
GTGGGCATCA TTGGCTTCTT CAAGGCCAAT GAGGAACAGC CTGCTGAGTG CGCATTC AAG	180
GGCTTTNNCC TGTTCCCTGC ACTCAAACCT GGGCCTGAAG GGACTGCAGC ATCAACCCCA	240
AGTCCCCGTT GGCTTCTACG TGGACGCGAA CCTNAGGNGA GGGTTGGNAG GAAAGGTTGT	300

TGCTTTCNCC CGGGTNG

317

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGCAGAGCCA ACATTGAGGC CAACGAGAGT AAGGNGGTCC GGCAGTTCCG GAGNACTCTT	60
TGCCCAGCTG GCTGGAGGAT GACATGGAGG TCAGCGCCAC AGAACTCATG AACATTCTTC	120
AATAAGGTTG TGAACACGNA CACCCTGATC TGAAAGACTG ATGGTTTTTG CATTGACACA	180
TGTCGCAGCA TGGTGGCCGT GAATGGGATA GCGNACACCA CAGGCAAGCT GGGCTTTGGA	240
GGGAATTTCA AGTNACTTGT GGGAACAACC ATTCAAAAAG GTGGNCAGGN CATATTACAA	300
ACAGTTTCGA CAATGGNACC GATTGNGGGA CCATTT	336

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGCAGAGCCA CAACCTCCCT GGCTCCTACC GCTGTGACTG CAAAGCCGGC TTTCAGCGGG	60
ATGCCTTCGG CCGGGGCTGC ATCGACGTGA ATNAGTGCTG GGCCTCGNCA GGCCGCCTGT	120
GCCAGCACAC GTGTGAGAAA CAACTNCGG CTCCTNACCG CTGTTCTGTC GCCTCCGGGT	180
TCCTGGCTAG CAGCGGNACG GCAAGCGCTG TGNAAGACGT GAATAAGTGT GAGGCCCANC	240
GCTGTGAGCC AGGTAGTNTG CCAACATGNT TATGGGNTCC TACCCAGTGG TACTGCCGCC	300
AGGGGTTACC A	311

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGCAGAGNAC AAGGGCCGTG GCGCTTCGCC CTCATCATCT ATGAGAACAT CCTCAAGTAT	60
GTNAACCTGG ACGCCTGGAA CCGGGAGCTG CTGGACAAGT ACTGTGTGGC CTACGGGTGG	120
GCATCATTGG CTTCTTCAAG GCCAATGNGA ACAGCCTGCT GAGTGCGCAT CAAGGGCTTT	180
NCCTGTTCTT GCACTCAAAC CTGGGCCTGA AGGACTGCAG CATCAACCCC AAGTCCCCGC	240
TGCTCTACGT GACGCGACCT AGGGAGGTGG AGAAAGGTGT GCTTCCCCGG NGNAGGACTG	300
GGACGGTTTT TCCAGTTCAA ATCACTCCAN CTATGGAGCC CATNCTTGTN GGNCANGACG	360
GGGTTGGTTT TGAAGTTCCA TGCCCAACAAC TGGGG	395

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGCAGAGCCA CAACCTCCCT GGCTCCTACC GCTGTGACTG CAAAGCCGGC TTTNAGCGGG	60
AATGCCTTCG GCCGGGGCTG CATCGACGTG AATGAAGTGC TGGGCCTCGC CAGGCCGNCC	120
TGTGCCCAGC ACACGTNTGA AGAAACACAC TTCGGCTCCT ACCGCTGTTC CTGAGACCTC	180
CGGGTTCCTG CTNAGCAGCG GACGGCAAGC GCTGTGNAAG ACGTGNAATG AAGTGTGAAG	240
GCCCAGCGNT TGCAGCCAGG NGTNTGGCCA ACATCTTATG NGCTTCCTAA CCCAGTGGNT	300
ACTNNCCGNC CAGGGNTNAC CAGCTTGGCT TGAAGGGATT GGGGCACAAC TGCAACAGAC	360
ATTCCGACGA GTTNTGCTTC AAAGGGNGGC CGGAATCCTT TTGNAACTTT CCGTTGTTNT	420
TNAAAGTTG	429

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CTCACTGCCA GTTCGTGCTT GAGCATCGTT CTGTGCAGGA GGAAGCCGGC TTTCACCGGC	60
AGGCGTGGTG TCAAATGCCC GTTAATTGTT AGCGGACACG AAAACCAGGC CATTACTCAC	120



AGTATAACG

129

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 213 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CTTACGATC GTTCTGNGCA GGAGGAAGCC GGCTTTCACC GGCAGGCGTN NTGTCAAATG	60
CCCGATAATT GTTAGCGATA CACGACAAAC CAGNCGCATT CACTCNACAG TATAACGNCA	120
GGCCAGTCGT CATAAACCGT TCAGGGGAGG AGCCCGGTCA CCCAATTGCG CCCCTGATAA	180
GTGCNGTNCG ATATTACAAA TTNCACTTGN TCC	213

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 115 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGCANAGGGA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	60
AAAAAAAAAA AAAAAAAAAA AANANAANAA AAAAAAAAAA AAAAAANAAA AAANG	115

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 60 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGCACGAGCC CCCCTTTTTT TTTTTTTTTT TTTTTTTTTT TTAAANGNT TNANNTTTTT	60
	60

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 180 base pairs
  - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGCACGAGCG CATGGGNGTC ATCCTCTGGG GTGACGCTNG GGTACACCAC AAGCACGGAG	60
ACCTGCCAGT ACCNCAAAGA TTACCTGACA CGGCTGCTGG TCCCCTACGT GGTCAATTTG	120
TCCTGGGCCA CCGNGTATTG CAGCCNGGCC GAGTGCCATG GCCGTNGNCG GCTGTGTGCN	180
	180

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 128 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TNCCATGNCA CGATATTTCC GCCAAGGACA TCGACGGGCA CATGGTTAAC CTGGNACAAG	60
NACCGGGGCT TCATGTGCAT CGTCACCAAC GTGTGNCTCC CAGTGAAGGN AAGAACCGAN	120
GTAAAACT	128

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 300 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CACCGCCTAT GGTNCTGACG CCAGGCCTGG GCAGAGCCCG GGCGTCTGGA GGCGCTTNGN	60
NGCCGTNCTT GGGCTGCGGA AAGGCTCAGG ACCCAAGAAG GAGCGGAGAC GCACTGAGAG	120
CATTAACAGC GCATTCGGNT AGTTGCGCGA GTGCATCCCC AACGTGCCGG CCGACACCAA	180
GCTCTCCAAG ATCAAGACTC TGCGCCTAAC CACCAGCTTA CATCGTCTAC CTNATGGGAC	240
GTNNCTGGCC AAGGTGCACA GTCTGGCGAT CCCGAGGGCT TTCANGCTTG GAACTCAAGN	300
	300

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TGNGTGAGGT GGCCCTGGGC AGAGAGCACC NTATCANCTT GGACAACCCC AGCTTGAAGA	60
CCCCACCTCC TGGCTTCGAC AGTNTCATTG CCCGAGGCCA CACCGAGNCT GATCCGACCC	120
AGGACACTGA GTTGGAGCTG GATGGGCCAG CAAGTGGTGG TNCCCCAGGG CCAGCCTGTN	180
CCNTGN	186

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TCTGNCCNTG TCATCGNAGA CTTCANGGTC TTAGCAGGGG ACAAGAACTT CATCACAGCT	60
GAGGAGCTGC GGAGAGAGCT GCGGGGCGNC CAGACCGAGT ACTGCATCGC CCGCATGGGG	120
NCCATACCAG GGCCCTGACG CCGTGNCCGG NGCCCTCGAA CTTACAAGTC CTTCTTCACG	180
GGCTTTGTAT GGCGAGAGGG NNCTGTGAGG	210

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GGCAGAGGNC AAGCCGAAGA AGCCCAACTA ACCCAATCGN AAGTNCCTGT CAAGTNCGGC	60
TNAGCATGGC CGNAAGCINN TGCCTTNANC CCTGGGGAGG GCCACACCCT GCAGGAGCAC	120
CAAATTGTCC TTGTGGAGGG TGGCCGCACC CAGGAACCTG CAAGGCGTNA AGCTTCACCG	180
TTNTGCGTGG NAAGTTANGA CTNTGGGCCA CGTGCCAGAA GAAAGTGAAC GGCTNGGGGC	240
ACAGTGGGCT GGGNGCCCCT NCAGAACATG AAACCTTTCC GNTTCTGGGT TGCNAAAGGG	300
TTCCTCC	307

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 421 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGCACGAGAG GGCTGGTGCC GGGANTCCAC GACAGACGAG CAGCTATTCA GGTGTGAAGC	60
TGTCAGTGGA GAAGTCCACA GTGCCTGCAG TCTGAGCTGG GAATCCTGTG AAGAGGCTGG	120
CAGGAGCTGG GAGCCTGAGA AATGAAATGG TGCCTGCTTA CCATCATCCT GCTGGATGCG	180
GGGCACTGGG ACCCCCTGCT GTNATGAGAA AGGAAGACCC TGGCAGTGAC TTTGGGGACC	240
CTCAAGGCCG TGGGACCCCA TGCGGGCAAC GTGATCTGGG TTGGACCTGC GCAAAGNTTN	300
CTTTGCTGGG AGGTTTAGCG TGGTTCAAGA TGGGAGTNAT GCCCAGAGTT GCGTGTGCTT	360
GGCANCTGGG TTCACAAAGG TTCTTNAANA ATGCTTTTGN CCATTGGGG AACAATTGCT	420
T	421

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 387 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GGCAGAGCNA ANCCCAGACA CAAGTTTTCA CTCCTTCCTG CGAGCCCTGA GGAAGCCTTA	60
CTGGGCAGCC CCGGGCTCAT TGAAATGCCC CGGNATGACT TGGCTAGTGC AGAGGGAATT	120
GAATGGTAAA CCACCGGGGT GAGAAGGGAA GGCTCCCCAT CTNCAGCCAG CCACATCCAC	180
AAGGTGTGTG TAAGGGTGCA GGCGCCGGCC GGTTTAGGCA AGGCTCTACT GTCTGTTGCC	240
CCTCCAGGAG AACTTCCAAG GGAGCTTTCC CCAGACATGG CCAACAAGGG TCCTTCCTAT	300
GGGCATGAGC CCCGNAGTGC AGTTCCAAAA TTCGGGAAGA AGTTNTGACG AGGTAGTTTG	360
NGGNGCGGTT TGTNGGAGTG GTTCATA	387

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 361 base pairs  
 (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GGCAGAGGGA ACACCCAAGG GTTGATATTT GTGGTCGACA GCAATGATCG GGAAGCAAGT	60
AAATAAGGCC CGGGTAGAGC TGATGNAAA TGCTGGCGGN GGAACGNAGC TCCGGGAATG	120
GCTGTGACTC CTTGTCTTTG CCAAACAAAC AGGTNTCTGC CTGAATGCTC ATGAANCGNC	180
TGCTGAGAAT GCACAGACAA GCTGGGCCTG NCATTCCCTT TCGTNCACCG TTAAGTGGTT	240
ACATTGCAGG CCACCTGTGC CCACCAGCGG GGNACGGGGC TGTNACGAGG GCCTGGTATG	300
GCTGGGCCAT TCAGCTTCAA AANCAAGAAG TGNAAGCCA GACAGCCCTA ACAAAGTACC	360
N	361

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 499 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GGCAGANAAC GGGATCCACT TCCGCAAGNC CCTTTGGNAA GGCCGGGTGG GCCANGCCTC	60
AAACTATGGC ATGAAACTCC CAATCCTGCG TTCCAACCCT GAAGGACCAG ATCCTGTATC	120
AAACTGAAGC GGTACAATGA AGGAGACCTT TGGCTACGAA NTGCCCCATT CAAAGAAGGA	180
GGGGGGACTT ACGTGCTGGT CTTGAAATTT GCAGAGGTCT ACTTTGCACA GTCCCAGCAA	240
AAGGTATTTG AATGTTACGA TTGANTGGCC ACGTCTGGTG NAAGGGACTT GGGATATCTT	300
TGAATCGTGT TGGGGCANTA GCACAGTTCA CGGTTGAAAT TATTACCTAT GAAGCATTCA	360
GAAAGGGGGA AGCTGAGTTT TCCAGGGGGA GGTGTTCCAC CTTTCACAGG GGAACTTTAC	420
ATTGAGTTTT NTTAAGGGGT ACTTTGGACA TTCCCAGGTT TNTGCACTTT ACATCATGGT	480
TGGGACCATG GGNTGTTTA	499

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 127 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GGCACGAGGG TGAACGTCAT CGCNTCGAAA GCGTCGNAAT AAGACGCACA CGTTGTCCGC	60
NCGNTGCTGG GTCNAAGGCC TACCACCTTC AGAAGTCGAC CTGTGNCAAA TGTGGGCTAC	120
CCTGTCA	127

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

AGGCCCNTNC CANTTCNGGG CCCCAACCCG TTTNTCCTGG GGGACCGTGA GAAGGTTTGT	60
TGCCCCAAAA ACCCAGGAGA AGGCCAGGCC GTTTTGGACC GTTTAAAGGT NTTNACGGT	120
ATCCCACCGN CTTNCGACAA GAAAAAGCGG GNTGGTGGTT TCCTGCTGCC CTAAAGGTCG	180
TGCGTTNTAN AGCCTAAAAG AAAAGTTTGC CTTTTTTTGG GGGCGGCTTT GGTTTAAGGA	240
GACTGGTTGN AAGTTACCCA GGNAGTTGAC ANGCCANCTT GGNGGGGGGA	290

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGCAGAGCTG TTCCCTNCCA CTGGNTGAGG NATCCTGCAC TGCNTACACC CTGAGNTGGA	60
AACATCGGGN TGTGANAGGT AGCACAGAGG NCTGTNCCCT TTTGTTTATG GTGGNTGTGG	120
AGGGAATGNC AACCGTTTTG GNAANCCGTG AAGGNACTGA GAAGAGNCCG CTGACCCACC	180
CCGGGTGGTA ACAGAGACCA GGGGGACAGG TACTTCCCAG GAACTGAGGG NNCAGATTAT	240
TGNGNTGAGG TTCAGCATCC CCTGGAGGNG TCGGGGTTTC CGCAGAACCC CACTTT	296

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GGCANAGGGA ACTTAAGCAA AAAATCAAAG ACATAAATNA TCAGATGGAT GAGTCTTTCA	60
GAGAGTTGGA TATGGAATGT GCTCTTTTGG ATGGAGAACA GAAATCTGTA AACAACTGGA	120
ACTTATGNAA GGAGNAAGGA GATTTTGGAT CATCTAAACC GGNGAATAGC TGANCTGGGA	180
AAAGAAACAT TGTTGGTGAA AAGACCAAGG ATGCTGACCT GTTTGATGTT GAAAGCAAAC	240
ACTTTGNAAG ACCTGGGAGT TCCAGCAGCT TGTAACATGA GAGCCGTCTA GATGTAGAAA	300
AGGTGGAAC TNGACTNCAA CAGCTCCNGC GTGNAAGTTG CTTGNATATT CT	352

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 58 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GGCAGAGCCC CTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTNNTTTTN AAGGGGGG	58
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(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 403 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GGCACGAGGT AAATNTGGTG TTTCTCCTAG CTGTAAACTG TGTCCCTAATC AGGATGGAAT	60
TTNNAAGGAG ACAGATGCTG GAAGATGGGT TCATATTGTT TGTCCCCTGT ATGTNCCTGG	120
AGTAGCCTTT GGAGATATTG ACAAATTACG ACCAGTAACA CTAACGGAAA TNAACTATTC	180
CAAATATGGT GCCAAGGAGT GTAGCTTTTN TAAAGACCCT CGCTTTGCTA GANCTGGGGT	240
TTGCATTAGC TGTGAATGCA GGGATGTNCA GAGCCTATTT CCATGTGAAC CTGTGCTCAA	300
AAGGAAGGTC TGCTTTCAGA GGCAGCGGGC GGAAGAGGNT ATTAGCAGNT CCATTCTTTG	360
CTTATTGTAA GCAACTNGCA GNTAGGTTAG TNAGAAAGTG GGA	403

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AGGGCGNGGA TTGGCCCGGG CCTGGCGGCC CGCGGGANCC TCAAGCCCAC GGNCAGCAAG	60
CTNGGCGCTC CGCTGAGNTC CTGCAGGGGC TGCCCAGAGTG CACGCGTTGN GCCACGGTCA	120
TCGGGNCACC ATCGTCAAGG CACGGGGCAA GCTCNNNCAT CCCGAGTGCT TCATGTGCAG	180
TGACTGGGG	189

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 488 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GCAAACCGCA TCANCTTTCC GGTGGTCAGC GACAACGTGT GGCCCTGGCC CGAAGCCTTG	60
CGAAGGCCCG AAACCTATTAC TGCTCGATGA GCCGATGGGC GCGCTGGATA AAAAGCTGCG	120
TGACAGGATG CAGCTTGAAG TGGTGGATAT TCTGGAGCGC GTCGGTGTGA CTTGTGTNAT	180
GGTCACCCAC GATCAGGAAG AGGCGATGAC CATGGCGGGG CGCATCGCCA TTATGAATCG	240
TGGGAAATTT GTCCAGATTG GCGAACCGGA AGAGATCTAC GAGCATCCGA CTACCCGCTT	300
ATAGCGCTTG ACGCNACCGT GGGAAATCAA GACCAAANTC AATCTGATTN CAAAAGCTT	360
CACGATTTN TGCCACGGTG TTAACCGCCG CATCTACCGN GCGGNAGTTA TTCAATTTAG	420
NCCCAGTTCT TCAAAAACCG TTCANTTTTG AAAGTATTCG AAGNCGATTT TGGNTAGTGT	480
TTTTAAAT	488

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GGCAGGAGCC AACCCAGCTA TGGCCTATGC CAACGAGGTG AAACGTGTGG TCAGCAGTGC	60
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ACAGGAGAAG GGCAGGAAGA TTGCAGCCTT CTTCGCTGAG TCTCTGCCCCA GTGTGGGAGG	120
GCAGATCATT CCCCCTGCTG GCTACTTCTC CCAAGTGGCA GAGCACATNC GCAAGGCCGG	180
AGGGGTCTTT NTTGCAGATG AGATCCAGGT TGGCTTTGGC CGGGTAGGCA AGCACTTCTG	240
GGCCTTCCAG CTCCAGGGAA AAGACTTCGT CCCTGACATC GTCACCATGG GCAAGTCCAT	300
TGGCAACGGC CACCCTNTTG CCTGCNTGGC CGCAACCCAG CCTGTGGCGA GGGCATTNA	360
AGCCACCGGC GTTTGAGTAC TTCANACCG TTGGGGGGCA GCCCAGTGTC CTGCGCTGTG	420
GGGCTGGCCG TCCTGAATGT NTTNGGAGGA AGGNGCAGCT TCAGGATCAT GNCACCAATT	480
TAGGCAGTTT CTGA	494

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 422 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GGCAGANCTG TGGACTGTTC CACCAACAAC CCCTCCNAGG CTAAGCTGCG GCGNGACTCG	60
ACGAATCCNT CCAGGTCGCT GAGAAGGTTG ACCAGGAAGT ACAACGAAGC TGCTAAAGTC	120
CTACCANTGG GAAGATGCTC AANACCTCCT CTTGGCTGG AGCAGCTGGA ACGAGCAGTT	180
TGAACTGGGG TGTGCCCCGC TGGCAAACCT NCACGCANGC GAAGACCAGT ACTGATCTGA	240
GGGTNACCAC GGTGGGCTTT CCNACACTTT CTGAACTCG GAACGTTNCC TTCCGGTGTT	300
CACTGANGGT GGTTCGTGAA AGCTCTTNTG AACTTCTGAA TTCCCATCCA CTGTGAACGG	360
TTCCCTTGTT AGGAANTTTT TNCAGGNAAG NAACCCCTAA AATTTTATGG GAGGACCGTG	420
GG	422

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 356 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ACGCCTGCNA TTGGTCAGGC TGACCTGGCC TCCCGTGGGG CCACTCGCTG CCTTAGGTGC	60
CTTCTGCTCT CTGGAACCAG AGGGACTAGC TGACTTTTGC CAAGGAAGCA GTGCCAAGAG	120

GCATGGTCNT GGTNNCCTGC CTGCCCCCGG GAGNNCACCT CTGTACACTT CCCTGAANAC	180
CTTCCCAGGT GTGGGTCACT GCCACCTGTG CCCATGGGCA CCCCAGAAGC ACCCACTGTG	240
AACCACTGNC AGTTTTTCTG CATGGCCCAC AGGCACTGGG CCTGTAANCC TTTCGCAAGG	300
GGTCCCGGGT CCCTTCCCAA NNAATTTTAG CCTTTNTAA NGGTTGGCAA CCAAAG	356

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CCGACCTACC GAGAAGAAAA TCTTCACCTA CTTTCATGGTG GGCGCCTCCG CCGTCTGCAT	60
CGTACTCACC ATCTGTNANN CTCTGCTACC TCATCTGCCA CAGGGTCCTG CGAAGGCCTG	120
CACAAGGACA AGCCTCGAGG GGGTTGCAGC CCCTCGTNCC TCCGCCAGCC GAGCTTCCAC	180
CTGCCGCTGC CACCACAAGC TGGTGGAGGC TGGGGAGGTG GATCCAGACC CAGGCAATAA	240
CAAGCTGCAG GTTCAGCACC CAACCTGACC CCCATCTGAC CACAGGGCAG GGTGGGGCAA	300
CATGCGGGCT GCCATGGGAC ATGCAGGGCG GTNTGGCAAG TGGAGAGGTN CTACAGGGNT	360
GAGTGACCCA TTTGGAGTTC ATAAGTATGC AATTTGGTTT TGGCAGTATT TTTTGACATG	420
GGACTNGGNT GTTTGNCGGG TTTAGTAACC CCAGGCCATG GCANCTNAA GGGCATGGTT	480
TTGAAAAAGG ATTAA	495

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GGCAGAGGGA AACTTTTCCT TTGTCCATCG AGGTGTTTCA TAAGTTTTTT GGTGTGTTTT	60
CTGGGTCGTC TATGTGTCAT ATGGTTTNAC TTTTCTCTCC TTTTTCGTTT TCAGAACATN	120
NTTCTGTCTG TTTTGGATTC ACTGCTTCCA TTTNACAGAA TGTGNACTCT TTAGACTCTC	180
AGTCCATCAT GCCATCGGGT ACTCTTGTTG CAGTGTAATT TTAATNACAT GCGGTTATTT	240
CCCTAACGAA TGTGCTATTC ACGTTCCATC TTNCAAATC CATTTTCCCA TCCAGCCAGN	300

GTCTACAATT TAGTGCCCNNT GGCTCCNATT TCGGTCCTCC TCCCCGGGGC TTTNCCCTGG 360  
CTGCGGTGCT GGGCCAAAAG CAGGGGTTTT ANTC 394

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 455 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GGCANAGGAG GGCTGGTGCC GGGANTCCAC GACAGACGAG CAGCTATTCA GGTGTAANCT 60  
GTCAGTGGAG AAGTCCACAG TNCTGCAGTC TGANCTGGGA ATCCTGTAAG AGGCTGCAGG 120  
AGCTGGAGCC TGAAAATAAA TGGTGCCTGC TTACCATCAT CCTGCTGATG CGGGCACTGG 180  
ACCCCCTGCT GTATGAGAAA GGNAGACCCT GCAGTACTTC CAGACCCTCA AGGCCGTGGG 240  
ACCCCATGCG GGGCAACGTA TCTGGGATGG ACCTGCGGCA AAGTTTCCTT TGCTGGGAGG 300  
AATAAGCGTG CTTCAAGAAT GGGAGTNATG CCCGAGGTTG CCGTGTNCTT GCACTGGGGT 360  
TCACAAGGAT CTGAACAGTG GTTCTGCCAT TTGGGAACAA CTTGTTCTTT GGTCAACCAT 420  
TTTTGATTNG TTNACANATC GGCTTCGNAA CCTNG 455

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 380 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GGCANAGCAA GAAATGGCAC CAGGAACAAC ATTTAACCCG GTCATTGGTG ATTCANCTNT 60  
GGATCCAAAA AAGGTTAAGA CCCTCGTTTT CTGCTCCGGC AAACATTTCT ACTCCCTGGT 120  
GAACAAAGAG AATCTNTGGG GGCCAAGAAG CATGACTTTG CCATCATCCG AGTAGAGGAA 180  
CTCTGGCCCC TTCCCGTTGG ATTCTTTACA GGAAGAGAAT GAGCAAATAC AAACATGTTA 240  
AAGATCATAT TTGGAGTNCA GGAGGAACCT CAGAAACATG GGTCCGTGGG TCGTTTGT TT 300  
CTNCCAAGGT TTGAAAAGCA GCTGGNCCTG CAAGCTTCCG TTCTGGTTGG GCCGGNCCCC 360  
TTTTGNCATG ACCCGNTGTT 380

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CAGTGACCGG TTCTNCAGCA CCCGGTGCTN GAGNTTTNGC AATGTCCCGC ACCGGGACGN 60  
TCATCCTGGG GACCTGGTAC ATGGTAGTAA AACCTATTGA AGAGCAATTT GCCTAACTGT 120  
GGGAGTGAAC TCATCCAAAC TCCATGCCAG TNNNNAGCNT C 161

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GGCACGAGGG TGCGCTGAGT CGGAGCCAGA GGCCGCGGGG ACACCGGGCC ATGCACGNCC 60  
CCAACTNAAG CTGCATCTCA AAGCCGAAGA TTCCAGCAGC CCAGGGGATT TCAAAGAGCT 120  
CAGACTCAGA GGAACATCTN CGGAGAGACC CCCGAAGCCC TCTCCAGGGC AGTCCTCATC 180  
CAGACGNTCC GCTAGTGNCA GACAGGAGCG CGCATGGGCC CCCGNNTCGG 230

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TGTGGGCCAC CTCACCAAGT GCAGCCATGC NTTCCACCTG CTGTGCCTCC TNGCCATGTA 60  
CTGCAACGGC AATAAGGATG GAAGTTTGCA GTGTCCCTCC TGCAAAACCA TCTATGGAGA 120  
GAAGACGGGG ACCCAGCCCC AGGGAAAGAT GGAGGTATTA CGGTTCCAGA TGTCGCTCCC 180  
CGGCCACGAG GACTGCGGGA CCATCCTCAT AGTTTACAGC ATTCCCCATG GGCATCCAGG 240  
GGCCCTGAGC ACCCCAATCC CGGAAAGCCG TTCCTGCCA GAGGGTTTTC CCCGCCAGTG 300  
GTTACCTTTC CAGACAACGG CCAGGGCCGN AAGTTCTTAG NAGCTTCCTG GAAAGTGGGG 360

CNTNGTAAGA GGNGGGTTCA T

381

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 299 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CTGCTTGTGT TTAATTCTGC CATTGCCAAC ATGTTACCT GTAACCACAC CCCCATACGG	60
AGCTGTGCAG CCCGGATGCT GAATTTAACA CCTGCTGACA TCACTGCCTG CCACCTGCAG	120
CAGCTCAATT ACTCTCTGGG TCCTGGGATG CTCCCCTGTG TGAGGGNACC ATGCCACCT	180
GNCAGCTTTC CTGAGGGCTT CTTCCAATGA GACCTTTGAT GGGCTGGGAC TGTCCAGCTG	240
CAGGGGAGGG TGGCCCTCAA TNTGTANGNA CCCCTGTGAA TNTCTNCTGG TGGTTTGCG	299

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 202 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GGCAGAGCAC CATCCTATCC AGCCTAACNT TTAATTGAAA GCAACAAAGC ACCTACACCT	60
TCCAGCTGAA GGNAGTGGA TNGTGGCGTC CCACCTGCGC TCAGCTTACG TTGGTGTCAC	120
CATCAATGTG CCTGGNACGA GAAATGAACA ACGNACCCTA TATTCAGTGN CCCCTTCCTT	180
AACACCTCTT NANAAGCTGC TG	202

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 231 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TTAAAANTNA TCCAGCTCTT NCTCAGTGAA AGAGGAAAAT CCCTCCATGG NAGAGGTCAA	60
CGCCTCGNTG GCATACAGAC TGGGGACCCT GGACATGCGG GNTTTTTTCC GNAACACCCA	120

AGNGGAANAT ATCGATTCTN CCTCGGGAAA GCCCCATCCA ACANTGGATG GTCCATCTGG 180  
GAGTTCCAGT ACCGCCCTNG GGGCCCGGTN ATTNATTTCC TGAACAACCA G 231

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 443 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GGCACGAGGA GAAGTGGCCT TAACTGTNCC AGGTCACACG TGGAAATAAG TACAAAAGTA 60  
ATGACTAAAA TAGGCCAAGT TGTCCGAGCA CTTTGTACAT AGGGGTATTA TACGACTGCA 120  
AATTGTGTGA TGTTTAATTG TCACAGANAG AGATACTCGT TTTAAGCACT TTTAGCCTAA 180  
TGTNCTGGAA AATTNCTTAA TGGATTTTNA TACTCTATTG GAAACATTTC CATATTGGTG 240  
NAAATGCCAC TNCATTCCTT TTNCCTGAGG GGGCAAATCT TGAGTAGGCA ATGGGGAAGG 300  
AAAGCCTGGG CAACAGCCAC CATTGTCTTT GTGGGACCTG ACATGGTTTA TTCCACCTNG 360  
GAAAAGGAGG AATTGCTTAA ATGGCACATT GGTTACCCTT TAGGTTAACC NCAGGTTTNC 420  
ANTTTGTGCT GGAATTNTTT AGG 443

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 121 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

AGCAAGTTTG GGNATNCTGA CCCTAAAGTA CCCCATTAAG CATGGGATCG TNACCANTTG 60  
GAAGGCATGG AGNAGTTCTG GGAACAAAAC TTTTAAATAA GNAGTTTNGG GTTGGGCCCC 120  
G 121

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 131 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGCTTTGGGC AGCTTGGAAG TAACCAANAA TAATGGGCAC TACCGTGAAG ATCCCAACTG	60
GTTTATAAAG AAAGCCCATG AGCATAAAAG GGAATTNANA GAGGGCCAGC TGCAGGNGGG	120
AAAAGCNTGT N	131

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 308 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GGCANAGGTT TGTTTCCATT CAGTTTCCTT CNNGCTTATG TTNGTCAGAG TTAGTATCTG	60
TGGGTTACAA CAAAGAACTC TGATAAACCC AGCAATAATC AATTAAAAGT GCAATAAGAA	120
GAAGCTGATA TACGTTATCC ATCAGAACCA TCAAGTATCT GGGAATAAAC TTACAAGCAA	180
GCATGGTAGA CCTTTAGGAA GAAACTATA AATCTTTGCT GAGGCCATAG GGAAAAAAAC	240
CTGANTGGAA GTGGNNCATA ATATTTTCCC TAGTGNGGAA AACTGGGTG GTNTGAAGGT	300
GTTGAATT	308

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 354 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GGCANAGCTA CAACAACACA TCCTAATGNG CANTAATTNT CCTTGCAATA CTCCTATTCT	60
GCCGGTANGA AAAGCCTCTG GGAACCTACC GTCTAGTACA AGATCTTCGC CTCATCAACG	120
NGGCAGTCAT CCCTACAGTC CCGGTAGTTC CTAATCCATA CACACTCCTC TCTCGCATCC	180
CCCCAACAG GTCTCACTTC ACTGTTCTGG ACCTTAAAGA TGGNNNTTTC TCTATCCCAC	240
TAGACCCCGC TTGTAACTT CCTCTTTGCT TTCCACATGG GNAGGACCCA GAACACCGGC	300
GTNTTTTAAA CAATTCACCT GGGACGGTTC TGNTTACANG GGNTTTAGAG ACAG	354

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

CCATGCCATA CTATGTTTGG CAAAATGTNA NTGGNAAAAC TGTATAATAA ACTTTTCATC	60
TTAAATTTTG GAAACTATCA GTAATACAGT AGATAAAAAT AAACAAATAC CNTTGGAGGT	120
AGTCTCAGAT CCTGGNATAC TCTCTCTGAT CTAGTTTCTT CCAGCGNATC CATTAGTTTG	180
ATTACCATAG GTGTGATTAA AATCCACCAG CTGGNGTCCA GTAACATTGG NTCCACCATG	240
TATGAAACCT CTGAAGGGGA AATNTCCTNG GATTTCTTCT GANAAATTAA TTACCA	296

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GGCACGAGCG GTCTGGCTTC ACAGGTCATT TCGCTCCCCC CGTTTCAGGT TGATCTCTCT	60
CGCCGTGAAT TATCTATTAA TGACGAAGTG ATCAAAGTGA CCGCNTTCGA ATACACCATT	120
ATGGAAACGT TGATACGCAA TAATGGCAAA GTGGTCAGCA AAGATTCGTT AATGCTCCAA	180
CTCTATCCGG ATGCGGAGCT GCGGGAAAGC CATACCATTG ATGTACTGAT GGGACGTCTG	240
CGCAAAAAAA TTCAGGCACA ATATCCCCAA GAAGTGATTA CCACCGTTCG CGGCCAGGGC	300
TATCTGTTTCG AATTGCGCTG ATGGAAAAAT TTAAGTNGGC TTTTTCCTCC CGTTTTTCGT	360
TGCGGGTACG TTTNCTGTTG GCAACGGCAA CGTAGTACCN GTGCTTTNN	409

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CTAATGCCCT CACCCCTTAA AACCAGAAAG CGCGCACAAAG TTTTAAANA GGAGACGACG	60
AGGAAGGGAA AGCTGGAAAT CCAGGTGTAA ATTAATGGTC TTCTGGCTTT CCAGGGNCAG	120



CCCTCCCCCTC CTTCCCGGAT CATAAATCTT NAGCATTTNA AAAATAACTG CANNCTNGGT 180  
GTGGTGGNTT GT 192

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 405 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

AAGCTCCGTN NAGTAACGAG CAGGGAAGAG GTGGATGTCC GAAGAGAAAG ACCTTGTGGA 60  
GGAAATCAAA AGGAGAACAG GCCAGCCCCT CTGCCATCTN CTGAACTGAA ACAAACATATC 120  
AAAGGAAAGG AAGTGGGGAC TGGGCACTTA TTTAAGGTTA AGAACAAACT GCATATGTNC 180  
TTANAATTGC TTTGCACTTT TCCCGTTTTN AGCGGAAGGA CCTGAAGAGT GGTNAGNAAC 240  
AGAGGCCTTT GAATTTTAAA TTATGGGTTA NTTTNATTGG TTATTAAGTG GGCAAAAACG 300  
GGCCNGTTAC CAACACCTTT TTTCNATTAC AGGGCCCCCG GGGGNTTTAG TNCCCGTCTG 360  
TGCTTCCGGG GTTAAAAGGN CCCC GCNTGA NATGGTCCCC TTTTN 405

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 348 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TGAATGCATA TGCAGGGAGA ATCCAAAAAC CATGCAGGAA GCTCCGAAGT ATGACGATGT 60  
CTTCCAGAA GTGAAATCGC TACTTTATTG AGCAAATAGC ACGTTGCGAG NCAGGCGGGT 120  
ATCCAAAAAA GAAATTGTTG CTCGACCCCG GATTGCGTTT CGGTAAAAAT CTCTCCCAT 180  
AACTATTCAT TACTGGCGCG CCTGGGCTGG AATTTGNACC ATTTTCAACC TGCCGCTTGT 240  
TGGTGGGTAT GTCACGAAA ATCGGTGGTT GGGCCANCTT GCTGAACGTG GGGGCCNTTC 300  
CGAGCGNNTN AGCGGTNGT TCTGGGCCTG TGCCGGGTTC ATTNGCCG 348

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 246 base pairs  
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

CNAGTGGAAT CCCCCGGCCT GCAGGANCAT NATCCCACGC NAAATGCGGT GAAATATTAT	60
CNCNATCGTA ACCCATGCCG TTAAAGANAT GACGATGCGG CANTTTATCG CNATCGGCCA	120
GATCGTTAAC TAATGANTTT AATGANCCCT CCTTTTTTGT TTCNAGAAAG TNTAGCCAGA	180
AACCCTCAGG GGGANTTTTG GTTATTGGNA AAAAANTGTT TNACCCTGTC CCGGGNGGTT	240
AACCGT	246

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 109 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GGAANACCTG TTTGGAAGTA ACAATAAGGA GGAGGACAAG GAGGCGGCAC AGCTGCGGGA	60
AGGAGCGGCT ANNGNAGTAC GCGGAAGNAA GNAAGGCCAA GAAGCCTGC	109

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 132 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GGAAGACCNC TATTGGNCTA CCGAAAGAAT GGTGTAACCC CATATATAAT TTCNTTTAAG	60
GNTGGTTTAG AAANTGGAAG ANTGTTAACA AATGTGGCAA TTTTNTNGGN TGTATGCACC	120
TGTGNATGCA TA	132

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 165 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GGAAGACCNC TGGCGCCGTT TTTNGNACAA NAAGGTGCTG CTGTCCTTTG GAAAGGCCTT	60
CAAGTGTAAG GAGCCTGGTT GGTTTCCCTT TGTTTTCTAA AACCAGGTCC ACCGGTTTTG	120
CCTGGNTGAA GCCAGNCTGC TTTTNCNAGC CCAGTNCCTT AACTG	165

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GAGNTNAACA TGGNCANNNC CAGCCAGACC NTGGCCACCT TCCTAGNTNN NCTGGCGCAG	60
AAGCTAAAGC CCCTGGGGNA GCAGGAGANT CGCGGTGATT NTGGAGCTNA TTNCNTGCGG	120
AGTGCGAGCC CCGGGGCCTG CCCTTCNACG GCCGCATCCT TGCCTGGAAC ATGCGCTACT	180
ACATGAACCA GGTGGAGGAG ACGCGCTACT GCTTGGACCA NAACCTNCTC AAGGAGTACT	240
TCCCCTTNCA GGTGGTCACG NACGGGCTTC TTGGGATCTA CCAGGAGCTC CTGGGGGTTG	300
GCTTCCACCA CGAGGANGGT GCANTNCCTT	330

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GGCACGAGAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAANNNN	58
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(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

AACANANCTN GAACTCCAC CCGATCAGAC GCCTCCTAAA NCTAGTGGA TCCCCGGCC	60
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TGGTTTAACG ATGAACGAAT TNACCGAATC GCCTCGGTAA ATTTNCCCGT AATATGGGCA	120
ACGTTAAGAA ATTGGAGCTT TTCCCCTACN AAGAGCTGGG NAAACANAAA TGGG	174

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 75 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

TGGCGCCGNT TTTNGGACAA CAAGGTGCTG CTGTCCTTTG GNAAGGCCTT CAAGTGTA	60
AAAGAGCTGGG NAAACANAAA TGGG	75

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 452 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GGCAGAGNCA ATTAATAAAC AAGCTAGATA CCCAGTCTAT TTTCTTTTGA GGATATTTTC	60
CTGTAGGTCA TTTTAATTGA TTTGTTTGAC ATGACTACAT TTATAATAAT CTANTATGGT	120
AAACCTAAGC ATCCTACATC TTGTCTTTAG CTTATAAAGA ATTTCCCTTT CTTGGAAGCA	180
TTAAGTGACT TCTGGTCCCT TAAAATATTC AAATGTGTTG TTTTGGCCAA AATTNCCATA	240
GGCAAAGAAG AATGGAGAAA AGAAATTGTA AAATGGTTCT CGGAGCTTCT TTGGGTAA	300
GGGTCTAATG CCAGGGACCA GCATACAAGT TNCGAGTTGG TGCTGTGGGG GGACCCCGGT	360
TTGTGAGTTC CAGAGGGTGT GTTTGNGNAC AGGCCAGTG GAGGCTCACA CCACACNGTT	420
CTGGGTCCG CTCAAGGTNG NGGCCGCCAG TG	452

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 323 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GGCAGAGCAG GTCTCAACTT CCAGCGAGAG AATGANAGCC CTGTGGTGCG GGCCANGGGT	60
GCCANCCCTTG ACCCTGGGTG AAGCAAGAAC GCCGACGNGG CCCTGCAAAA CCTCCGGGTG	120
GGTCATGAAC AGTGCACAGG NTTCCATCAA GCAANTGGTT TCCGGAGCTT GAGGACANTG	180
AATTTTGT TN CCGAAATCCT TAAATCTTTA GGCAGAATTT TTNAAGTTAA AGACGGGGGA	240
GGAAGGCTTT TNAGGGACCC CTGGGTGTTC TTAAGCATNA AGNTTCGNGT TNTACCCTGA	300
GGTTAACCAC GGTTTCGATCT TAA	323

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 321 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GATACGCCCT TTGGCAAAGA ACCTGGNGTN TAGANATGTG GTGTTTCGNT CCATAATTNT	60
GGAGATCCAA AAAGGAAGAG GCTGTGGCCC TAAAAAAAAT CACGTTTACC TGCCAGCTGC	120
ACCACCTACN TCCAAANCAG CTGGCCACGN GCCTTGCCTT GGGAATTTNA AAANACAGCN	180
ATGAATCTTG GCTGGCNTGG ACGTNACGAN GAGCCGATCC TTGTCCTCCC CACCGTGCCA	240
TTATAAACAT GGGCGGNATT TCCNACCAAC TTACAAGGGG CAGGTTCTNG AGGGCACGTG	300
AATTGGNCCA GGNTTCAAAT T	321

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 64 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GGCAGAGGTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTNG GNAATTTTTT TTTTTTTTNN	60
GGGN	64

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 193 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GGCACGNGAA CGGGCTGGGC CGAGCCCGCA CTNTCGCGGN TCCGAGAGGA CNNGCGTCGC	60
ATCGTGCTGC CAGCCATCGA CAANATCAAG TACAGCACGT TTAAGGTGCA GCAGTATGCG	120
AGACGNNGCC CATGGCTACA ACTGGGGCCT CTGGTGCATN TACATNATAT CCCCCGCAGT	180
ACTGGANTGG ACC	193

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GGCANAGGGA GGAAATGTGT TACAAAGATA TATGTACAAG TGTATTCATC ATTTTCCTGT	60
TTATAATTAA TAAAATGAAA ATGAGNGGGN ATGTTGGGTT NTANGGTTTG N	111

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

GGCAGAGCAA ACTTCAGGGA AAGCCATGCN CATTGGAGCA GAGGTTTACC ACAACCTGAA	60
GNAATGTCAT CAAGGAGAAA TATTTTTTTT TNGGGGTGNG	100

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

AACAATTAGC TCCAGGAAAT AACAGTTATT TNATCATAAA ACAGTCCCTT CAAACACACC	60
CCNNCCGTTT GTNT	74

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 290 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GTACCATTG TCTGACCTCT NTAAAAAATG TGATCCTACA GAAGTGGAGC TGGNATAATC	60
NGNTAGTTAC TGCTACCCAN AGCAATATCT GTGAATGAAG ACAGTGCTAC AGAGGACCTG	120
GCTACACTTA TNNACAGAAA CAAGTGCTAC ACAGCTGTGG ANCCCACTCG NGATATGGTG	180
GTGNAGAACC ANAATGGTGG TAAACAGCCT TTAACCCAG AATGCCTGGC TNATCCTGGA	240
CTGANTTTGA AGTCATTGCT GGAAGTCNTA GCGCTTTTC CTTNGAGAGG	290

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

NGTAGNGGNT CAGACCCAAA GNCTATGAAG TTAATGCTAC TCTGAAGTCT CTCAACA	57
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(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 287 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GGCAGAGGNA GACCCCGGTN TNACGGAGTT AACGTACATG ACCTACGTAA GGGAAGACCT	60
GCGNGTGCTG CAACTGTNAN AAGCGCTGTG GNCNCTGGAA CGTGGTCTTC GTAATCAANA	120
GCTCCAAAAG CATTGGGTAC ACCAACTTNA CACTGGNGAA GAAACTTCGT GAATCAACGT	180
GGTCAACAGG CTGGGTGCCA TCGCTAAAGG ACCCCAAGTC CGNGAACAGG GACGCGTGTG	240
GGCGTGGTGC CAGTACAGCC ACGAGGGCAC CNTTGAGANN CATNCCA	287

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 418 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GGCANAGCAA CCCCATAGGC GGGATCAGCA AGACGGACCT CAGGGCCTTC GTCCAGTTCT	60
GCATCCAGCG CTTCCAGCTT CCTGCCCTGC AAGCATCCTG TTGGCGCCGG CCACCGCAGA	120
AGCTGGTAGC CCTTGGCTGG ATGGACAGGT GTNCCAAACC GACGAGGAAG ATATGGGGAT	180
GACATATGCG GAGTCTTCGG TCTATGGGAA ACTCAGGAAG GTGGCCAAGA TGGGGCCCTA	240
CAGCATGTTA CTGCAAATC CTCGGCATGT GGGAGACACA TCTGNCACCC CGAGACAGGT	300
CGCTGACAAA TGAAGGGGTT TTTTTTCCAA GTACTCCATG AACAGACACA NGATGACCAC	360
G TTCACAACC GNGTTACCAG TCGAGGAACT ACAGCCCTGA GGNCAACAGT TTNATTTG	418

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 191 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GGCAGAGCTG ACTGAGTGGG ATTGAAGGGG AGGTAGGGTG GGTGTGCCCT ATGAATGTAG	60
GGCCTGCTGC ACCCTGGGGA GGGGACCCGG ATGCAGTNNA TGCCCAAGTT CCAGCGTTCA	120
GACTGCCTGG GAAGCCCTGA GAACTCCCTG NACCCAGCAG GACGCCCCAT CCTTGGGTTT	180
NNGGGGGTAG A	191

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 224 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GGCANAGGTA TCATCAAGAG CCACCAGGGC CTGGACCGNC AGTAGCTGAG CTTTGGANCC	60
CGGTCCTTCT ACTACAAGCT GCGTGCCGCT GAAGCAGTAC ACACCCANGG NCAAGTACCA	120



TGGCAACGTG ATGCTACTGC GCGCCAAGAA CGGGTGGCGN CTACGGCAGG GNNCCTGGGC	180
GCGGACTACA ACCTTTNCCA GGTATGCAAC GGGAAAGTAT NCGT	224

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 269 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GGCANAGCGG GATCCCGGGG ACCTCTGGCG ATCCACAGAT GCTGGAGACT TAGATCTACT	60
TGGAAGAACC ACGTTTCTGG CTCTTCTCAG GCACGGGAGA CCTACTAACA GAACGGGACT	120
TGCTCCGGCT CCGGCTCCTG CTCCTGCTTC TTGACCGGCT GTANGATTTG CGACTACGGG	180
AACGGGNATC GGCTACGAGA CCTGAGAGGA ACTTCTGGTC CGGGATCGAG ACCTGNCTTC	240
TTGNACCTAC TGTGNNCTTT TGCTGCCTT	269

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 377 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

CGNGCACAGG ACCAGGNCCT TGGTGAGAAA TTCCCAACCT GGGCNAACAA CCAAACCAGA	60
ATTAGAACTN CTGGGGCACA ACCCGAGGAG AAGANGAATC ACCTCCAGCT TTACGATCGG	120
TTTAAGAGGA CTCATCAATC TTGGCAACAC GTGCTTTATG AACTGCATTG TCCAGGCCCT	180
CACCCACACG NCGNTACTGA GAGATTTCTT TCTCTCTGAC AGGCACCGGT GTGAGATGCC	240
GAGTCCCGAG TTGTTGTCTG GTTCTGTGAG ATGTCGTCGC TGTTTTCGGG GAGTTGTTAT	300
TCTNGGAAAC CCGTNTTCTT GATGTGGCCC TATAAGGTNA CTGGCAACTG GTGGTGGGAT	360
ACANGGCCNG GCATTTT	377

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 354 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GGCANAGGNA AAAAAAGGAA ACACCGCAAA CGGTCCCGGG ATCGAAAGAA AAAGTCTGAT	60
GCCAATGCAA GTTACTTAAG AGCAGCTCGA GCTGGTACAC CTTGAAAAGG CCCTCGACTA	120
CATAAAAAAT GGAGTTGACA TCAACATTTG CAATCAGAAT GGGTTGAACG CTCTCCACCT	180
TGCTTCCAAA GAAGGCCATG TAGAGGTTGT TTCTGAGCTG CTGCAGAGAG AAGCCAATGT	240
GGATGCAGCT ACAAAGAAAG GAAACACAGC ATTGCACATT CGNATCTTTG GCTGGGCAAG	300
CAGAGGTNGG TAAAGTCTTT GNTTACAATG GGGGCCATGT TCATGGANCA TTTN	354

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

AAAGCTGGCA TCCCTNACCT CCTGATCTGA AAAGAAAAGC TTTCAGGNAT TCATCACTAA	60
GCATTTNGTC CACTGTNTGT TTGTCTTAAG ATTGCCTTTA TCAGATTAAG GAATGTNCAT	120
TTNATTCCTA GTTTGCCGAG AATTTTTTATT GTCATAGGAT GTTTAATTTG GCCACATCTT	180
TTTCTGCATC TGTTGGGAGT AATCAAATTA TTTTAGCTTA TAATCNCTTA ATATGGTGGT	240
TTACATNGG TTTTATAAAN GTTAANCCAA ACAGGGTGGT CTGGTATATT GCCANGGTAA	300
	300

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GGCANACCCG GATTGAATAG TNTTAACCAG CTTCCNTGGC TTGCTGAACT GCATGAGGCT	60
CTNACGCACT TGTTAAGCGG CCCCTCCACC AGCACCTTCT GCTCCTNATA GTAGTTCAGC	120
AGGTGGTTCC AAAGCGGCTG CTTTGAATAG TGCCCTTCGG GTTGCCCAACA ATGAATGACG	180
CCATACCTTG CTCTGGTCAG GGCCACGTTN AGACGCCTGG GGTCATTTAA AAAGCCAATG	240

CCTTGGTGCT CGTTGGCCCG NACACAGGGN CAGGNTGNTG AAGTCCTTTT GG

292

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TCTCTCTCCA GTGTAAACTC TTTAATGTCG TGTAAGGCAC GNAAGTCGAC TAAATACCTT	60
GCCACAGTNA CTGCATTGTG AAGGTTTCTC TCCAGTATGT ATTCTCTAAT GTNGTGCAAG	120
GTGTGAATTG TAACTNAAGA CTTTGCCACA TTCATTACAT TTGTNTTNTT TTGTTTGT	180
TTTGTTTTTT NTTTTTTT	197

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GACACGAGCT NGAGCCCACC CTGGAGGGAG GAAGAGGTNG TCACCCCTGA CTTCCAGGAG	60
CCTCNGGTGT CCAGTGGGGT AAGAAGAAAC CCTGNATTTT GGTAGGTAGA AGCANGAGTC	120
TCAACANACC CTNCAGCCCT GACCCCTGGG GGANCCCATG ACTGGACCT	169

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

CTTCCTGCAC AGGAAGGACG TCCTCGGTNN CTCGNAGGAG GAGGNCATGG GGCTCCNNGA	60
GGTCAGCGTT TCGNACATCA AGCCNCCAGC CCCANAGCTG GGCCCCATGC NANANGGCCT	120
NNGCCCTCAG NAGGTGGTCC GGAGGCATAT CCTGGGCTCC ATCGTGCAGA GCGAAGNCAG	180
CTACGTGGAG TCTCTNAAGN GGATACTCCA NGNCTACCGC AACCCCTAA T	231

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

NGTTTGAATT GANCCCTCAC TAAAGGGGCA AAAGCTGGAG CTCGCGCGCC CAGAGCGAAG	60
NTGCGGACCG CGCCGCGACC TTGGNTTGAG CGCATTNGTT TGCTGGAACA CGCCAACCGT	120
CAGGCGAGTA ACCTGGCCTA TGGTGACCAG CGCCGTCTTG AGATTGCCCC CTGCATGGTG	180
ACGCAGCCGG AGATTTTAAT GCTCGACGAA CCTGCGGCAG GTCTTAACCC GAAAGAGACG	240
AAAGAGCTGG ATGAGCTGAT TGCCGAAC TN CGCAATCATC ACAACACCAC TATCTTGTTG	300
ATTGAACACG ATATGAAGCT GGTGATNGGA ATTTCGGACC GAATTTACGT GGTCAATCAG	360
GGNACGCCGC TGGCAAACGG TACGCCGGAG CAGATCCGTG AATAACCCGG ACGTGATCCG	420
TGCCTATTTA GGTGAGGCAT TAANATGNGA AAAANTNCAT GTTTGTCCTT TGGACAAAGT	480
CAGGCGTCCA CTTANGGTAN ANTNCCAAGG CGGTTGCATG AGGGTGAGCC TTCATATTCA	540
ATTCAGGGGC GNGATTTT	558

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GGCACGAGGG AGCNCAAGCA GGATTCTTCC CGAGTCCCTG GCATCCTCAG AAGCTTCAAC	60
TCTGGAGGCA ATGGGTCGAA AGGGAGAAGA TGACTGCAGT NCCTGGAAGA AACAGACCAC	120
CAACATCCGG AAAACCTTCA TTTTATGGA AGTNCTGGGA TCAGGAGCTT TCTCAGAAGT	180
TTTCTGGTG AAGCAAAGAC TGACTGGGAA GCTCTTTGCT CTGAAGTGCA TCAAGAAGTC	240
ACCTGCCTTC CGGGACAGCA GCCTGGAGAA TGAGAATTNC TGTGTTGAAA AAGTTTCAAG	300
CATGAAAACA TTGTGAACCC TGGGAGGACA TCTNTGAGAA GCACCACCCA CTAATAACCT	360
GGTTCATTNC AGCTTGTTNT CTGNGTGGGG NAGCTCTTTG AACCGNNTTC CTGGGAGCGG	420
GGTGTCTNCA CAGAGNAAGG ATTCCCAGTT TTTGTCANTN CCAGTAGGTT TTTGTCGGGC	480

AGTGNAATA CCTACATGGG GGATTGGGAT GTCC

514

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

AGCAGGTATG GTGTTCCAGC AGTTTTACCT CTNCCCGCAT CTGNACAGCG CTGGNAAAAC	60
GTCATGTTTG GNCCGCTACG GTGTCGTNGC GCGAACAAAG AAGAGGCGGA AAAACTGGCA	120
CGTGAGCTGC TGGCGAAAGT CGGTCTNGCA GAACGTGCAC ATCACTACCC NTCCGAACCT	180
TCTGGTGGTC AACAGNAACG TGTGGCGATT NNCCGCGCGC TGGA	224

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GGAACAAAAG CNTNAGCTCG TGCCGCCGGC AGGTGCACAC TAGTGGATCC AAAGAATTCC	60
NGCANAGTCA CAGCTGATTC CTGGGNAGAG GCTGAGAGGC ACTCCTGGNA TCTCTGGAGA	120
GNGGCGTCTC CCAGCTGT	138

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GCTGTAGNTN GTCAGANAGG TAGCGAGGAA CAAGAAGCGA AATTAGTTGC CGTTCATTTA	60
ATCGCGGCAA ACCTGGCAGN GCATGNTTCA CATGGTATTT GGANCATCCC AAGNTATGTA	120
CGN	123

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GNGTAGCNNG GAAGNCACAG CGCATCTCCC CGCTGTAGGN TTCCTCCCAC AGAACCCGTT	60
TCGGACCTTC AAAGCGTCTG GTGGAGATGC TGTGCCGCT GCTGCTGCTG CTAACCCATG	120
TGCCTGGGCC GTTNAGNTC AAGAAGGCC CNGGGCGTNN TCCCT	165

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

AACCCTNCAC TGAAAGGGCA NCAAAAGCTG GGGCNCGGGC GCNCTGCAGG TTCGTACACT	60
AGTGGATCCA AAGAATTCGG CACAGTTGTG GTTTNTCTCA NCGCCTNGGT AGCCGGTAAC	120
AAACGNGGGT TCCCNNGAT TGGACCGACG CAGCCANGCC NCTGTGGACT TGTTATCAAA	180
AGAAAGCTAA CTGCTAGATC TTTATCGAGT TAAGAGTGTG GATCTGCATC CTACAGAGCC	240
ATGGGATGTT GGCAAGTCTT NNACANNGGN	270

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

AGCCCNNGGA TGTGCCACTG AGCCTCGGCC CCATCGTGGG GAGCTNTNCC CATCCNGCCT	60
GTAACCCACC TCTGGNCCCC ATCCATAGAT GATAGGGACC TCTCAACTNT AGG	113

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

TGNCTTNGGC TTTGTCCAGC ATNAAAAGGC AGAGCGAACG TTTTCACTGC AGGCTGTTTC	60
CCNCCAGGGC AAGTGGGACA GGGCGAGTNC TGACGTCTGC AGGCATGGTG TGCATTTAGG	120
GGTGGGCGGC ACCGAGGGGG CATCATTTGG CATAGGCGGG CCCGGGGGTC ACTGGGCTAG	180
ATGACTGGCT GGTGCTGGG GGCAGGTGTC ACAGCCTTTG CTGNGCACCC TTTAAGTNGA	240
GGACAGAACA TTGTTGGGAG GAGTCCAGGC ATAAAGTNAC ATAAACAGCG NCGGNGAATG	300
GGACCAGCGC ACCTTNAGAG GTGGATTCAT TAGCCTTNAG TCAACTGGGG T	351

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 247 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GTGGNACACT TTCCACGGCC TCTTCAAGTC CACGCTGGTN TGCCCCGATT GTGGCAATGT	60
ATCTNTNACC TTCGACCCCT TCTGCTACCT CAGTGTTCCA CTGNCTATNA GCCACAAGAG	120
GGNCTTGGAG GTCTTCTTTA TCCCCATGGA TCCGNGNCGC AAGNCAGAGC AGCACTGGGT	180
CGTGGTTCCC CAAGAAAGGC AAGATCTTCG GGTCTAATGT GTGGCTCTGN ACAAACACAC	240
GGGGNAT	247

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 254 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

AGGCAGGTGT CCAAATGGGC AATNCCTGCT GGGAAGCNCT ATTGNTTGGG AACATGGGTT	60
TNACCCTGNT GGGCAGATGC CAGTGAACAA GACCATTGGT GGAGGGGACG ACTCCTTCAC	120
CACCTTCTTC CTGTNAAANT GGTGCTGGAA AANACGTACC CCGGGCAGTT TTTGTGAGNT	180
CTGGAGCCTA CGGTCATTGA ATGAGAATCC GAAATGNGCC CANACCGACA GTCCTTNCCA	240

NCCAGAGCAG CTCC

254

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GGCACGAGGT GCGTGATGN CTCCCGGGGC CACGGTGGGG TGAAGGATGG CGAGCCGGAC	60
ATACCATTNT TGGATGTATT TTTTTTAAAA CAGCAATAAT TAGCCATTTT AAAGGAGGGA	120
TGTACCTGTN TGTGTNCATG TCCACGTNTT TGAGCGTGTG TNTGTGTGTN CAAGTGGGTT	180
CTTGATATG TGTAGTGTGA GCATGTGTGC ATGTNTGAGC CTGTGCACGT GCATGTTGTA	240
GGTGCATAAG CATGTACACG CGTGACATGC ATGTCCGTGT ACACGTNTAT AGGTGTACAT	300
GTNCATGAGT TGTGTACATG CGTGACACGT GTATAGGATG TACGTGTGTN TNCGCATGTG	360
TGCGNGTAAC ATGTNTTTGT GNTCTTGGGG TATGCATAAG CCATACACGT G	411

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GGGCACGNGC AGAAGTCAAG GTCANTTAAA TGAAAAGCCC TTACCTGAAG GTTGGGAAAT	60
GAGATTCACA GTGGATGGAA TTCCATATTT TGTGGNCCAC AATAGAAGAA CTACCACCTA	120
TATAGATCCC CGNACAGGAA AATCTGCCCT AGNCAATGGA CCTCAGATAG CCTATGTTTCG	180
GGACTTCAAN GCAAAGGTTT AGTATTTCCG GTTCTGGTGT CAGCAACTGG CCATNCCACA	240
GCACATTNAN GATTACAGTG NCAAGAAAAA CATTGTTT	278

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

TGGGGCAGGA CCAAAGGCAA GATCCATGCC AACGCTGCTG ACCAACCCCC AAAACCAAGC	60
TGGCTTTGGG TCTGTGTCTG GTGCCACTGG GCAATGTGGC CTAGATGGAA GGGTGAAGGG	120
GTCCCACTCT CAGTGTTCCT CCTGTGTTCT TCCTCCTTCC ATCTTATCTC TATCTCTGGG	180
CTGGTTTGTN AGCTGAAAGA GTTCACACAT ACCTGGGGTG GGCCTCTGTC TCCTCGACAG	240
AGTGGGACTG AGGAGCGAGG CCTGAAGCAT TACTGGTTCA CATCCTGGCC CGGACCAGAA	300
GACCCAGAC CGGGCCCCC CACTCCTGTA CCTGGTGCGG GAGGTTNGAG GAGGCAGCCC	360
AGCAGGAGGG GNCCCACTNT TGCCCCATT CATCGTCCAC TGGCAGGTGG GGTNCTCCCA	420
GCCAGCCATG GN	432

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

TTGNCAGGTN CGACACTAGT GGATCCAAAG AATTCGGCAN AGCTGATNTG ATGCGTCACA	60
TGNTTATGGC CAACCCCCAG ATGCAGCAGT TGATGGAGCG GAACCCGTNG ATCAGCCACA	120
TGNTCAATAA CCCTGAACTC ATGAGGCAGA CAATGGAGCT TGCTCGGGAA TCCAGCCATG	180
GATGCAAGAG AATGNTGCGG AACCAGGACC GGGNCCTGAG CAACCTTNTN GAGCATCGCT	240
GGGGGGTATA ATGCCCTCNG CCGTATGTAC ACGGGACATN CAGGAGCCCA TGTTTCAGTG	300
CTGCCCCGGG AACAGTTTTG GCAACANTCC NTNCT	335

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

ACCTTCTTTA AATCCGTCAA TAGCCTGCCA GCCAGTAAGC TGTGCCAGTT TGTCAACAAT	60
CGCAGGCCGG GTACNGGNTG NATATAGACG ATTTTTTTTC CCGGCGTGGC TTTCAGCTCA	120
AGCGGGGCCG CCCCAGCCAC CCGTTCCTTC CTCATATCGA CTTTACCTAC ATTACCACTA	180

TTTCAATGCT GGTTTTCGCG GTTGGCGGAG CAGNAGNAAG ATTTCTCCTT ACGTTAATCA	240
AACGCGCAAC CCAGGAAAAG AATTTCCAAA AGGGATGTTA TGCCTGGCGG TGGATGGTTG	300
CGGTTTGTGN CCATTCTGGG CTCGCTGGCG ATGGGGGATG GATGTTTTGA TTCGNGTAAT	360
ATCCCGGATG GACTTTAATG GACCCAAGGT CANTTATTTA CGGCCTTTCC ANAAGTTNGG	420
GNNG	424

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 351 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

NNNAGNGCCT NCAGGTCGAC ACTAGTGGAT CCAAAGAATT CGGCAGAGAA AAAAACAAAG	60
CCATTGACAA GTTACAGATT TCCAGGAAGA AGGCAAAAGA AAAAGGAGCT TAGACAGGGA	120
AGGAAGAGTC CCCTCTATCC TTAAGTTCTC CCATGTCCGT TGTAAGAGGG CTCCACAGCT	180
CCACAGAAGA AGAGGGNAGG AAGGACAAGC GCTGGTCAAG GTTATGCAAT CCCAACCTGC	240
CATCTTCACT GCACCATTAA GCTGGNTATT CTGAAATATG CTTCTTTCTC GACTTTCCGG	300
CANATTTTAA ATTNAACATT AGAATCCAAC CGGTCGACCT GNTNGTCATT G	351

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 518 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GGCACGAGGA ACTGTGGATC TCCTACAATT TTATTGAGAA GTTGAAAGGG ATCCACATAA	60
TGAAGAAATT GAAGATTCTC TACATGTCTA ATAACCTGGT AAAAGACTGG GCTGAGTTTG	120
TGAAGCTGGC AGAACTGNCA TGCCTCGAAG ACCTGGTGTT TGTAGGCAAT CCCTTGAAG	180
AGAAACATTC TGCTGAGAAT AACTGGATTG AAGAAGCAAC CAAGAGAGTG CCCAACTGA	240
AAAAGCTGGA TGGTACTCCA GTAATTAAAG GGGATGAGGA AGAAGACAAC TAATGCCACG	300
CTTTCCACTG TGTGTAACT TATTTGAAAT GTCCNTAGGA NCATTAGATA ATTTTATGTG	360
ATTGTNNNTT TTAAGATTCT GTATGGGGCA AAGTTTCNTA AGTTAAACCG TTCANNCNTC	420

NCCANCTTTT TTTTCCCTTA ACCTATTCCG TGNTTTNCCC CCAAACCTGGT ANGGCCANCC 480  
TNTATATCCC TTCCCNTTT TAGGAACCCN CAATTTTC 518

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

CCGNNAGNGN CTNCAGGTCG ACAGCGCTTC CTGTCCACGA ATCATATCCG CTATTTTCTC 60  
GCCAATCATA ATTGTCTGG CGTTCAAATT CCCGGTGATA ATCTGCGGCT TAATCGACGC 120  
ATCCACCACA CGCATGCCTT CTAACCCGTG TACGCGGCCT TCGCCGTCAA CCACGGACAT 180  
CTCGTCGTAA CCCATTTTGC AGGTACCGCA CGGATGGGAA GGCGGTTTCG GCGTGGTTAC 240  
GCACGAACTC ATCGAGCTGT TCATCCGTCT GGCATTCGAC ACCGGGGCTG ATTTGCGGGC 300  
AACGATACTN ATCCAGCGCG GGTGATGCA TGATNTCGCG GGTGATGCGA ATTGCGTCGC 360  
GGGAACCTCT GCCAGTGCCT GCTCGTGCGA CATGTGNTTG AAACAGAATN CGCCGGATGG 420  
TAGTGCGGGT AGCGGGGTTT NATGCCGNAC NGG 453

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

AGGGCNAGCT NACTGANGC TACCAGGAGA TCTCCANGCG AAACCTCAGCC TCCTCCCAAG 60  
CTCCCTNTGG GATCCTAGCC ACAAGCTCTC CAACAATTAC TATTGCACTC GAGAATGGCC 120  
GCCGGGGAAT CTNAGCCCN TTGCCATCAT GCATNTGCGT TCNACAGAAG NNGCTGGTGT 180  
GCAGGCAAGA CAGCAGAGAG CTCTGCTGTG AGCTGACCAC TGAGCNGGNA GGCGNTGCNT 240  
CCANNTTCTT NTATTAAAGA GNTTGGGGCT TNNCTTCGGG CCACCTTTAN CTGTTTACAC 300  
TGCAANCTTN AGGGNCACCG GATGANTTNG CCNCCTTTGG GATTTTCNAC CAGGGGGGTT 360  
TTGGACNCAN TTTTNTGGNC AACTAGGGGG GNTTGGGTTT CNNTTGGGTT TTTTTTGN 420  
AATTAAAAAN AAGGGGGNGT TTTTAAAAAA AAA 453

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 548 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

TTTTTNCGC GGNCGGTGGC GCGGCAACCG CCAGANGATC CAGAAGAAAA GCAGATNGTT	60
GGCGAAGATG GAAATCGCCA GGCCAATCAN TCGCCACGTC GGTTCAGCC ACTCANTGCT	120
GTTCAGGTGC AGGGCGCTAA TAATCATTTG CTGCGCCGAA CCGGCAACCG AGGTGATCGA	180
AAGCTTCACA ATCAGCGCAA TCAACAAACC AATCAGCGAA ATAAAATCTC GCAGATATTT	240
TACCCAGAAC TTCTCCTGAT CTTGCGGCGA GCNTTCCCAG ACATCGCGCG NACTGGGCCA	300
CGATTCTGTTT CACGCAGGTT AACCCATCCA NTTGATGCCG GNANTAAAGT GCCACCGCCA	360
GTCCGACAAG CCCTACAGTC GTTACGCTGC TGGNACGGTG GTGTTGNNGG TGTTTTNC	420
ACGTGGTGGC TNNCGTTGGG TNCNTGNNGT TTTTGCAGAA TTTTTCGNA GATTNTCCNG	480
TAGGCAACAT GGNTGGGGAG GNCCAGCAAC AAGGCCCCNG NGGGCAAANG ACANCNTCAA	540
AATGGTNT	548

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

CCATCAGAGA GGCTGGCTCC AGCATCTTAC GCATGTCCAC ATTGTGGTCA GTTTGCAAGA	60
AGTCACCCGT GATATGTGGC AAAACAGCCG GACTCCCGAC ATAAAGTGCT GGAAGGAAGA	120
CTGTGAGGGA CACAGTTGTA AAGGTTCTCG AATTGTATCT GTCTGATCAG AGAAACAATT	180
TAATGTCCCA GATCAAAGTC GAGAGGCAGG CTCTGGGAAC TGGGCTGTGA GCAGCCAGAG	240
AAAGGCGGCA GAACCAGTTT CTTCAGGGCA GGTCTCTTTT ATCTGCTTGT CTGGATTGCC	300
TAGTGGACAC TCCATTGGCT CCCAGAGGCC TTCCTGGTNC ATNTCNTCCC TCTGGCTGGG	360
TCCTTGATCT TTGCAGATGG CTGCGTCCCT GGGGCCAGGA GCACCAATGT GTGCCGNTGC	420
TGGNCAGGTA NGGNGGTATN CNAGGTNATG TTNTTCCAGG TTCACCNGTG CTTGGTGTG	480

CGGTTTATTG AGTGAANTCN GT

502

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GGCAGGAGCC AAACACTCCA GAGACCGACG AGTCCCTGNT CGACCCCAAC ATCTTGCTCTC	60
TCAACATCCT CTCTTCCGGA TACATCCACC CAGCCCAAGA TGACCGGACC TTTTACCAAT	120
TTGAGGCTGC GTGGGACAGC TCCATGCACA ACTCTCTCCT GCTGAACCGG GTCACCCCTT	180
ATCGAGAGAA AATCTACATG AACACTCTCC GCTTATTATC GAGATGGAGA ACTGCACCCA	240
GCCGGCTGTT GTCACCAAGG AACTTCTGGC ATGGTCTTCT ATTCCCGTGA ATGCCAAGCT	300
GGCCAGCCTN CGNGGCTNCC ATNCCGCAAC CTNTTTTTGGN CAGTGGGGAG GCCTTTCGGG	360
CCTNCAGAGA GTGAACCTGT GNANTGGTGT GTTANNAGNT TCAGCNTGTG GCCACGTGGC	420
TGANGCGGGN CAGCCCAGGG NTGCAGCGNC GGNGCCGNAG NGTTCNGGGA CACATTGTGG	480
GCTNTGTTCC GGGCGAGGAG AACTGGCAGN TG	512

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GGCANGAGCG AAATACACAG AAATGGACTA CGCCCACCT GGTAACAAAG CAGCTTTCAC	60
TGTAAGCCTG GATCCAGGGC CCCTGGAGCA GTTCCCNCAN TCCATGGAGC CACAGCTCAG	120
GCAGCTGGGC CTGCCCACCG CCCTCAAGAG AGGTGTGGTG ACTCTGCCTG TCTGACTACG	180
AAGGTGTGCA AGNGGGCGA TGTGCTGACC CCAGAGCAGG CTCGNNTCCT GAAGCTTTTT	240
GGGTATGAGA ATGGCTGAAT TCAAGGTGAC CATCAAATAC ATGTGGGATT CACAGTTCGG	300
GAAGGTTTCC AGCAGATGGG NAGACGGATT TGNCCAAAGA AGCGCATTTT AAGTTCCACA	360
GAAGNGTTCA GATTCCAGAA GGTTGNNTGA TTGAAAAGGG NNTTCGGGAC TTAAGGTNTT	420
CCTGGGAAGT TTTTGGGTTT TCATTGGGCC CTTCAGGATT TTTTCCGCC CTTTGGNGAG	480

GGCAGTTTTT TATTTNTTCT TAGNAA

506

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GGTCAACATG GNGCCCGACC AGTACCANAT GGGGAGCACC AAGGTNTTTT TCAAGAACCC	60
ANAGTCGCTT TTTCTCCTG GTAGGTAGNT GCGAGAAGCA AAAAGTTCCG ATGGGTTTTT	120
GCCCGTAAAC CCATNCCCAG GAAGGTTCTN GTCGTGCGGN CACGTTGGGT CTGTTNCC	178

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

CGGTGACCAT GTNTGGCCTG GGNTGTAAGA AGTACGTGGN GGCCAACATC TCCCATAAGT	60
AACGCACAAC TGTNAAATAT ACAATNAAGA CTCTAGCCAG CTGTNCTGAG ACCGTAATCT	120
TNATGCTGCT TGGNATCTNA GCCGTGGACT CTTCTAAGTG GGCCTGGGNT TCTGGGCTGG	180
TGCTGGGCAC CCTCATCTTC ATCCTGTNCT TCCGAGCCCT CGGTATTGCT GGCACCCTCT	240
GCTTTCCAC TCTNCCTTCC TGTCCCGCCC CTCCCTGCAG CTCATCTCCC TATGTGAAGT	300
CCACATCTTT GTNAATTCCT AAAGCCTCCT CTTGTTGCTC ACCTGTCCCA GCCCTGTAAA	360
GACCTCAGCC CAGATAATTG GGTCCCATCG GGTCCCAAGT CCTTCAA	407

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

GGCAGAGCTT NGTGGGAGCC TCGAGCCTTC ATCATGCAGT GTATTTNTTT CTGTNGTAAT	60
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CCAGCTGATC CATTGATCAG TGGGGTTGGG GACGCTTCTN TNCTGCTCAT TTATTGCTGT	120
GTACAAACCA CCTCTAAGTG AAGGGCTTTA AAACAAGATC GTTCATTTCT TTTGCACATG	180
GGCATTGGGG TANCTGGGCG CACTACGGCA CTTCTTACCT GGGGCCTCAT CAGTNNAGAT	240
GGGGCCAGGT TGGGTTAGCC CCAAGGCTTC TGGCATTGGN CTAAGAAGGC CTTCAGAACA	300
ATGAGGGCTT TGGGCGGCTG GGGGCTCCCC ACCAACAACC CTTNCACCTT CGTGGGGCCT	360
TCCAGGTTAG CCTGTTCCAC CTGNCNCAGA ACACACACAN CCAGTCCCAC AGGTTCANCC	420
CTT	423

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GGCAGAGGNC AAGATGGCCA CTGTNATCCC TGNCCCCCTG AGCCTAGGCG AGGANTTCTA	60
CCGCGAGCCA TCGAGCACTG CCGCAGTTAC AACGNCGGCC TGTNNCGTAG CGCAGCCTGN	120
NAACTGCCCT TCCTCGACTC GCAGACCGGC GTGGCCCAGA ACAACTGCTA CATCTGGATG	180
GAGAAGACCC ACCGCGGGCC GGGTTTNGCC CCGGNACAG ATTTACACGT ACCCCGCCCCG	240
CTGTTGGAGG AAGAAACGGA GNCTCAACAT CCTGGAGGAC CCCAGACTTC AGGCCCTGCG	300
AAGTTACAAG ATCGACTGTG AAAGCACCCC TGGAAGAAGG AGGGTNGCCT TCCGGNAAGG	360
GCCGGTTNCT TCGAGGGTTT TATTGTTNTG CCANAGTACG GGGGGAGAAA GAAAGGTTT	419

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

AGTGGTATCC AAAGAATTNG GCANAGGNCG GAAGATCTNA AGACACAAAG GCCCAGTCCT	60
ATGGGAGAGG GAGCTGCAGG GNGCGGGAGC TGGGACATCC CANGGNTCAT GAAGTGGGGG	120
NGCAGCCCCC ACGCCTGGNA AGCTGAGGGA AGGGCTCATC TCCCCTNTAT GGGGGGNCAG	180
GAAGGGANTA CCTGNCCCT GACTTNGTTG GGATTGGGAA CTNAACCCTG GGNGGCCCT	240

CTGAGAGCCC ACCAGCCACA GGNCANTGAA TGCCAACAAA GAGCCCGTTG CTGGAAAGGT 300  
CTGTAGCCTG NGA CTCAGTG GNGCTGCCTC CTGN 334

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 385 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

GGCANAGGGN GAGGGCAGAG GAGGAGAGTC GCGGGCGGCC GCTTGGGCGC ACTTNCCGGG 60  
TCACCTTGTC CCGGAGGAGN AAATGGCTTC CCTGAGGCAA GTGTACCTAC ATTCCCAGCC 120  
CACCAGCCTG ACGCCCAGCC AGGGAAGAGA GTACCATGGA TGGCATCATT GGAACAGAAG 180  
AGCATGCTGG TGCACAGTGA AAATCAGTGA TGCTGGCAAG AGGAATGGTT TAATTGAACA 240  
CCAGAACTT GATGGCCGAG AGCAGAGATG GTCTGGTGTC TGTTTACCCA GCGCCCCAGT 300  
ACCAGAGCCA CCGGGTNGGG GGCCAGCACA GTGNCGGNCA GTCTGGNACA GCAGCAGGAG 360  
TTAAGCCNTT TGTCAGCAGT TGGTT 385

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 317 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

TGGCINNAGGA CCAGCCATCG GAGGTGACTG ANAGATATAA TTTGGGACAG GTCATCAAGA 60  
CTGAGGAGTT TTGTAAATC TTCCGGGCCA AGGACAAGAC GACAGGCAAG CTGCACACCT 120  
NCAAGAAGTT CCAGAAGCGG GACGGCCGCA AGTGTCGGAA AGCTGCCAAG AACGAGATTA 180  
GGTATCCTCA AGATGGTGAA GCATCCCAAC ATCCTACAGC TGGTGGATGT NTTTTNTGAAC 240  
CCGCAAGAGT TACTTTAATN CTTCTGGGA GCTGGCCACG GGGAGGGAGG TGTTTNACTG 300  
GNATCCTGGG ACCAGGG 317

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 383 base pairs  
(B) TYPE: nucleic acid



- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

GCGCCTGCAG GTCGACACTA GTGGATCCAA AGAATTCTGC ACNAGGTNTT NTTGGTGTG	60
GGNNGCTGGT CTGGGGACAG GTCATTGCCA CCATCCCCAC CAGCCAGCTC AAGTGCCTGT	120
NGGAAGCCGG GCACGGGCCN GGNAAGGGAC GAGATGACCG ACGTAGGGAG CTGGCCGAAG	180
GAGGTAAGAG AATCGACCAT GTCGAGCGGG AACTCCGCAG GGGNCCCAGA TCCTCTGGTT	240
CCGGGGCCTG AACCGNATTC AAACGCAGCC TGGGCCTCTN CCCACCACTT CCCAGAAAC	300
GGCGCTCGTC TNAGGNCCTG GGAAGGCTGC CTTTCCGGTT CGTGGGGGTA CGGGGNTGTT	360
CCCGCAATG GGTTCCTGG TCT	383

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 234 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

ACCTGCGCGG GGNCATCCCG AATNCNTTTN AGCACATCTN CACCCACATC TCCCGCTCCC	60
AGAACCAACA GTACCTGGTC CGGGCCTCCT ATTTGGAGAT CTACCAGGAA GAGATTCGAG	120
AACCTNCNCT CCAAGGAGCC GGGNCAAGAG NGCTAGAGCT GGAANGAGAA ACCCCGAGAA	180
CTGGCGTCTT ACATGCAAGG GACCTCTTCC TGCCTTGTT CACCAAGNAA TGNG	234

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 265 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GAACATGNCG AGGCCATCGT AAGCNGGAAG CAGGAGGTGC TGCAGGNTTG GAAANAGCTG	60
CTGTAACTTG TNAAGGTTGC CCGCTTGCTT GTTAAGCTCC ACAGCCGNCG CCCTGGCCTT	120
CCACAGCCAA GTCCGCGAAC CTGNTCTCCT GGTGTTGGT CATCGCCGCN AGANTTGGGG	180
CAGCCGNCAA GCCCAGGTGC CCCTNAATCC CTCCTGGGGC TTCCNGCCTC CCCCTGGTGG	240

GCCTACCCCT GGCAACCCCC AGCCC

265

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

CTGCTGTNCG AGGCCGGNCC CCGGTGGGCT GNNAACGCTG GGACCTGCAG AAGCACTCTT	60
TCCTAATTNT AATCGGCGAT ATCGGTACAG AGAGTCANCT GNNGGCCGTG CGGGCCAACC	120
TTAAACAAGG GAATTCTTTC CTGGTAACAT TGACCTGTNA TCCTTTGANT TGAACCAACA	180
GTTGAAACTC TTCATTACCC GGCACCTAGC TCACTTCTCC TCAAAGGTCA AAGGCCAGAG	240
GACCCTTTGC CACCAGAGTG AAGATCCTAG AGACCATCAT CCTGGTAAAT CCCAGTGNCA	300
GACAGCATCA GCTCTGAGGT TTCATCATCT TCTTTAGGCA GTTCNTCAGT TTATAAACTA	360
TTATTTTGAA TGGGGCAAAG TTTTNGGAGC CTNGGGGGGN GACCTNAT	408

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GGCGCNCCTGC GGGAGNNGGG CTTCCCGTAC ATNACGCCGG TGCAGTCCGC AACCATCCCT	60
CTNTTCATGC GAAACAAAGA TGTCGCTGCA GAAGCGGTCA CAGGTAGTGG NAAAACTC	120
GCTTTTNTNA TCCCCATCCT GGAAATTNTT CTNAGAAGAG AAGAGAAGTT AAAAAAGAGT	180
CAGGTTGGAG CCATAATCAT CACCCCCACT CGAGAGCTGG CCATTCAAAT AGACGAGGTC	240
CTGTGCATT TNACGGAAGC ACTTCCCCGA GTTCAGGTGG AATTGGATGC AGTGTCCCTG	300
TTAAGTTCAT GGGGCTGTTT TNTCGAACTT NAATCAAAGG CTGTTTTTCT TGTGTAGNC	360
CAGTTTCTTT TTGGATTCCG AGGCAGGAAT TCTGGAGGAA NTTTTTGAGA GGTTTAAGGC	420
AANAAGGTNG GGGACCATCA TNTTGGGCCA TTCCAAGGCC GTTTTGGNGG ACATTTT	477

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

GCCAGCACCC GAACATNATC ACCCTCAAGG ATGTCTATAN TGGTGGCAGG TTTGTGTACC	60
TGGTAATNGA GCTGNATGCN TGGTGGGGAA GCTCCTGGAC CGCATCCTCC GGCAGAGATC	120
ACTTCTCGGA GCGGCCN	137

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

GGCAGAGCAG ACTGTCCCCG TGTTGTCTGA GGCAGACCCC TCAGGTTGGT GAGCAGGGTG	60
CTNTGTGGCC GAGGGCTGGG TGGGCTGGCC TTTGCAGTCA TCTCACCATC TTCACGAGCT	120
TNTNTCTCTT CAGTCACGCC GATGATGGAG CTGAAGCCCA ACGCAGTNAG CNACCGTGCG	180
CTGGGTCTGG NAACACCCAC GCTGGACTTC GGCCGACGAG TGCCCCAAGC CAGAGCTGCT	240
GGCCATCCGT TTTCTNGAA TGCTGAGAAG TGAAGCCAAG GCCCTGGGNG ACCTGGCCTT	300
GACTTNGGGG NTTACCTGN	320

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

GGCAGAGGTT GGTCTTTGCC ATGTCCTTTG TCCCGNCAG NTTCACTCTT GTCCTCATTG	60
AGGAGCGAGT CACCCGAGCC AAGCACCTGC AGCTCATGGG GGGCCTGTCC CCACCCTCTA	120
CTGGCTTGGC AACTTTNTCT GGGAACATGG TCGGGGGGCT GCTTGGACGG GTGGGGGCCC	180
AGCCACTGCT TGCCACTGCC CTGTNTGGNC CCTTGTNAGN CAGGGGCTTG TCCAAGATGG	240
CCTGGGTAAA GTTTTGAGGG ATTGTGGGAG ACTTTNTGGC CTTCTAATT CAAAAAGCAA	300

GGNGGTTCAA GGTGGGAACA GGGCTNAGGG TGGGCAGTGC CCAACTNNTT TTAGGGTTGA 360  
TAAAAGGT 368

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 122 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

GAGGGCCATT CAGTGNATGG GGAAAGGTGA ACATNCCATC GTGTACCTCA AGCCCAGCTA 60  
TGGTTTTTGG TAAGTNTTGG GGANGGAAAA NTTCCAAATC CCACCAAATG CTGGAGCTGG 120  
NA 122

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 200 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

CTCAAACCTCG CCTGGNAGCA CCCATCATCC CCNTGCCGGT CCTNACCTCT NCCTGGAGCN 60  
GTCCCCCGGC TTCCTTCCCC ATCCAAGGAG GAGGAGGGAC TAAGGGCTCA GGTGCGGGAC 120  
CTNGAGGAGA AACTAGAGAC CCTGAGCACT TNAACGGGCA GNAGACAANG CAAAGTTAAA 180  
AGAAGCTGGA GAAACANAAA 200

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 338 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

TGTGCTACAT CACCTACGTN AGCAATCAGA CCTACCAGGA GCGGACCTAT AAGCAGCTNC 60  
TCCAGGAGAA GGCAGCTTTC CGGGAAGCTG ATCGCNCATA GGAGCTCGAC CCCAAGTGCA 120  
GGGGGCTGCC CTTCTCCTCC TTCCTCATCC TGCCTTTCCA GAGGATCACA CGCCTCAAGC 180

TGTTGGTCCA GAACATCCTG AAGAGGGTAG AAGAAAGGTC TAAGCGGGAG TNCAGTGT	240
TTT TGGAAATGCTC ANAAGGGNGC TGGAAAATGG TGGTAAAGGC ATGNAACGAG GGC	300
CGTTTCAGG NAAAATGAGC CGCACGGAAC AGATGATCAG CNTTTCAG	338

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 108 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

ATGCGCTNCT GGTGTTCTNA GTGGCCAAAG TCTNTGCCCA GCCCAACNTG GCTGAAATGA	60
TTCAAAAAGG TGAGCAGNTA TTCCTGGTAG CCAGAGCTGT GTTCATNG	108

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 142 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

AAGCCCACAT NGCCACCCCG GAGCAGCTCT ATCCNGNCTA CNTTGGGGGC TATAAGCAAT	60
GTAATGCTGG CTGGNTTGG GATCAAACCG TAAGTTATCC CATCCAGACC CCACGAAAGG	120
CCTNNAACGG GGACATNGNT GG	142

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 147 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

AATNCANTCT TAAGGCCAG GGGAACACAA TGAAGTATGN ATTGACTGAA TGCAGAACCT	60
GGTTGTGGNA GAGCNAGCTG AATGTTTGGC CCAGAAGAAG CCTGTTCTGT TTTGGGAGCA	120
GTNANAACCA GNATATGACG TGAGAAA	147

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 295 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GGCAGAGNCT GCAGTTTGCA GNGCCCGGAT AACCGAGGCA GTGGCCCCTC CCGCGTCCCC	60
AGGTTTCAAG GACGCTAGGN CTCTCCGCGG CCCTGAGGCT TCGCACTGGG GAGTGGGGCC	120
GCCAGATGGG ACGTGTTTCAT GAAGGGCCTG TCCATGGCCA AGGAGGGCGT TGTGGCANCC	180
GCGGAGAAAA CCAAGCAGGG GGTCAACGAN GCGGCGGAG AAGNCCAAGG AGGGCGTCCT	240
CTACGTCGGA AGCAAGACCC CNGAAGGTGT TGTACAANGT NTTGGCTTTC AATGG	295

(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 331 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

NANGNGCTCT GCCAGGTNCG NACACTAGTG GATCCAAAGT AATTCGGCAG AGGATGGAGC	60
GGCAGGTCCT CCCAGACCCC GAGGTGCTGG AAGTGTGGGG GACAGGCAGG ATGGGCTAAG	120
GGAACAGCTG CAGGCCCCAG TGCCTCCTGA CAGTNTCCCC AGCCTGCAAA ANATGGGTCT	180
TCTGCTGGAC AAGCTGGCCA AGGAGAACCA GGACATCCGG NTGCTGCAGG CCCAGCTGCA	240
NGCCCCAAAG GGAAGAGCTT CANAGCCTNA TGCACCAGCC CAAAGGTTAG GAGGGAGGAG	300
AATGCCCAGC TNCGGGGGGG GTTCTGNAGC A	331

(2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GAGGCGCTGC GTCTTTCCAG CGTTTCGCAT CCGGAATACA TTGGACGCGT CGGAAGTTCT	60
TTAGCGATAT CGGCGGGCGG GCGCTACTAA TGCATGGTAC TGAAGGTGAA GTGTATGCTA	120

ATCCGCAGCG CTGCCCCGAG ATCAATCTCA TTGACCGTGA AAGGGATGCG GGTGCTGTAT	180
GAAAAACAGG ACACTGCTGG TAGCGAGTTA CTGCCACAAG CAAAAGATCC GGAAACCACG	240
GCGCATGGGT TGAGCCGTTG CCTTGCTGGG AGCGGAACCG ATTCCCGAAT CGCTGAAAAT	300
CCAGATGGNT TNCTNGCCTG GTGGTTACGG GTTAAGCGGG CAACTTTTCA GCGACGGNCT	360
TGGGGGCGTT TAATCCGGGC ATTNAATTC CTTTTCTCTA	400

(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 417 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

GGCAGAGCCC CACCGTGTTT AAAAATACTACA CTGCAAGCTT TNAATTCGAN AAGCGCCGCA	60
TTGAGCTCAA CATGTGGGAA CATTGAGTT CCTCTNACTA TGAATAATNT CCGGCCTCTG	120
GCTNATNCCT GAATTCTGAA TGCTGTGCTC ATTCTGCTTC GAACATTAGN CGACCAGANA	180
CACTGGGACA GTGTTNCTTC AAGANAGNGG CCAAGNGGNG ATTTCAAGAG TTCCTGNCCC	240
CATGCCCAAG GTTGTGCCTG GTTGGGCTGT TAAACTGGGA CATGNGGGAC TTGAACCTGG	300
GCCCACACTG MNGGGAGCTG TTCCAGGCAG AGGGCTTATN CCCTGTTAAC ACATGNGCCA	360
AGGGCACTGT GCCTGGGCCA GCAGGTGGGG GGGTGTGTGC CNATGTTGNG TGGTNCT	417

(2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 100 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

GGCAGAGTGG TGCTGGACAG TGACCAGCNG GTCAGTGCAG CTAGNCCACT NGCCCACGCC	60
TACTTNGGCC AGTACCACGA CCCCAGGAT GAGCCAGAGG	100

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 375 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

TACCTGGATA TNCNCGTNTA ACGCCGTGGG GGTCTGGNCC TAAGTGTGTA AGCNTTGCAC	60
GCCGTGGAGA AAGACGTGTG GACCGCCTGT GCCAGATGGC ATCCCCCACA AACTCGCNCT	120
ATGGGCAGAA GGAGTCCTCG GAATCAAAAC TTCGACTACA TGTTCAAAAT TCTNAATCAT	180
CGGCAACAGC AGCGTGGGCA AGACGTCCTT CCTCTTCCGC TAATGCTGAC GAACTTCGTT	240
TCAGGNCTGN TCTTCGTNAG CACCGTGGGG CATCGACTTT CAAAGGTTCA AGACCATCTA	300
TTCGCAACGT CCAAGAGGNT TCAAGTTGGC AGNTTTGGGG ACACAGCAAG GGCAAGAGCC	360
GGTTNCCGGN NCCTT	375

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

GGCANANCGG CAGGAGGCTC NATACTACAA GCTGGGGGAG ACCACCCTGG AGGAGTGGAA	60
GAGGCGTATC CAGGAGAATC CAGGGCCCTG GGGAGAGCTG GCCACGGACA ACATCATNT	120
AACCGTGCCG ACTGCAAATT TTCGTACTCT GGAGAACCCCT GAGCCCGNTG CTCCGCCTCT	180
GGGAATGAGG TGATGCAGGC TGTGGCGCGA CTGGNAAGCT GAGCCCTTCC CTTTGC GCCT	240
GCTTCAAAGG ATNTTGCCG ACGTGCAGAT CTTCACTGGG NTGGGATGCA TNCAGGTAC	300
CCCATCCATG TGCCATCTGG AGTTCAATGN CAGGAGCTTC ATTCAACGGG GAAGCTCCTT	360
CAGGAACCAA GGGGCTGTTG GGGGCCCCGT TCCATGAGCT GGGGCCGCAA CCAGCAGTGG	420
CAGGAGTTGG GGAGTTCCCA GGGACAATAC CAACGGGGGC NACTTGGAAN CTGTTGGTGG	480
TGTGTTATGT GCATGANAAC GTCTTTGGGG NNTTCTT	517

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:



AGCTGGNTNN CGCGCGCCTG AATTCGCCAG GAAGCAGGTA TGGNGTTCCA GCAGTTTTAC	60
CTCTTCCCGC ATCTNACAGC GCTGGAAAAC GTCATGTTTG GCCCGCTACG GTGCGTGGNG	120
CGAACAAAGA AGAGGCGGAA AACTGGCAC GTNAGCTGCT GCGGAAAGTN GGTCTGGCAG	180
AACGTGGCAC ATCACTACCC TTCCGAACCT TCTGGTGGTG AACNGTCAGC GTGTGGCGAT	240
TNNCCGCGCN GTGGCGGTGG AAGCTGNNGG	270

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

GGCACAGTTT CATTCCTGGT TTAAAGGAGT TCACGGGCCA TGTGGATCGC ATCTTTGAGG	60
ATGTCAAAGA GCTCACTGGA GGCAAAGTGG CAGCCTACAT CCCTCAGCTG GCCAAGTCAA	120
ACCCAGACCT NTGGGGTGTG TCCCTGTGCA CTGTGGATGG TCAACGGGCA CTGTGTGGGG	180
CCACACAGGG ATNCCCTTCT GCCTGGCAGT GCCTGGTNTG NNAGCCCCTN ACCTATGNCC	240
ATCTCCATGA AGGCACCCTN AGGCACTGGA CTTACGTGTC ACAANGTTTT NTGGGNCAAA	300
AGAGCCCAAG TGGGCCTGGC GCTTACGAAC A	331

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

TTGNAGGTCG AACTAGTGG ATCCAAAGAA TNTGGCNGAG CNAGGGGTGA AGTCCTTNAG	60
GCCCTGAATG GTCAGCTTGT CCACAGGGTG AATCTTGTTG TAGTCAGCCG GGTCANNNAG	120
GTNAGAGGCA GCAGGACCTG TTTNNTTCAGG TTGGTCTCTG GAAAGCAGGC GGCATTCCGT	180
CATCGGGGGC CTNACTAGCC TGGAGAGCTT CATTTTCTAA ACCCATCTGG GGCTCTGGGA	240
AGATGCCCCCT TAATCCTGNT GCCTGGGAAC AATNCCCGGG TCAGTGAAC TATGGGNGCC	300
CTGGGTGCTG CTTCCCTTTC AACTAGGGGT NCCCCTAGCA AGTNTGACGC TGGGTGCTGG	360
AGGTTTGCAA GGNCTTTCCT NGTTGGCACA TTGCATGGAT N	401

(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 316 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

ACTCACAAGC TTGNNTTGA NCACCAGCCA GGTGACATCT TTGGCTGTNT GGCCGACATC	60
GGNTGGTTTA CAGGACACAG CTACGTGGTG TATGGGCCTC TCTNCAATGG TGCCACCAGC	120
GTCCTTTTTG AGNAGCACCC CAGTTTATCC CAATGNCTGG TCGGTACTGG GAAGACANTA	180
GAGAGGTTGA AGATCAATCA GTTCTATGGC GCCCAACGG GCTGTGCCGG CTGTTGCTGA	240
AATACGGTGN ATGGCCTGGG GTGAAGAAA GTGATGGATC GGTCCNTGCC CTGNGGGACC	300
CTGGGGGTCA NTNGGG	316

(2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 571 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GATCATTATG CTAAGNTNGT NTGNGNCTCC AGGTCGACAC TAGTGGATCC AAAGAATTTCG	60
GCACGAGCAG TTGGTGAGG ACAGAAGGTC CGGTGGTTAA AGAAGGAAAT GGAGAAATAC	120
GCTGACCGGG AGGATATGAT CATCATGTTT GTGGATAGCT ACGACGTGAT TCTGGCCGGC	180
AGCCCCACAG AGCTGCTGAA GAAGTTCGTC CAGAGTGGCA GCCGNTGCN CTTCTNTGCA	240
GAGAGCTTCT GCTGGCCCGA GTGGGGGCTG GCGGACAGTA CCCTGAGGTG GGCACGGGGA	300
AGCGCTTCCT CAATTCTGGT GGATTCATCG GTTTTGCCAC CACCATCCAC CAAATCGTGC	360
GCCANTGGAA GTACAAGGAT GATNGACGAC GACCAGCTGT TCTACACACG GNTCTACCTG	420
GNCCCAGGAC TGAGGGAGAA ACTNAGCCTT AAATCTGGAT CATAAATTNT GGGATCTTTC	480
AGAACCTCAA CGGGGCTTTT AGATGNAATG GGTTTTAAAA GTTTTAATNG GGAACCGGGT	540
GCGTATNCGG AANGNGGGCT AAGGACAAGG T	571

(2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

GGGAACATNG AGACTTGGGC CACCCAATTN GAGAGGATCT TGGACAGAAA CCCCTTCATA	60
AAACCTNAGC CTCAAAGGGC TTCNCTGACT GTGANAAAAA AAAAAAAAAA ANTCC	115

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

GGTCNTGATT AACCTCATGA AGGGGCCAAA GNTCGGGGNC NGCGCCTGCG GGTCGACACT	60
AGTGGATCCA AAGAATTCGG CAGAGCAGCT TTTTNGATGCC TTTNAAGATG ATAGGTATCT	120
GTNCATGGTA ATGGAGTACA TGCCTGGTGG AGACCTTGTA AACCTTATGA GTAATTATGN	180
ATGTGCCTGA AAAATGGGCC AAATTTTACA CTGNTGAAGT TGTCTTGCT CCTGGATGCA	240
ATACACTCCA TGGGNTTAAA TTACACAGNG GTGTGNAAGC CTGACAACAT GCTCTTGGGA	300
TNAANCATGG GACATCTAAA ATTTAGGCAG ATTTTGGGCA CGTGTATGAG GGTGGATGAA	360
ACAGGGCATG GTTACATTGT GNATACGGCA GTTTGGGAAC ACCGGATTTA TATNNTCACC	420
TGAGGGTTNC TGAAAATCCA CAAGGGGGGT TGATGGGTTT TCTTATGGGG CGGN	474

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

TACAGCGATC TNCGAGTGGN ACATGNTGGG TCCAAAGANT CGGCANAGGG ACAATCTCTA	60
ACTAGTGTCA TGGCTCCATC TGGGGCTGGG CTGGGGTCAG GACTCCGTCT GAGGCTGTNT	120
TTTGACTGTN AGGTAGCCCA GGCTGGGCTG ACTCCTGATT GTGCAGTTTT GCATCTTCTC	180
CCTGCTGAGA GTCCACCAAA GTNTTCTATG GTAGACCCAG TNTCTGGAAG TNATCATCAN	240

GCAGCAGCAA CAGGGNGTGT TGTAGGTCAG CAATGGGGAG ATAGGCAATG CAGAGGTGTC	300
TNTTCCAGNN CCCTGGAGAG CCATTTTGTC GGNANTTGGA GCTGGTNAAT NAGAGGNTGC	360
TTGAGCAGTG TCGGAATAAT CCCGTCAGGA CAGCTGCTAG TTCAAGCTGG TTTGGTGAAT	420
GTATGGANTA CTGAGAGGTG AGTGCAAAAG GTTGGCTGCT TCTAAGTTTG GTGAGTCATT	480
GTTTTNTTGC TNATTGCATG TTGGGNAAGA TACCACCTCA NTGCTTACGT TATCAGCN	538

(2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 353 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

GGCAGAGGTC ATGATGGAGG TCGAGTCCTC CTACTCGGAC TTCATCTCCT GTAACCGGAC	60
AGGCCGTCGG AATGCGGTCC CTGANATCCA GGGAGACTCA AAGGCTGTAA GCGTAAGGNA	120
AGCTGGCTGG AGACATGGGC GAGCTGGCAC TCGAGGGGGC AGAAGGACAG GTGGAGGGGA	180
AGCGCCCCAA ACAAGGAAAG CTGGGCAACC AGCCCCAGAG CAGCGATGGG NACCACCTTC	240
GTTTTTGAAA TCTGAACCTT GTTCCAAGAA GGCTTGACG AGAGACCCTT NTGTTCCCCT	300
TCCCANAGGG GGGGAACCTT GGGCAATTGG GCCCANAAAN GCTTTTTTTTT TTN	353

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 374 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GGCAGAGCCC AGCAGGGAAT AAAATTTTTN NAAACCCTAG TGCCATATGN TGAAGGGGCC	60
CCTGCTTTTA AGGGAAGGGC TCCTGCCTTT NCTNACGCTT CTNTCCACCC CAGGTATGAT	120
CTCATGTACC AGTGCCTGGA GTGCTGACCC CAAGCAGCGC CCGANCTTTA CTTGTCTGCG	180
AAATGGGAAC TGGGAGAACA TCTTGGGCCA GCTGTCTGTG CTNATCTGCC AGNCAGGACC	240
CCTTATGACA TCAACATCGA GAGAGCTGAG GAGCCCACTG CGGGGAGGCA GCCTGGAGCT	300
ANCTGGCAGG GGNTCAGCCC TACATGGGGG TTGGGGATGG CATTGGCNTN GGGGCATGGG	360
GTGGCACTNC CCAT	374

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 402 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GGCAGGAGCA ACTGCTGGTT CTCCTAGAGG CCTCTCCTCA AACTCGCAGN CTGCCTGATC	60
ATTGCTACAG AATGAACTCT AGCCCAGCTG GGAACCCCAA GTCCACAGCC CTCCAGGGCC	120
AATGGGAAAC ATCAACCTGG GGCCTTCAGC CAACCCAAAT GCCCAGCCCA CGGACTTCGA	180
CTTCCTCAAA GTCATCGGCA AAGGGAATA CGGGGAAGGT CCTACTGGCC AAGCGCAAGT	240
TTGGATGGGG CGTTCTATGC AGTGAAAGGT ACTACAGAAA AAGTCCATCT TTAAAGAAGN	300
AAGAGAGCCA CATTATGGG CAGAGCGCCA TMTGGCTTTC TGAAAGAACG TCGGGGCACC	360
CCTTNCCTGT GGGGGNCTGN GCTNATTCCT TTCCAGAACA AC	402

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 334 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

CAGACGCTGT CCAGCTGGNA GTAACAGTGG GGCCTGGTGA ACGTCGGATC GGCCCAGGGG	60
AGCCCTTGGN AACTCCTGTG CAATGTGTCA GGGGCACTTC CCCCAGCAGG CCGTCATGCT	120
GCATACTCTG TAGGTTGGGA AGATGGCACC TGCGAGGGCA CCTGGGCCCT GGCCGCTGG	180
TAAGCCCAGC TGGACACAAA GGGTGTGGGN CAGCCTGGGC CCTGGCTATG AAGGGCCGAC	240
ACATTGCCAT GGNGCAAGGT GGCATCCAGA ACATACCGN TTAGNGTTAG AGGCTGCCAG	300
GNCTGGGTGA TGCGGGCAAC TNACCGTTGT CTTG	334

(2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 369 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

GGCAGAGTTT GTTTTGAAGG AGACCGGNTG GCATTCTTCG GGACAGAGAT ATCTTTCAGA	60
TCCAATGGAG AAGCACTCCA GCAGCTATAA TCAAGGTGGT TACAACCANG ACAGCTATGG	120
ATCAAGCAGT GGGTACAGTC AGCAGGCGAG TTTGGGGCCA NNCTCAGATG AGTTTGGCCA	180
ACAGCCTACT GGCCCCACTT CCTTTACCAA TCAGATTTAA CAGAGTAGCA TTTGCATTCT	240
TCTGCAGTGC GCCTCACCAT CTTCCATTTT AGTGGGCAGA AGAATTTTTT AAGGGTTTCA	300
ATCAATTATT ANTGCAGAGA GTATTGANTG TNAATGCAGA GCTCTCTAGT NTTNCATTAA	360
GGCAGCAAT	369

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

GGCAGAGCCA AGGCGNTGGC TNGAGGGAGT CAGCGGCCTC GGGCTTGGGG GCCTGTTGGA	60
GGAGGAAGGA GCCGGGGCAG GTGCTGCCAA GAAGGAGGTG CTGGAGCCTG GCAGGGAAC	120
CTCCACCCTC NTGGAGGCCG CAGCCTGNAT GGTGAAGGCC AGCCAGACAG AAGACGTGGA	180
TGGNACCTGG GGCTCTTCAG CAGCCAGGTG GAGCGAATCA GGGGGCCAGC ACAGACTTNT	240
CGGCGACCCT CCAAGGCCC TCCTGCCAGA TCCCCAGTT CAGGACTTTT TCCTTCATTG	300
AGGACACCGA GATCCTCGAA CANTNCCCAT GTTATCGGA GCCGTGCCAA TTTGGGGGCG	360
CAATTTTGG GGGCAACGGG GCCCCGGTCC ATTCGGNCTG GGGGGTTACT TTGGGNCTTT	420
NGGGGNAGC ANAATTCGGA TG	442

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

CGGCTTTATT TGTAGGCGAG ATCTTTGTNC GCNTCATATG GTCCACACGG GAGATCAGCC	60
CTATTATTGT NAGAGTGTGG GAGTGCTNCG ATAGGCCNCG TGTCTTTGAN ACATCAGAGA	120

GNCCCCGTGG AGA

133

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

GGCACGAGAA CACCTATGGN TTTCCAATGG ATCTAACTGG ACTAATTGNT GAAGAGAAGG	60
GCCTGGTGGT AGACATGGTT GGCTTTAAAG AGGAGAGGAA ACTGGCCCAG CTGAAATCAC	120
AGGGGCAAGG GAAGCTGGTG GGAAGACCT CATTATGCTG GACATTTACG CTNATCGAAG	180
AGCTCCGGGG CACGGNGTCT GGAGGTCACA GATGATTCCC CAAAGTTACA ATTNACCATT	240
TGGNGCTCCA GTGGTAGCTA ATGTATTTNA AGANACACAG TGGGCTACGG GTGAATGGTT	300
TCTGCGNCAG GGGAGNAAGA TGTTCCTGG GGAGAGGTGT TCCCACAGGT CCAGGAGTTG	360
TTGGGAGTTG GTTGCNTGGG ACAAGANCCN GTTTTT	396

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

TGGCACGAGT GCGACGCGGT GGTCAACATG TGGATCTTGG GTCTGAGGAA AGAATTTNAG	60
GAAGCCAGGA AGTGGGTGTC GAAGAAGTTA CACTTTGAAA AGGACGTGGA CGTCAACCTG	120
TTTNAGAAGC ACGATCCGCA TCCTGGGGGG GCTCCTGANT GCCTACCACC TGTTTGGGGA	180
CAGCCTCTTC CTGAGGAAAG CTGAGGATTT TGGAAATCGG CTAATGCCTG CTTTTCAGAA	240
CACCATCCAA GATTCTTAA CTTCGGGATG TGAAACATCG GTNACTGGGA GTTGCCCACC	300
CGTNCACGGT GGAACCTCC GACAGCACTN TGGGCCGAGG TGACCAGCAT TTCAGCTGGN	360
AGTTTCCCGG GAGCTCTNCC CGTTTTTCAC AGGGGGATNA AGNAAGTTTT TCAAGGGGG	419

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

NNANACTGAG TGGATCCAAA NAATTCGGCA GAGCAGTGGA AGATCAAAGC AATCGGGCAT	60
GTAATAGAGG ANGGCGGTGT CAAAATAAAG CTAACCGTAA TCANCACCCC AGGCTTTGGA	120
GACCAAATCA ACAATGAAAA CTGCTGGGAA GCCCATTAAG AAAGTACATC AATGAAGNCA	180
GTACGNGAAA GTTCCTGAAA GGAGGNGGTT CAACATCGCC AGGTAGGAAA CGCATCCCTG	240
AAACTNCGT GTCCACTGNT GCCTTTGACT TGCATCTCTC CCACAGGNCA CTCCTTGCGA	300
ACCTCTGGGA TCTTGAAGTT NCATGAAACA CCTTCGGCAA GGTNTGANA CCTCATCCCT	360
GTTCAATTGCT TANGGCNTGG ACACCCTGGA CCCTGGTGGG TGAANGTCT GATTTTCAAG	420
CCAAGGGTTT CGCCAAGG	438

(2) INFORMATION FOR SEQ ID NO:164:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 554 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

NTNTGACTNC AGGTCGACAC TAGTGGATCC ANAGAATTTCG GCACGAGAGC CGGCTCGGGG	60
AGAAGCAGCT CANCTGGGAC ATAAGGTGAC ACAACTGGCA AGCTATTTTA AGCCCTTNAN	120
CTTAGCCGCA GTTGGTGTGG CCTCCAAGAT TCTTGATCAT CAGCAGCAGA TGACGGTGCT	180
GGACCAGACC AAGACTCTCG CAGAGTCTGC CTTGCAGATG TTGTATGCAG CCAAAGAAGG	240
TGGCGGAAAC CCCAAGGCAC AACACACCCA TGACGCCATC ACAGAGGCCG CCCAGTTGAT	300
GAAGGAAGCC GTGGATGACA TCATGGTGAC GCTGAACGAA GCTGCCAGTG AAGTGGGGCT	360
GGTTGGGGGC ATNGTGGACG CCATTNCAGA AGCCATGAGC AAGCTNGATT GAAGGCACTC	420
CTCCAGAACC AAAGGGNAAC ATTTTTTCGA CTATCAGACG ANTGTGGTTT AAATACTCCA	480
AAGCCATTTG CGGTTGANCA GCNTNAGGGA AATGATGACT AAGTCGGTTT ACTAACCCGG	540
AGGGNGTTTG GGAG	554

(2) INFORMATION FOR SEQ ID NO:165:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 465 base pairs  
(B) TYPE: nucleic acid



(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

GGCACGAGGG CCCNCGGCAC TAAGTCATCT TGGAGTTATT AACCACTGGG CCCTAGGCAC	60
TAAGTNATTT GTGGAATGTA AAGGTTCCCTA GCGAGCATCT CACCCCAGGC TCCAGGGCCT	120
CCTGAGTGCA CTGAATTTAT TTTGCACAAT ATCGTGCACA TGAGCTCATC TGNGAAGAGC	180
ATCCAGTCTT CATCAGTCTA CCAAACCTCA GGAACCACCG TTTCCCCCTC AGTTCCTTGC	240
AATCTGTTCA TTTAAGGATG AGGAACCAAA GTCCAGGAAA GAGGAAGGGG TTGCCCAGGG	300
TACTGGATAG TMTTCTGCAG AGTGGGACAA GGGCTCTCTG GGTNTTCTG ACTNCACCAN	360
ATCTNGTTCA CCCCTGNACC TGGACCTCCT TGAACCTCA GTTCTCCCT GAGGGGACCC	420
TGCACACCCA CAACTTCANA ACAACATTTT CTTANAANCT AGNGG	465

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 320 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

ATNANTTTAG AGTCAAGTAT GAAACANACC TGGCCATGCC CCANTTTGTG GAGAACGANA	60
TCCATGGGCC TCCGCAAGTC CATTGAATGA CACCAATATC ACACGACTGC GAGCTGGAGA	120
CAGAGAATCG AGGCTCTCAA GGAGGAGCTG CTCTTNATGA AAGAAGAACC ACGAGGAGGT	180
AAGTTAAAAG GCCTTACAAG CCCAGATTGC NAGCTCCTGG GTTGAACCGT GGAGGTTAGA	240
TGCCCCAAA TTTTNAGGGA CCTCGCCAAG NTCATGGNCA GACNTCCGGG CCCCAATATG	300
AACGAGCTGG CTCNGTAGGA	320

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 154 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

GGCACGAGAT GATCCTTNAG TNCCTNAAAT TGATCGGATC TACAAAACAG ATAGAGAAAA	60
---	----

TTACATCGCA TACTTCTGAA GTCCATTCCN GAGCTATTCT GTTGTGACTT TTNTCGNGAC 120  
CGATTCCGGCA GGAAGACANC TGATNCCTGT CCGG 154

(2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 497 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

GGCACGAGAA GCCTGAGACT AGGGAGGAGA GGGTTGCTCC AAAGTGGTTC CTACACAACC 60  
AGGAGGCAGC CCTAGGAACT TCAGATCAAA GCGGATGGAC TTTGGATTAC AGGAGAAATA 120  
TTTAGTGGTA TCTGGAAAAG AAATACATTA AAAAGAATAA AATAACTTTG AAATTAAAAA 180  
ATCCCAACAA TCTTTTGTTC CACATTTTAG CTGCGGATCA GCATTTAGGG TAAAGGTGTA 240  
ACTTCCTCCT GAAGGTACAT CCTTGGCTAG AAATCTGAAA GGCCAGGTCA TTNCTTTGGT 300  
TCTCTGGAAC CGGATTTAGG CATAGTTTCC ATTCAAGTTT TTCTNGGTNC TTTGAAGTNA 360  
ACCTTTTCCA NTATTATTCC ANTGGGTTTA GGGCTTAGTT ATTATGAATG TNCCCTCAGA 420  
TGGGCAACTC CGGTTTTTCAN CCNTCAGGTC TAGCCCTGGG GAAGGAAGNA GGAGGGCCAG 480  
GTTTCNGGTGG GTTCAAA 497

(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 80 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

GGCACGAGGG AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 60  
AANAANANAN 80

(2) INFORMATION FOR SEQ ID NO:170:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 262 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

GGCAGAGCC ATGCCCCGCT ACGCCGACGC GTCGNNACGC AACACGCTTA GCGGCTTCTC	60
CTCAGNCCAC ATGGGCAGTN ACGTTCCCAG CCCCANAGCC AGGGTCACCA CGCTGTNCAA	120
CCCCATNGTG GNCTCGGTCT CCAGACGGAC CGCACCCCGA GGTAAGTGGG GCAGTGTCCG	180
GACCAGTGTG ANGNAGCAGT GGTCTTGGCA CCGATGTGGG CTCCCGGNTA GCTGGCAGAG	240
AACGCGCTNG NCCCACCCCA GG	262

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

AGAGCGCGCC TAACCGTAAA GGTCGTTACC TGTATATGGA ACCCAAGCCC TACCTGGAAG	60
TCTNCCTGCA CTNGGAGCCC CGGNCCAATN TGAGNAACTG ATCGG	105

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

CACGNNNCGG CACGNACCG TTCACCTTCC AGCCAGAAGG GGTCACGTGG CGGGAGCAGA	60
AGGAGCAGCG GGCCGCCCTC ATGGTGGGCA TGNTCGTTGG CGTGTTCGNG CTCNGCTGGT	120
ATCCCCTTCT TTCTACCGA GTCATCAGT CCCCTGCGGC TCCTGNGACA TCCCCGCCA	180
NCTGAAAAG CANCT	195

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

GGCACGAGCA CACACGNACC ANCATCTACA GGACGTGGAC ATTNAGCCCT ACGTCAGCAA	60
GATGCTAGGC ACTGGCAAGC TGGGTTTNTC CTTCGTACGC ATCACGGNCC TGCTTGTTNGC	120
GGGCAGCCGG CTCTGGGTGG GCACCGGCAA CGAAGTGTTG CATCTCCATC CCCCTGAACA	180
GAGACTGTGG TCCTGACACC GAGGCCAGCT CCTGGGGNTC CGAGCCAATT AAGAACATCC	240
CCCACCTCTG GGGAGGGCGC CCGTCCCGGG GGCATCATCC ACGTGTATNN GCGATGACAG	300
CANTNAACAG GGGGGGNCAA CAG	323

(2) INFORMATION FOR SEQ ID NO:174:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 248 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

CCAACCCTGG TGTGGTACCA NCCCGATGGC ACTCGGGTGG TCAGTNAGGG ACACACTTTG	60
GAGAACTGCT GCTACCAGGG AAGAGTGCGG GGATATGCAG GTCCTGGGT GTCCATCTGN	120
CACCTGCTCT GGGCTCAAAG GCTTNGTGGT CCTGAACCCC AGAGAGAAGC TATACCCTGG	180
AGCAGGGGGC CTGGGGACCT TCNAGGGTNC TGNCCATTAA TTTNNGCGGA ATCCAAGATC	240
TCCACCTG	248

(2) INFORMATION FOR SEQ ID NO:175:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 242 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

GGCACGAGCC AATGTGGCAG CCGCCCTGGG GGTGGCAGAG CTCCTNTTCC TGCTGGGGAT	60
TCACAGGACC CACAATCAGN ACCTTCGNGT GGNTCTTCGT GCAGGGGCTG CACCTNTACC	120
GCATGCAGGT TGAGCCACGN AACGTGGACC GTGGCGCCAT GGCTTGCTAC CATGCCCTGG	180
GCTNNGGCGT CCCTGGCTTT GCTGCTGGGC CTGCTGTGG GGCCTGGACC NTNAGGGNCT	240
NT	242

(2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

TGAAGGAGTN CTTNCTTNN ACGAAACGCT CCAACGANTA CCACCTGATT AATTGTCCCC	60
AGTACTTCCT GGACAAAATC GACGTGAATC AAGCAGGCTG ACTATTTCCC GAGCAATCAG	120
GACCTGTTTC GNTGCCGTTT CCTGATTTCT GGAATNTTTG AGANCCAAGT TCCAGGTGGA	180
NAANGTAAAC TTCCACAT	198

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

AGGGCCAGCG GGACAGGGCA GAGNTCATCN TTTGCAGAA TNTGGGGGGT GGGGAGGCAG	60
GGCCACAGGA AATAATTGGG GTNCAGCTCC AGCCCCCTCCA ACCAGCCCCA GAAGTAACCA	120
CGGTCCAGCT CCAGCCAGCG CANGAGGTGA CCACAGTCCA GCTCCAGCCA GCACAGGAAG	180
TAACCACGGT CCAGCTCCAN CCAGCACAGG AGGTGACCAC GGTCCAGCTC CAGCCCGTGG	240
CCGGCCAGNT NTCCAATTCC ANTGGGGGAG CTNTGG	276

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

GGCAGGACCT CGTCCAGCGA CTCAAGTCTC ANCGGATTGC AAAGTTCGCC TTAACTATG	60
CCACCAAGAA GGGGCGGGGC AAGGTCACTG CTGTCCACAA GGCCAACATC ATGTGANGGG	120
GCATGGCTTT GTNTAGGGAT GGGTTCCTGG GAAGGTAGCC CCTGTACTTT CTNGGGTAAT	180
TCTGTCCNCT TTGGGCNATG GGACAGGTAA ACTT	214

(2) INFORMATION FOR SEQ ID NO:179:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 266 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

```
GGCACGAGGC AGGATGAGCG CTGGCAAGAC CTCAATGTGA TCAGCAGCCT GCTCAAGTCC      60
TTNTTCCGAA AGCTGCCCCG GCCTNTTTTN ACTGATGACA AATACAACGA CTTCATNGAG    120
GCCAACC GCA TTGAGGACGC GCGGGAGCAA TAAGGACGNT GCGGAAGTTG ATCCGGGGAT    180
CTCCCAGGAC ANTACTATGA AANGNTTCAA ATTCCTTGTG GGGCCATNTT TAAGACCATG    240
GGTGGACCAC TTTNAGTTCA CCCTTT      266
```

(2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

```
TTCCAGAGGG CCACANAGGT GCTCNGCGCC GCCCAAGGAG ACCATNTCCC TGGCCGAGCA      60
                                                60
```

(2) INFORMATION FOR SEQ ID NO:181:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 190 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

```
GGCANNGGGA AAGTGGGGNT TAAAAAGGGA GAAGCAGACC TCTGNATGNA TCTGCCGCTT      60
GAACATGTCA GCTTTNAGCT GAAACCTCCC GACGCGCCAT CTCCTCATTC AAAGGTCTGC    120
NTCTCCCTTT TCAACCCCAA CTTTCCTTCT NNAAGGGTTT TCCTGNAGAC TGCATTTCNT    180
GGGTTTTCCT      190
```

(2) INFORMATION FOR SEQ ID NO:182:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

```
GGCANAGACA ACCGTGAGAA GCTCAGCGAG TCGGTGCTGA TGAAGGGGGA GCGGGTNATC      60
GCNATCCTAA AGCTCATTGA GCACCCCCAC GTCCTAAAGC TGCACGACGT TTNATGAAAA      120
ACAAAAAATA TTTGTNACCT GGGTGGCTCA GGAGACCAAN ANTGTN                      166
```

(2) INFORMATION FOR SEQ ID NO:183:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 167 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

```
GGCAGAGGTG TGGACGGCAT AAATGTAATA NNATATGCTG TGTGGATAAG GAGCACAAGT      60
NTCCTTTGAT TTGTGGGAGG AAATCCGTT GTGGCCTTCA TAGGTGTGAA AGGAACCTTG      120
TNCATCGTGG GAAACTGCCC CCAGANGCAA TGCGGTTTGN NTTTTTN                      167
```

(2) INFORMATION FOR SEQ ID NO:184:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 163 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

```
GGCANAGCGG CANGAGCCAC AATGAAACCA AGGAGGTAGA AGATGACTGG AAATACGTGG      60
CCATGGTGTT GGACAGAGTA TTTCTTTGGG TATTTATAAT TGTNTGTNTA TTTGGNAACT      120
GCAGGGCTTA TTTCTACAGN CCCACTTACT TTGGGGGGGG GGN                          163
```

(2) INFORMATION FOR SEQ ID NO:185:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 329 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

GGCACAGCAA GCNTTCACAG GTGGTGGNAT TTTTGGGGGC CCAGCTAAGC CCAGCCCGCC	60
GGCGGCAGCA CATGCAGGAG CGCAGAGCCA CCCAAACCTC TCCACTATTT AATCAGGAAG	120
GGTCCCCCTA GCCCTAAGGC TTCTTTTTCG TTCCAGGTGA AACACAGNAA GANTCAGCCT	180
TCCCAGCAGC CNGGGGGGAG ACCCACAAGC CCCTAAAAGC NTGCACTCAA GAGGGGGCCC	240
AGTNTTCACC AGGAACCTTG GAGGAAGTTC CCACAGGGAG CGCAAAGTNC GGCAGGCATC	300
GNCCTTCCGG GGCTTCTTNT TNTGGCATT	329

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

AGCAAGGNAG CTCTGGCTGA NACCACCGGN NAGACGCACC TCCGGGACCA CACCCACCAA	60
GGCTCCTGCC CCTNTTGTTT CTGGGGTCCC CAGTTGTTCT TAGGGCCTNC TGTGGGGCCA	120
GGCCCCGANTG NGCTGTGNGA GCACTTCATT ACCGAAAGG	159

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

GGCACGAGGC GCTTTCTNCC NATTGTNTGG TTTTACTTTT GTNCTGGTAT GAATTCGATT	60
CCATTTTAAT NCATCCTGTT AAATNAAGTT AAATGAGGGG AAANCAAAAC CAAAAGGNAA	120
AAAAGGCACA GAGTGAGAGA CAACCCAGCA CAGGACCCCC AGGAAGGCAA GCAGTAACGC	180
TCCAGCAGCC GGGTTGTGCT GCCTGGGCCC AGGCTTCTGC NAGGTGGTTT ACAGGCGGGA	240
ACCATTGNTA CCACAACCAC CAAAGGNGGT GGGAGTNCTG TGTGTGCCCC CTTTACAGAA	300
GAGGAGACCG NGNNCTCAGA GAAGATCCAG CAGTAAGATT TAGAGTCAAG GTT	353

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

GGCACGAGGC CAGCNTTCGC CAATNNTTGG AGAGTGGGGT TNTGGGGTCA GGTGGGGGAC	60
CCCCACGGGG TCTGGANTTC TNCCGGGAGG AGATCACCAC CTTTCATCGAT GAGACACCTC	120
TCCTTTCTCC GACTGCTTCA CCAGGGCACT CTCCTCGTCG GCCCCGGCCA CTGGGNCTNT	180
AACCCCGCCG ACTCTTCCCT TGGNTCCCT GAGAAGCAGA GCCGTTGGAC TTCCTTTGGG	240
AACTGAAGCG CAGGGAGACG CTGCTCCCTG ACGGGGGGTG AAGAAAGTNC CAAGGGCTTG	300
GGGAGGATCC TGGGGCCCAG GCAACCCCAT NTTTTCCCA GNTGACCTGT NAAGCCCAAG	360
CAGGNTGTTG NAACTTCAGA GGAGAAAGTT GA	392

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

GGCACGAGCT GGGCTCATTC CCAGCCAGCT GCTGGAGGAG AAGCGGAAAG CATTTNTNAA	60
GAGGGACCTG GAGCTGACAC CAAACTCNGG GACCCTATGC GGCACCTTTT AGGAAAGAAA	120
AAGAAGCGAA TGAATGTATT TNACCACCAA GNAATGCAGC CTGGTGAGCA GCGCNATCTC	180
CCTGTNTCCA GAGTTTGACC GTNATGAGCT GCTCATTTAT GAGGAGGTGG CCCGCATGCC	240
CCCGTTCCGC CGGAAAACCC TGGTACTGAT TGGGGGCTCA GGGCGTGGGA ACGGCGCACT	300
GGATAGGAAC AAGCTCCTTC ATGTGGGGAT TCCAGATTCG NTATGNGCAC CAAGGGTGCC	360
CTAAAACTT CCCGNGGGNC CGNAAAAAT CAGAGCGGGG AAGGTTGAGG GTTTAACAGT	420
TTTTTNTTCC CCTTGGGGGA AGATGGNAGG	450

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

GGGCAGGGAC GCCCTGGCGC CTCTNTAGGC CGACTNCTCG AGCTGCTTAC CAAGCTGGGC	60
CGCGACGACG TGCTGCTGGA GCTGGGACCC AGCATTGAGG AGGATTGCCA AAAGTATATC	120
TTGAAGCAGC AGCAGGAGGA GGCTGAGAAG CTTTTACAGG TGGCCGCTGT AGACAGCAGT	180
NTCCACGGA CAGCCAGAGC TGGGCGGGGC ATCACCACAC TTGAATGACC CCCTGGGGCA	240
TATGCCTGAG CCGTTTTCGA TGCCTTCATC TGCTNATTGC CCCAGCGAAC ATCCAGTTTG	300
TGGTAGGAGA ATGATNCCGG GNAACTGGAA CAGACAACT ATCGACTGAA ATTGTGTGTG	360
NTTTNGACCG GATGTTCTTG CCTGGNA	387

(2) INFORMATION FOR SEQ ID NO:191:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

TCACCGATTG GGATTNNGAC ATTGGAAAAT TCCGACGTTT TCTTTGGTGG TGTGGTTCTG	60
GGAATCCACG CCAANGGGAA GCGCATAANG NACTGGTTTG ACTGC	105

(2) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 336 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

GGCAGGAGN AGAGCTCAGC ATCACCCTCA CGCTGCGGAT GCTGATGCAC GGGNAGGAAG	60
TGGGCAGCAT CATCGGGAAG AAGGGCGAGA NTGTAAAGCG AATCCGGGAG CAGAGCAGTG	120
CCCGGNTCAC CATCTCCAAG GGCTCCTGCC TGCAACGCAT CACCACCATC ACCGGGTCTA	180
CAGCAGCTGT TTTCCATGCA GTCTCCATGA TTGCTTTCAA ACTGGATGAG GACCTTTTGTG	240
CCTGCTCCTG CAAATGGTGG AAATNTCTCC AGGCCTCCAG TGAACCCTGN GGCCTTGTTN	300
ATCCCTGGCC AGTTCNTTTN GGCTCACTGG TTTGGG	336

(2) INFORMATION FOR SEQ ID NO:193:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

GGCAGAGGTA AGCCATATGT NTTCGACAGA GTGCTACCTC CCAACACGAC CCAAGAGCAG	60
GTTTACAATG CATGTCCGAN AAATTGTCAA AGATGTCCTT GAAGGTTATA ACGGGACGAT	120
TTTTGCGTAT GGGCAGACTT CATCAGGAAA AACCCACACC ATGGAGGGGA AGCTGCATGA	180
CCCCCAGCTC ATGGGGATCA TCCCACGANT TGCCCATGAT ATCTTTGACC ATATCTACTC	240
CATGGGATGA GAAACCTGGG AGTTTCACAT AAAGGTTTCC TATTTTGAGN ATCTTACTTG	300
GGACAAAATA AGGGACTTTA CTTGATTGTT TTCCAAGACC AACTTGGGCT GTTCNTGAA	360
GGTTAAAAAC AGGTNCCCTN TGTAAGGGG GTTNCATNGG GCGG	404

(2) INFORMATION FOR SEQ ID NO:194:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 282 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

GGCANAGGGT GGAGAAGCTC NACTACAAGA TGGAGCTCTN CAAGGAGATC CGNGAGGNAC	60
ACCTGGCCGC ACTGGCGAGG GGCTGCGCGA GNAAGGAGCT GCACGNGGNC GAGGTGCGCA	120
NGAACAAAGGA GCAGCGAGAA GAGATGTCGG GCTAAGGGCC CGNNACGNGG TCGCCCATGC	180
CTGACGAACG TNAACACGTT CGGGTTTTTG GTTTGTTC GTTCACCTCT GTTTAGATGC	240
AACTTTTGTT CCTCCTCCCN CANCCNGGNC CCCAGGTTCA TG	282

(2) INFORMATION FOR SEQ ID NO:195:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 405 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

GGCAGAGCT TTCTTGGGCG GGTCTGTAAG AGAGAGGCCA CGGTCCTGAG CTACGATGGC	60
TCCATGTACA TGAAGATCAT GCTGCCTAAC GCCATGCACA CGGAGGCAGA GGATGTNTCC	120

CTGCNTTTTNA TGTCCCAGCG GGCTTACGGA CTCATGAATG GCCANCACTT CCAGGGAGTC	180
TGCCGACACC CTACGCCTGG AGCTGGATGG GGGGCAGATG AAGCTTNACT GTCAACCTCG	240
ACTGCCTGCG CGTNGGCTGC GCACCNAGTN AAAGNCCCG AAACGNTGTT TGCGGGGTAC	300
AAGTTCATTG ACATGAGTGG NCACAGGNTT GAGGGTGGTC CGGCCGTGGG CAAGAGNCTT	360
GCAATTGTTT TTGGGACAAC GTGGACTTTN GGAGGGGACA ATTNG	405

(2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 337 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

GGCAGAGCAG ATAACAGCCA TGTTGTTGAC TAAGCTGAAG GAAACTCCTG AAAACAGCCT	60
CAAGAAACCA GTAACAGATT GTTTTATTTT AGTCCCCTCC TTCTTTACAG ATGCTGAGAG	120
GCGATCTGTG TTAGATGCTG CACAGATTGT TGGCCTAAAC TGTTTAAGAA CTTATGAAAT	180
GNCATGACAG CTGTTGCTTT GNAATTACGG AATTTATAAG CAGGATCTCC CAAGCCTGGA	240
TGAGAAANCN TCGGATAGTG GGTTTTTNGT TTGGTTAGGG GGCCATTCCA GCTTTTCCAA	300
GTGGTCNNGC TTTGTGCTTT TTTAACCAAG GGGGAAA	337

(2) INFORMATION FOR SEQ ID NO:197:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 287 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

CTTCNAGGTG AGCCAGCTCT ATNACTGNAN ACTGGATCGT GGTCAACTGC TCCACACCGG	60
CCAACTACTT CCACGTNCTG CGCCGGCAAA TCCTGCTGCC CTTCGCAAG CGCGCTGAAT	120
TATNTTCACA CCTGAAATCT CTGCTGAGGC ACCCAGAGGC CAAGTCCAGC TTTGAACCAA	180
ATGGTATCCG GGACCAGNTT CCAGGGGGTG AATTCCTGAA GATGGGGCCG AAGNACGGGC	240
CCTTGANCNA GGTGAAGGGG TTAATTTTTT GAAAGGGNAA GGTTTAT	287

(2) INFORMATION FOR SEQ ID NO:198:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

GGCAGAGCTT CTNCAAAGCT GCCCTCTNCC ACTTCATAGT AGNCGAGTTG AATGCCAAGC	60
TTGCNCTTNA GAAATATGAG GAAATGTTTC CAGCATTNNN NGNTTCAAGA GNNTGTAAAT	120
NNTTGAAAAA ACTCCTAGAA GCTCATGGAA GAACAGNNCA GTGNAAGCTT AACTGAAGC	180
AGTGTAAGGA ATTTGAACTC AATATCTCGC TTGGNTCAGT GGCTGNCCAC CATGTTGCTT	240
CGCATCAAAA AGTCCATCCA AGGGGNTGGA GAAGGAGATG GAGACCTAAA ATGNNTGTTT	300
TTGGNCTTTG TGGGCATGCA GCTAACTCCT CTTTAGTTTT GTTCTTAGGG TCCAAGTGAT	360
CTTTTATGGG GATGCCNCTT TTAATGGGT TAATTTTGTT TGGNATATGA GGCCCAACGG	420
GCCNGTGNN A	432

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

GGCACGAGTA CGAGTCCCTT CAAACCGCCA AAAAGAAGGA TGAAGNCAA ATTGCCAAGC	60
CTGTTTCGCT GCTTGAGAAA AGNCGCCCCC CAGTGGTGCC AAGGCAAAC GCAGGCTCAT	120
CTCGTAGNTC AAATAACCT GCTCCGAAAT CAGGCCGAGG AGGAGNTCAN CAAAGCCCAG	180
AAGGTGTTTG AGGAGATGAA TGTGGATCTG CAGGAGGAGC TGCCGTCCCT GTGGAACAAC	240
CGCGTAGGTT TCTATGTCAA CACGTTCCAG TGGCATCGGG NGCCTGGTGG AAAAATTNC	300
ACAAGGAGAT GAGCAAGNTC AACCAGTNCC TCAATGANTG TGCTGGTTCG GNCTGGNNGA	360
AGCAACAGGG GNGCAAACAN CTTTCACGGT NAAGGCCCCG NCCNTTGAC AACGGGNCTT	420
GAAAAGGGGT ACAAGGGGCC TTTTAACTTC CAGTTGGTTC CCTTGCNGGN ANCCCCGGGG	480
TTCCGGGTTA ACCAGGGGCC A	501

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

GGGCACGAGT GCAGATGAAG ATGTTGATCG GAAACACTGG GGCAAGTTTC TGGCTTTT	60
TCAGTATGCA AAATCATTTA ACTCAGATGA CTTTGNTTAT NAAGANCTGA AGAATGGAGA	120
CTACGTCTNG ATGAGGTGGA AGGAACAGTT TCTGGTCCCA GATCACACGA TCAAAGACAT	180
CAGTGGTGCT TCTTTTGCCG GGTTCTACTA CATCTGCTTT CAGAAGTCAG CAGCCTCCAT	240
AGAGGGCTAC TACTACCATA GGAGTTCAGA ATGGTATCAG TCCCTCAATC TAACCCATGT	300
TCCTGAACAC AGTGCACCCA TCTTATGAAT TCCGGTGACA ACGGGTTNAG NNCAGCAACC	360
AAATTAAAC TNGAACTTNG GCAAAAAAG	389

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 240 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

GGCAGGAGGA CACTGCCGTG GAGAACATGC CCAGCCTGAA GATGAAGGTG GTGGAGGTGC	60
TGGCTGGCCA CGGTCACCTG TATTCCCGCA TCCNAGGCCT NCTCAGCCCC CATCCNTGC	120
TGCAGCTGAG CTACACGGNC ACCGACCGCC ACCCCCAGGC CCTGGAGGCT GNCCAGGCCG	180
AGCTGCAGCA GCACGANGTT GNCCAGGGCC AGTGGGATCC CGNAGACCCT GCCNCAGCG	240
	240

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

GGNACGAGCC CGACGGAAGN ATCCAGGGCA CCCCANAGGN TACCAGCTCC TTAACCCACT	60
TNAACCTGAT CCCTGTGGGC CTCCGTNTGG TCACCATCCA NAGCGNCAAG CTGGGTNACT	120
ACATGGCCAT GANTGCTGAG GGA CTGCTCT ACAGTTNGCC GCATTNACA GCTGANTGTC	180

GCTTTAAGGA GTGTGTCTTT ANGAATTACT ACGTCCTGTA CGCCTCTCCT CTCTACCGCC	240
AGCNTCGTTG TGGCCGGGCC TGGTACCTCG GCCTGGACAA GGAGGGCCAG GTCATGNAAG	300
GGAAACCGAG TTAAGAAGNC CAAGGNAGCT GCCCACTTTT TNCCCAAATT TCTGGNAGGT	360
	360

(2) INFORMATION FOR SEQ ID NO:203:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 330 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

AGGAGGCCGG CCTCACCTTA ATGAGGACGT TNTCGTAGCT GGTGGGATTN ATGACGTCAT	60
AGCAGATGAC CACGAGGTGG GTGTNCTGGT AGGACAGGGG CCGCAGCCGG TTNATAGTNT	120
TNTTGCCCTG AANGCACAGA GCAGCGGGGG TNAGGGGACG TCCCCTTCCC TGTTTGGA	180
CTGAACGGGT GAAGGGGAAG GGGCCAGGCA AGTAAACCCT GNCTTTAGGG CCTTCAATTT	240
CCCTCATCTT ATGACAATGG GGCAGCAAAG CCAGGTAGTG CTGGCACGGG CTNTNTGGGT	300
CGCAAATTGT TTGGGAAGGC TTNAGGNCNG	330

(2) INFORMATION FOR SEQ ID NO:204:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 245 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

GGCACGAGCA GCCTGTACCC TAAAATGAGT GCCCATAAGC GCTCCTTGGA TTCCTCATT	60
NAACTGCTGC ACAAGGATCA GCTGGATGAA ACTGTNAATG TGGAGCCTCT AACCAAGGCC	120
ATCAAGTACT ATNAGCATCT GTGACAGCAT CCACCTTGGC CGAACAGCCT GAGGACTGTA	180
ACTATGNCAG CTGGCTGACC ACATTAAAGT TCCACGGCAG AAGTTGGCCT TTTTGGTNT	240
TNGNN	245

(2) INFORMATION FOR SEQ ID NO:205:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 230 base pairs
  - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

ACCAGGCTTT GGCTCAAAAG AATGGATGGN GTTTCCTCT TGTTGCCAG GCTGAAGAGC	60
AATGGCGCGA TCTTGGCTCA CCNCAACCTC CACCTCCAN GCCGGGGTGC TCNTNNCACT	120
GCCGGGNAAG GTGATAGCCG CTCCNAACG CTAATTAATG CGNCTACCTC ATGATGCGGG	180
AGAAGNTGGG NCGTCAATCT GCCCTGAGCA TCGTGAGGTC AGAACNTGA	230

(2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 235 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

GGCACGANCG GCGCGCAGC CAACCCCGA GGAGCGGCCG GNTGGCGTCC GNGCGCCCAG	60
GAAGTTGGGG ATGTCCTACA AACCCATCGC CCCTGCTCCC AGCANCACCC CTGGNTCCAG	120
CACCCCTGGG NCCGGGCACC CCGGTCCCTN ACAGGTAAGC NTCCCGTCGC CGTCGGGCTT	180
CAGTGCCAGG NAGCCGGCGC CTCCTTTGAA AACCGCTGTT TTNAACGNAC TTTTG	235

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 314 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

ATCAGGGGAA ATCAAACGGA CTGTCACAAG GATCCTGCCA GATCCTGATG ATCCAAGTAA	60
GTCCCCTGTT GGGTCACCTC TAGGGNGCGC CATTGCAGAG GNCCCCAGCG AGATGCCAGG	120
GGATGAGGTG CCTGTGGAAG AGCACTTTCC TGAGGCAGGC ACAAATTCAG GGAGCCCCCA	180
GGGGGCCAGG TAAAGGGGAC GAGAGCATGA CAAAGGCCAG TAACTCGTCA TCTCCCAGCT	240
GCANTTCTGG GGCCGGGTC CCAAAGGGGG CTTGNCCCAG GTTTNACAGA CAGGCANGAA	300
GCAACAGNGC ACAG	314

(2) INFORMATION FOR SEQ ID NO:208:



- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 348 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

GGCANAGGTC CCCGCAGAGG AACNTNCTGC CCAACCGGTT GCTGACCAAG GTGGCCGAGA	60
TGGCGCANAG CNATCCTGGT CTGCAGAAGC AAGACCTGTG CCAGGAGCAC CACGAGCCCC	120
TCAAGCTTTT NTGCCAGAAG GACCAGAGCC CCATCTGTGT GGTGTGCAGG GAGTCCNGGG	180
TGCACCGGCT GCACAGGGTG TGCCCGCCGA GGAGGCAGTG CAGGGGTACA AGTTGAAGCT	240
GGAGGAGGAC ATGGAGTACC TTCGGGGAGC AGATTCACCA GGACAGGNAA TTTGCAGGCC	300
AGGGAGGAGC AGAGNTTAGC CGAGTGGCAN GGTCAAGGTN GAAGNAGC	348

(2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 137 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

ATCCAGACCG ACTTCCGCTG CTGTGGCGTC TCCAACTACA CTNACTGGTT CGAGGTGTAC	60
AACGCCACGC GGGTACCTNA CTCCTGCTGC TTGGAGTTCA GTNAGAGCTG TGGGCTGCAC	120
GCCCNCGGCA CCTGNTG	137

(2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 363 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

GGCAGAGCC GCCTCCTCCC GCCGAGTCAG CAGCAGCAGT GAGCTGGACC TGCCCTCGGG	60
NGACCACTGC NAGGTTGGGN TCCTGCAGCT CGACGTGCCC CTNCTCCGCA CCCAGCTCCG	120
CGGCTCCCGC CTGCTCGATG CCATGCGCAT GTACCGCCAA GGTTACCCTG ACCACATGGT	180
GTTTTCCGAG TTCCGCCGCC GCTTTGATGT CCTGGCCCCG CACCTGACCA AGAAACACGG	240

CGGTAAGTAT ATCGTGGTGG ATGAAAGGCG GGCAGTGGAG GAGCTGCTGG AGTGCTTNGG	300
ATNTGGAGAA GAGCAGCTTG NTGCATGGGC CTGAGCCGGG TTTCTTCCG GGTGGGNACC	360
TTT	363

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

GGCAGGAGGG CTCCAGGGNA GCCCTCTTCC CGGTGGCTTT AATATGAGTN TCGAGGGAGG	60
TCAGGGTAGG GGCAGCTACC ACGCCTGAAG CCCTAGAGGT CACCAGGCGG CGCGGGTAGA	120
TTCGGGGGAA GCGCGCAGGG CTGCGCTAGG GACCCGCCGG GTCACCCTGG TACATGGNTG	180
GCTTTTNTTT ACAGTTTGTT CTAAACATCA GAAATGTTTG TCCGCTTTTA AAAACAAAAT	240
TGGCAGTAAC AGTTTATTAT TGGGTAGCTT GATGGAACCT GTGGATTACT TAATTAAAAA	300
ATTAATAATC TGNCTTTTTA ATTGGGGNTT TACCANTTTA GTGTTNTTGG GNTTTAAAA	359

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

GGCANAGCTG CCGCCGTCGC CGCCACCCGA GCCGGAGCGN GCTGGGCCGC CAAGGCAAGA	60
TGGTGGACTA CAGCGTGTGG GACCACATTG AGGTGTCTNA TGATGAAGAC GAGACGCACC	120
CCAACATCGA CACGGCCAGT NTCTTCCGCT GGCGGCATCA GGCCCGGNTG GAACGCATGG	180
AGCAGTTCCA GAAGGNGAAG GAGGAACTGG ACAGGGGCTG CCGCGAAGTT CAAGCGCAAG	240
GTGGCCGAGT GCCAGAGGAN ACTGAAGGAG CTGGAGGTGG CCGAGGGCGG CAAGGCAGAG	300
CTTGAGCGC TCTNCCANGC CGNAGGTANA G	331

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

CCAGAGGTTT GCTGGCCACT GTCAGTGTGT GTNTGAGGCT GATCGCCAAG CGCATGGTCC	60
GGANGAACTN CCTNGTGATG AACCTGGTGN CTGTAGAAAC CCTGGGGTCN ACGTCCACCA	120
TCTTCTCAGA TAAGACAGGG NANTNTNACT NAGATCCGCA TGATAGTCGC TNTCATGTGG	180
TTTGACAACC AGTTCCACGA GGCTGACACC ACTGAGGTNC CAGTCAGGGG ACCTCATTTG	240
ACAAGAGTTC TNTACACCTN GGTGGTTCCT NTNTTCA	277

(2) INFORMATION FOR SEQ ID NO:214:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 102 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

CTTGAAGGGG GCCAAACCCA AGCTGATGTC GGCCATCTCC AAGACCTTCT NGCCGGCCCA	60
CAANAGCTAC ATCATCGNTG GTNGTNTGGG TGGCTTCGGC CT	102

(2) INFORMATION FOR SEQ ID NO:215:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 154 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

CTTTGCGTCC TCAATTGCCN CGGGGCTCNC GCTGGGGCAC AAACNACTCG ACGCAGCGCA	60
GACGCCCAAG GTGAAGGTTG CCCACGGGGA TTGCCCCGTC CATGNCCAAT GCCATGGGNG	120
TGCAACTGCT ATGTTCCATC CGNNCAANCC GCGT	154

(2) INFORMATION FOR SEQ ID NO:216:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 341 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

GGCACGACCG GGCTCGAGAG CCNCCNCGCA TGCCAGTNCC CATNCGGGGC CGCCGCCAGT	60
NAACGNCGGA GAGGTGTTCC CCCACACTG GGGCTCCCAC TACTGCGAAG GAGTGACCCA	120
CGAAGGCCAC AGAGATGGCC GGGGCTTCGG TGAAGGTGGC GGTGCGGGTC CGCCCNNTCA	180
ATTCCCGGGN AAATAAGCCG TGNACTCAA GTGNCATCAT TGCAGATGTT TGGTAAGCAC	240
CACCACCATT GTTAAACCCC AAACAGCCCA AGGGAGACGC CCAAAGGTT TCAGCTTTGG	300
NACTNATTGC TAACTGGGTT TGGGACAATC TNGNACCTNG A	341

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

CTNACTGGTG CTTNCTGCCG TCGACTGGTA TGCAGTCAGC ACTGTGAGCC ACTTACCTNC	60
AGGTGTNANC TCGGGGCCAG CCCCTTGCAT GTGGACCTGG CCACCCTNNG AGAAGCTTAA	120
G	121

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

GGCACGNGGT AAATGCTATG AAAATAGTTA CTACACTATT GTTTATNTGT ATTTTTATTG	60
AATTGTTTTG GGGTGGGGGG CAGCTGTATC TTTCTTAGTA ATAGAACCCC TGGTTTTAGC	120
TGGGCACATG AACTGCCNTC AATAAAGATT AAAGTACCCC AGCCTTCCTT GAGATTGTGG	180
CCATGTGACT GAACTTTAGA CAGTGAAGAT ATAAGCAGAT ATCTNCTGTG GCAGTGTTAG	240
GAAACTATTA AAGACAGTAA GGAACATTGC CCTTGCCTT CTTGTTCCT TNCTTCATTT	300
TTCTGCCTGG GAATGCAANG TGNATGGNTA ACACCCTAGC AGNCTTTT	348

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

```
CCTGGACCCA CAGTCGGCCA GTGGGTACCT GCAGCTGTCA GAGGTCTGNA AGNGCGTAAC      60
CTACACCAGC CTGTACAAGA GTGCCTACCT TCACCCCAG CAGTTTGGAC TNGTAAGCCT      120
GGGGTNTTGG GCAGCAAGGG GTTCACCTGG GGCAAGGTCT ACTAGGTAAG TGGAAGTNGA      180
GNGTGNAGTT NCTGGTTCTT AAGGGATGAA GTAAG                                215
```

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

```
AAAAAAAACC CAACTTGACC TAGTTGTCAT TTATAGANCA CTCCATCCAA CAACAGNAAA      60
ACACATAATT TTTTTCAAAT GTACACGGAA CATTTGNAAG ATAGNCCACA TTCTGGTCTA      120
TAAACAAGG CTCAGTAAGT TTAGAAGNT TCAAGTTATA CAAAATATAT TCTCTGACCA      180
CAATTGANTT AAATAAAAAA TACCNGAAAG NTATCTAGNG ATTCCCCAAA TATTT          235
```

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

```
GGCACGAGNA GTTGGAGGAG AAGAATCAAG AACTGCAGCG GGCAAGGCAA AGAGAAAAAA      60
TGAACGAGNA ACATAATAAA CGTTTATCAG AACTGTGTTGA CAAGCTGCTT TCAGAATCTA      120
ATGAGAGGCT TCAACTTCAT CTTAAAGAGA GAATGGCTGC TTTGGAAGAT AAGAACTCTC      180
TTTTAAGAGA AGTTGAAAGT GCAAAAAAGC AGTTAGAAGA AACACAACAC GATAAGGATC      240
AGCTTGTCCT AAACATTGAA GCACTGAGGG CTGAACTAGA CCACATGAGA CTTAAGAGGT      300
GCTTNCACTT TCATCCATGG GCCGACCCCA CTTGGGGCAG TGTTCCCAGA TTTTCAGGTT      360
```

TCCCCATGGC AGACGGGNCA CACAGACTTC NTACCAGCAN CCAGTGCAGT NGTTGCGGGN 420  
GCCCACAGAA A 431

(2) INFORMATION FOR SEQ ID NO:222:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 251 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

GGCACGAGCC GTGATGCCAA GCTGCCAGCC TCGCGCTCCA TCCGCAACCT CTTTGGCAGT 60  
GGGAGCCTTC GGGCCTCAAA GAGTAACCGT GTGACTGGTG TNTACGAGCT CAGCCTGTGC 120  
CACGTGGCTG ACGCGGGCAG CCCAGGGATG CAGCGCCGGC GCCGACGAGT CCTGNACACA 180  
TNTGTGGCCT GATGTCCGGG GCGAGGAGAA CCTGGGCAGG CTNNTAGGCC CCGGAGTNGA 240  
CAGTTTTTCAT T 251

(2) INFORMATION FOR SEQ ID NO:223:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 261 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

TGGGTNCCCC GGGNTGCANG AATTNGGCAG AGGTACAAGC TCGNTGCCTA TAAAGCTGAT 60  
GATCCAACAA TGGGGGAGGG CCCAGACAAG GCACGTTCCC AGCTCCTGGA TCCTGGATCG 120  
AGGCTTTGAC CCCAGCTCCC CTGTGCTCCA TGNAATTGAC TTTTCAGGCT ATGAAGTTAT 180  
GAATCTGGCT GCCTATCGAA AATGNTGTAT ACAAGTATGA GACCANNGGC ATCGGGGGAG 240  
GNACGTGTNA AGGGGGTTCT C 261

(2) INFORMATION FOR SEQ ID NO:224:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 392 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

GGCAGAGGNA CAAGCTCGAT GCCTATAAAG CTGATGATCC AACAATGGGG GAGGGCCCAG	60
ACAAGGCACG CTCCCAGCTC CTGATCCTGG ATCGAGGCTT TNACCCCAGC TCCCCTGTGC	120
TCCATGNAAT TGACTTTTCA GGCTATGAGT TATGATCTGC TGCCTATCGA AAATAATGTA	180
TACAAGTATG AGAACCAGCG GCATCGGGGA GGCACGGGTG AAGGAGGTGC TCCTGGAACG	240
AGGACGACGA CCTGTGGGAT AGCACTGCGC CACAAGCACA TCGCNGAGGT GTTCCCAGGA	300
AGTTCAACCG GTTTTTGNAA AGATTTTTTC TTTTAGCAAG NGGATTGAAT TACTGGAGGG	360
AAGGCCACC NTGCGGGACC TNTNCCCAAT TG	392

(2) INFORMATION FOR SEQ ID NO:225:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 380 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

GGCAGAGCCC GACGGAAGCA TCCAGGGCAC CCCAGAGGAT ACCAGCTCCT TNACCCACTT	60
NAACCTGATC CCTGTGGNCC TCCNTTTGGT CACCATCCAG AGCGCCAAGC TGGGTCACTA	120
CATGGCCATG AAATGCTGAG GGA CTGCTCT ACAGTTCGCC GCATTTNACA GCTGANTGTC	180
GCTTTAAGGA GTGTGTCTTT GAAGAATTAC TACGTCCTGT ACGCCTCTGC TCTCTACCGC	240
CAGGTTTCGTT NTGGCCGGGN CTGGTACCTC GGCCTGGACA AGGAGGGCCA GGTCATGAAG	300
GGAAACCGAG TTAAAGAAGA CCAAGGCAGN TGNCCAATTT TTNCCAAGA TNCTGGGAGG	360
TTGGNCCATG TAACCAGGGG	380

(2) INFORMATION FOR SEQ ID NO:226:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 488 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

GTACTGCTTC CAGTTCCTGC CCTTTGGCAA AGGCCTCATC AAGAAGTGCC GGACCAGCCC	60
TAATGCCTTT NTGCAGATCG CGCTGCAGCT GGCTCACTTC CGGGAACAGG GGTAAGTTCT	120
GCCTGACCTA TGAAGGCCTC AATGAACCAG NAATGTTCCG GGAAGGGAAC GGACTGAGAA	180
CTGTGNCGTT CCTGTNACCA GCGAAGTTCC ACAGCCTTTN TGGCAGGCCA TGNATGGGAG	240

GGGTCCCACA CAAAAGCCAG ACCTGCAAGA ATCTTTTTC AGAAAGGCTT GCTNAGNAAG	300
CACCCAGGAA TATGTNACCN GCCTGGGNCC ATGAAACCGG GGGCAGGGG ATTCGNAAAN	360
GGCANCTTTT TTTTGGCCTT TTAATTTGGG TTNTTCCAAG TTAACCTAGG GGGTTCANTT	420
TTTCCTTTTT CCTTGNTTGA GGGTGGTTTT NGGGGAANCC TTGGGGGNTT TTTTCCAACC	480
AGGCCAGT	488

(2) INFORMATION FOR SEQ ID NO:227:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 492 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

GGCAGAGGNC AGGACGAGCT CAGCTTTAAG GCCGGAGACG AACTCACCAA GCTGGGNGAG	60
GAGGATGAGC AGGGCTGGTG CCGTGGGCGG CTGGGACAGC GGGCAGCTGG CCCTCTNACC	120
CTGCCNAACT AACGTGGAAG GCTATCTAGA AGGCCNCCTN CCCTGCCATA CTGCCCCGTTA	180
ACTCCTCCCC ACTGCCGCCC CTCCCCCTNC CCACTNCTGC GTNCTCCTTC CCCTCGCCAT	240
AGAAGTTTCC AGACATATTT TCCCGAATTC AAGCTTTTTT ATTTTTTTTAA AAAGTTCAAA	300
ACCAGGAACA AAAACAAAAG TNATGCCANG AGGACAGAGN CATTTNGCAG GGGCCCANCT	360
GGNAGGGTTT GGGGTGCTTG GGGGTTTTTG GGAGTGGGGC CCCCAGGGTT AGGTTAACCA	420
GTTNTTNAGG TANTTTAGGC CCCAAGCATT CAACAAACAT CTGGGTTCTT TTTCTGGGGT	480
TTCCACCCAA AN	492

(2) INFORMATION FOR SEQ ID NO:228:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 97 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

TTCCATAATG GCTGTNCTGA TTTACATTCT CATCAACAAT GNACAAGTGC CCTTTNCTCT	60
GCATTCTCCC TAGCATTTTT TTTTTTTTNT CTTTTNG	97

(2) INFORMATION FOR SEQ ID NO:229:

- (i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

```
GGCACGAGGG ACCCGCCCGC NATGGGGGAC GAGGACGACG ATGAGAGCTN CGCCGTGGAG      60
CTGCGGATCA CAGAAGCCAA CCTGNACCGG GCACGAGGAG AAGGTGAGCN TGGAGAACTT      120
CGAGCTGCTC AAGGTGCTGG GCAGGGAAGN CTACGGCAAG GTNTTCCTGG TGCGGAAAGG      180
CGGGTCGGGC ACNACGCGGG GTAAGCTNTA CGCCATGAAG GTGCTGCGCA AGGTGGNCGC      240
TGGTTGNCAG GGCCCAAAGT ACGCAAGNGT CAC                                     273
```

(2) INFORMATION FOR SEQ ID NO:230:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 398 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

```
GGCAGAGGCG CCCCCAGCC CTCCTGACG CTCAGCCTCG GGCCTCTCT CCAACTCTCC      60
CGGCCCACCG TGGCATCGGG AGGCCATGCT CAGGTCTGAA GCAGGTTTGG GGCCTGCTGA      120
CAGCAATAGC CCGCCTTTGG GAAACCCCTT GCTGTGAAAC TCTCTGCACT GCAGTGAACC      180
TTCAGTCACG AACCTGCCTC TGCCCCTTCG GGGGACGCCC ACACAAAAGG GNAAGTGCTT      240
GGCCGTGCTG GTTCCTGCCC TGCTGGTGGG CCTGNCCGGG GNTTGGGCGG CCGGTGAAGC      300
GGGATTGCAA TGGGGATGAG GGTGNACAGG GGCCTGGTTC CTGTTCTCTA GNGCCNCAGT      360
NTTGTTCCTT CCTGNCCAGT TCCTGTTCCA AATGCATG                                     398
```

(2) INFORMATION FOR SEQ ID NO:231:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 301 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

```
GGGCACGAGA AAACCTTTTAC AATNAGCATG AAGAGATAAC CAACCTCACT CCACAGCAGT      60
TAATAGATCT CCGGCATAAG CNCAATCTTC GGGTCTCTGG TGCTGCACCT CCTAGACCAG      120
```

GAAGTAGCTT TNCTCATTTT GGGTTTGACG AACAACTTNT GCACCAGATT CGGANATCTG 180  
 GATACACACA GCCCACTCCA ATACAGTGCC AGGGTGTGCC TGTGGCATTAGTGGTAGNG 240  
 ACATGATTGG TATTNCCAAA NCAGGTAGTG GGNAAACTNC AGCCTTCATT TGGCCCATGT 300  
 T 301

(2) INFORMATION FOR SEQ ID NO:232:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 209 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

ATNGTTTGGG AAGCGCATAT TGCTTCNTC TTCCCCGAAT TCTGGCAACT NTTCTCCTG 60  
 CNATNATGGG CCCTTGGGCA TCATGAACTT NATTACTCCT CACTGGCTGG AATTCAAAC 120  
 GCCCATCTGT AGTGGTCCCG TCGTTGACC ATGCACCTNA GAATCCACGN GANACGGAGC 180  
 CCTCCTTGNC GGACGGGCTG GACGNTTTG 209

(2) INFORMATION FOR SEQ ID NO:233:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 106 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

GGCAGGAGGA GGAGCAGACA GCGGTGGNCA TCNCCAGCGT CCAGCAGGCG GCGTTCGGCG 60  
 ACCACAACAT CCAGTACCAG TTCCGCACAG NGACAAATNG AGNACA 106

(2) INFORMATION FOR SEQ ID NO:234:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 358 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

TTATGAGCAG GGAGATGAAG AAGCAAATCT TGGTCTGCCC ATCANTCCAT TCATGGATCG 60  
 TNCTTCTCCT CAACTAGCAA AACTCCAAGA NTCTTTTATC ACCCACATAG TGGGTCCCT 120

GTNTAACTCC TATGATGCTG CTGGTTTGCT ACCAGGTCAG TGGTTAGAAG CAGAAGAGGA	180
TAATGATACT GAAAGTGGTG ATGATGAAGA CGGGTGAAGA ATTAGATACA GAAGATGAAG	240
AAATGGGNAA ACAATCTTAA ATCCAAAACC ACCAAGGAAG GGAAAAGCCA GNCGGGCGNA	300
TATTTTNGT CCAGCTTAAT GGCACCACCC TTCACTTNGN AAAACCCCCA AGGTTTTT	358

(2) INFORMATION FOR SEQ ID NO:235:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 471 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

GGCACGAGGA CAACCGGGAG CAGCAGCATT TCCTGCAAGA TTGTNACGAG CTGAAGCTCT	60
GGATCGACGA GAAGATGCTG ACAGCCCAGG ACGTGTCTTA TGACGAGGCC CGCAACCTGC	120
ATACTAAGTG GCAGAAGCAC CAGGCATTCA TGGCCGAGCT GGCTGCCAAC AAAGACTGGC	180
TGGACAAGGT GGACAAGGAA GGGCGAGAGC TCACCCTTGA NAAGCCAGAG CTGAAAGCCC	240
TGGTGTCCGA GAAGCTGAGA GACCTGCACA GGCCTGGGA CGAGCTGGAG ACCACCACCC	300
AAGCCAAGGC CCGCAGCCTN TTTTATTGCC AACCGAGCTG AGCTNGTTTG NCCCAGAGCT	360
GTTGTNCCCT GGAGAGCTTG GCTGGAGAGC CTGCAGGCCN CAAGTTGCAC TCCNGTTGAC	420
TACGGGNAAA GGACCTTACC CAGCGTTNAA CATCCTTNTT CAAGAAGCAG C	471

(2) INFORMATION FOR SEQ ID NO:236:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 500 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

GGCAGANGAT CTA CTGTGTN AGGNGAGAGG GCAATTAAAA AGCTGAAGAG AAAGGAGGCC	60
CTCTNTGTAT TCCGTTCCCT CCTCCTTAAT GCCTCCAAGG GTCCTTGCAT CCCTAGTCTC	120
CTAAACTCCA GCTCTGAATT CGCCATCAAC CCATGGAGCA ATTCCAAGGC CCCAGTTACC	180
CATCACCTCC ACACCAGGTG CAAGTTTTGT TTCAGCCCCA AAGGCACTGA GCATTTCTAG	240
TTTGCCCCCT CTGCCCTGNA ACCCCACAGC ATGCCTGTTT GCAGCTCCCT GTGCCCTCGG	300
CACTTCCCCA GGCTCATTTG AAGCAGGTGT GCCTTCGGCA GTTCCCCTAA ATTCCCAGGT	360

GCCTCATNCC TNATGNGNTA ATGGCNGTGA GGGGAAAANT TTTCAAGAAG GTGGAAGAGG	420
CAGCNGGATT NGTTAGGGGT ANCTGTNGTT CANCTTGAGA TGCACAGTGA AGGTTAGGGT	480
AGNTGGGACA GGCCTACCTG	500

(2) INFORMATION FOR SEQ ID NO:237:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 295 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

TGTATTCACC TATTNATTCT GTGGNTATAC ATAGTGTTNG GGTAGTGGA AACTGGGAA	60
GCTTGGGCAG TAGTTNCTCA AGGATTGAAG CTTGTTTCTT TAGATCTGNA GGTAGATATG	120
ACTAGGGGGA AAAACANTGG TNGAGATAAA GGCTACCATT GAAAACCCTG TAGCTCCTAT	180
CTGTGCAATT ACAATCTGGA TGCTTCAGGN AGCCCTTTTT CTGGGTGCAC ANATGTAANA	240
TANCCTACAA GTCTTGAGC AANCCTGTTC TCCTTTACGT TCACAGCTGT GTTCC	295

(2) INFORMATION FOR SEQ ID NO:238:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 437 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

GGCAGGAGCN AGTATATGCG GCAGGCGGGA TGGGCCTGGA CCTACGTCNA CACAACCACC	60
TCCAACACTA TGACATGCTG AAGGACATGT GGGTNTCCCT AGCACCCATG CCCACCNCGA	120
GATATGCTGC CACCTCCTTC CTCCGAGGNT CCAAGATCTA CGTGCTGGGG GGACGNCAGT	180
CCAAGTACGC GGTCAACGCT TTCNAGGTCT TTNACATCGA GACTNGNTCC TGGACCAAGT	240
TTCCCAACAT TCCCTATNAA GCGGGCCTTN TCCAGCTTTG TNACCCTGGA CAANCACTTG	300
TACAGNCTNA GGAGGCCTGC GGGCAAGGTC GCNTNTTACC GGAAGTCCCA AGTTCCTGAG	360
GGACGATGGG ACGTTTTTCC GNAATGGNAA ACAGGGGGGG GTTNGCTGAA GATGGAAAGG	420
TTCGTTNTTT TCCTTNA	437

(2) INFORMATION FOR SEQ ID NO:239:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

GGCACGAGCC TCAGCCTCGC TCATGCGCAN TNTCTNAGGT GCTTTGGACC ATGGTGATCC	60
ACATCGGCCT GAGCGTNAAG AGCTTGGCGG GAGGTTTGGT GCTGTTCTTC TTCTTCACTG	120
CCTTTGCCAC CCTNACCGTG GCCATCCTCC TGATCATGGA GGGCCTCTNG GCCTTTNTCC	180
ACGCACTGCG CTTACACTGG GTTGAGTTCC AGAATAAATT CTACAGCGGG ACCGGTTTCA	240
AGTTCTTACC CTTCTCCTTC GAGCATATTC GGGAAAGGGN AAGTTTGAAA GAAGTGAAGN	300
CCCTTTAAAG GGCCCGTGTG CCCCCAATGT TAACCTTCCC GGCNTTCCTT TCCAAAAGTG	360
GATTAAAGTN GTGGCNTTTT TTTGCCTTNT G	391

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

GGCACGAGCC ACAGTGCAAG CCCCTGTCCC CTGGAGAGAT CCTGGGCTGC ACATCCCCC	60
GACTGTCCAG AGAGGTGGAG GCCGTTNTGT ATCTTGGAGA TGGCCGCTTC CATCTGGAGT	120
NTGTNATGAT TGCCAACCNC AATGTCCCCG CTTACCGGTA TGACCCATAT AGCAAAGTCC	180
TATCCAGAGA ACACTATGAC CACCAGCGCA TGCAGGCTGC TCGCCAAGAA GCCATAGCCA	240
CTGCCCGNTC AGCTAAGTCC TGGGGCCTTA TTCTGGGNAC TTTGGGCCGC CAGGGCAGTC	300
CTNAAGATTC TTGTAGCACC TGGTAATNTN CGATTNCGAA GCCTTGGGCC TTT	353

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

GGCACGAGCG GANCCACGGA GCCCACGGAG GAGCCCACGG AGGAGCCCCA GCGTCCGAAC	60
---	----

GGGCAGACCC CCTCGAGCCG CGAAGGAGCC CGAGAAGCAG CCACGATGTG CGGAATNTTT	120
GCCTACATGA ACTACAGAGT CCCCCGGACG AGGAAGGAGA TCTTCGAAAC CCTCATCAAG	180
GGCCTGCAGC GGCTGGAGTA CAGAGGCTAC GACTCGGCAG GTNTGGCGAT CGATGGGAAT	240
AATCACGAAG TNAAGAAAG ACACATTTCAG CTTGGTCAAG AAAAGGGGGA AAGTCAAAGG	300
TTTTTCGATG GAAGGAACTT TTACAAAACA ANGTTTCAGGC ATTGGGCTTA AAAAGTNGGN	360
GTTTTTNAGN ACCA	374

(2) INFORMATION FOR SEQ ID NO:242:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 291 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

GGCAGGAGGC CCCAGGTACT ATGCAGCTGT GGAGGCCAAG AAGGAGAGAA TGAGCAAACA	60
CGCCCAGACC TTTGGGGCCA AGCAGCCCAC ACATCAGGGG GGCCCTGCAC AGGACCGCGG	120
AGTGTACCTG TCCCTCCTGG CCTCCCTCCG NACACGTNCC CAGTTNCCCG TGGTGGTGTT	180
CANCTTCTCC CGGGGCCGCT GTGATGAGCA GGCCTCAGGN CTNACCTCCN TTGACCTCAC	240
CACCAGTTCG GAGAAGAGCG AGATCCACCT NTTCTGNCA GTGCTGCCTT G	291

(2) INFORMATION FOR SEQ ID NO:243:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 256 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

GGCAGGAGCC TGTTTGAACC TCTNCNAGTC CTGGAGACTG GTGCCCTGAG CTCCAACCAG	60
CGGGCCTCAT CCTACACCCT CACCACCGCA ACTTNTNACC CGAGCAAGAA GCAGCTCCCA	120
GAGAGAAAGA ACGTTCCCAC CTGCNTAGCC ATGGGAGAGG ACGCTGCACA GGCCGAAAAG	180
TTCCAGCACC CTGGGTCTGA NATGCGGCAG GAAAAGCCCT CGAGCCCCAG CCCGNTGCCT	240
TCNTTCACAC NAAGNC	256

(2) INFORMATION FOR SEQ ID NO:244:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

CCCCCAGAGC TGGACAGCCG GGNTGGAGTG CAGTGGTGTA ACCAAGCTCC CTGACAGCCT	60
CTNTNTCCCA GCTAAGGTGA TCTTCCTGCC TCGGNCTCCC AGGTAGCTGG NGTTACAGAT	120
CGAGCGGCAC NTT	133

(2) INFORMATION FOR SEQ ID NO:245:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 253 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

GGCANAGGNA TCCGCAGGGA CTGGCTGACC ATNAACAACA TCAGCCTGNA TGAAAGGCGG	60
CTCCAAGGAA GTACTGGTTT GTGCCTGACT GCCGAGTNAC TGTCCTGGTT ACAAGGATGA	120
GGNGGAGAAA GNGAAAGNAG TACATGCTGC CTCTGGGACA ACCTCAAGAT CCGTGATGTG	180
GAGAAGGGCT TCATGTCCAA CAAGCACGTT TTCGCCATCT TNANCACGGG GCAANGAAAC	240
GTNCTTNCAA GGG	253

(2) INFORMATION FOR SEQ ID NO:246:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 424 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

GGCAGAGCCC CTATCAACTC TTTGGTCGAT CGGCTGGCCC TTCTCCAGGT CAGGAGGATT	60
CTNCAGCAGC TGGGCCTGGA CAGCACGTGT AAGGACAGCA TCGTGGTGAA GGAGGTGTGC	120
GGANCGTGTC CCGGCGNGCG GCCCAGCTCT GCGNTGCTGG CCTGGCCGCT ATAGTGGA	180
AAAGGAGAGA AGACCAGGGG CTAGAGCACC TGAAGGATCA CTGTGGGTNT GGACGGCACC	240
CTGTACAAGC TGCACCCTCA CTTTTCTAGA ATATTGCAGG AAAGTGTGAA AGGAACTAGC	300
CCCTCGATGT GATGTGGACA TTTCATGCTG TTCAGAAGAT GGCAGTNGNA AAAGGGGCAG	360

CACTGNTTCA TTGTTGTGGG CCAAGAGTTT ACAGNAGCAC AGAGGGGGAA NTAGGAACCC 420  
TGGG 424

(2) INFORMATION FOR SEQ ID NO:247:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 439 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

GGCAGAGCAG GTCTGGGCGG GGCACGTTTC CACGGTCTGA CCCGCCTNTC CCGCTGGTGC 60  
CAGGTTGTNT CCAGCGGTTT AAGTGCTGCC AGGTCAACAT CGAGGNAAGG GCTAGGCAAG 120  
TTTTGGTGGA TCCTGCGGAA AACCTGCTTC CTCATCGTGG AGCACAACTG GTTTAAGAAC 180  
CTTCATCATC TTCATGAATT CTNCTGAGCA GTGGCGCCCT GGTGAGGTCC AGGGGAGAGT 240  
NTGAAGGAGG GATTGGCTGG GGAAGGGTGT AGAGAAGCCA GTGGGAAAAG GCTGAGGCCA 300  
AAGCCCAGTG GCTCTNAAAA CAGATTGGCT GTGGTNCCAA GAAGAATGAT CTGTTAAAT 360  
GCTTTTAGGC TGCTGTTTTG AGCCTNTGGG ATTAGGATTC CNAATTGTTC ACATNGTGAT 420  
NCCCTTTAGC ACTGTNCCC 439

(2) INFORMATION FOR SEQ ID NO:248:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 471 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

AAATATGCTG CCAAGATGGG GAATCCAGCT GCTGAGCTTT GACAATAAGA TGGAGCTGGC 60  
AAAGGTGGTA AAGAGCCACC CCAGTGCCAA GGTGTGTCCA GCAGAGGGGC ACTGCGTGTT 120  
TGCATCAGGA TGGTCTGTG NCATTGCTAC CGATGACTNC CACTCCCTGA AGCTGCCTGA 180  
GCCTNAAAGT TTGGGAGTGT CACTGAAATC CTGCAGACAC CTGCTTGAAA ATGCGNAGGA 240  
AGCACCATGT GGNAGGTGGT GGGTGTGAGT TTTNACATTG GGCAGTGGCT GTNCTGAACC 300  
CTTCAGGCCT ATGGTNCAGT TCCATCGCAA ACGGCCCGGN TTCGTGTTTT GAAAATGGGG 360  
CACCCNGGTT GGGGTTTACA AGTTTGCCAC GTTCTTGGG ACCCTTGGGT GGGTGGGGTT 420  
TTCNTGGGC ACCAAAAGGG GGGCCNAAAG TGNAGGTTTT NNAAGGGGTT T 471



(2) INFORMATION FOR SEQ ID NO:249:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 319 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

GGCACGAGAA TGAACCGTGG GGATGACACC CCCCTGCATC TGGCAGCCAG TNATGGACAC	60
CGTGATATTN TACAGAAGCT ATTGCAGTAC AAGGCAGACA TCAATGCAGT GAATGAAACA	120
CGGGAATGTG CCCCTGGCAC TGATGCCTGT TTTTGGGGCC AAGATCAAGT GGCAGAGGAC	180
CTGGTGGCAA ATGGGGCCCT TNTNAGCATC TGTNAACAAG TTATGGAGAG ATGCCTGTGG	240
ACAANGNCAA GGCACCCCTG AGAAGAGNTT TTTCCGAGAG CGGGCAGNGA AGATGGGNCC	300
AGAATTTTCA ACCGTATTT	319

(2) INFORMATION FOR SEQ ID NO:250:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 97 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

CCAGGAGGTG TTGCAGTNAA CCAAGATCAC ACCACTGCAC TCCAGCCTAG GCAACANAGA	60
CTCTNTNTCA AAAAAAAAAA AAAAAAAAAA AAAAAAN	97

(2) INFORMATION FOR SEQ ID NO:251:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 245 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

AATTTTCAGTA ACCGAAAAC TAAGCCTTAG TATGAAAAC TGAGGATTTA TAATTGAAAA	60
TGAAAAAACT ATGTTACTNT CTATCATCAG AATTATAGTC TTTGGTGCTN NGTTTTCAAT	120
GGGGCATATT ACATAAGGTT GTTCTTTTCA CCCCAGAG ACTACTAGGT TACCACTCTG	180
GGGCATTGNC TTTCCACCTT AACCCCTNAA CCAGTAAGNC TNTTACACCC TTTGTAGGC	240

CCACT

245

(2) INFORMATION FOR SEQ ID NO:252:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 182 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

CTGCTGCCCA ACCGGTTGCT GACCAAGGTG GCCGANATGG CGCACAGCAT CCTGGTCTGC	60
AGAAGCAAGA CNTGTGCNAN GTGCACCACG AGCCCCTCAA GCTTTTTTGC CAGANGGACC	120
AGAGCCCCAT CTNTTTGGTG TNCAGGGAGT CCCGGAGCAC CGNCTNGCAC AGGGTGCTGC	180
CC	182

(2) INFORMATION FOR SEQ ID NO:253:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 391 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

GGCAGAGGTT CTTGTCTAT GGCACCCGTA CGTCCAAAGA CAAGAGTGGA GCCTACCTCT	60
TCCTGCCCCG TGGCGAGGCC AAGCCCTACG TCCCCAAGGA GCCCCCGTG CTGCGTGTC	120
CTGAAAGGCC CTTTCTTCTC AGAGGTGGTT GCGTACTATG AAGCACATTC ACCAGGCGGT	180
CCGGCTTTAC AATCTGCCAG GGGTGGAGGG GCTGTCTCTG GACATATCAT CCCTGGTGGA	240
CATCCGGGNA CTACGTCAAC AAGGAGCTTG GCCCTGCACA TCCATACAGA CATCGACAGC	300
CAGGGGTATC TTTTTTCAAA GACCTCAATG GTTTCAAGG TGGCAAGCCC CGAANGGTTA	360
TTNTGAAAGG AAGTTNCCNC TTTCCNGGGC C	391

(2) INFORMATION FOR SEQ ID NO:254:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 212 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

TTTNNNCACG GCTCTCTNGT AATGCAGAAT CTGGGTGANA CTTCCACCCC CACACAAGNC	60
TCGNTGCTCT TCGGCACGGG TCAACGGCAT GATAGGGCTG GTNACCTCAC TTTCAGAGAG	120
GCTGGTACAA CCTGCCTGCT GGGACATGNC AGAATCGANC TCAATTAANG TCATNCAAAA	180
GTGTGGGGTA AGATCGAGCA CTGCCTTGCT NG	212

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

GGCAGAGNAT CAAATATGCT GCCAAGATGG NNAATCCAGC TGCTGAGCTT TGACAATGAG	60
ATGGAGCTGG CAAAGGTGGT AAAGAGCCAC CCCAGTGCCA AGGTTTGTCC AGCAGAGGGG	120
CACTGCGTGT NTGCATCAGG ATGGTTCTGT GCCATTGCTA CCGATGNACT CCCACTCCCT	180
GAGCCTGCCT GAGCCTAAAA GTTTGGGAGT GTTCACTGGA AAATCCTGTC AGACACCTGC	240
TTTNAAAATG CCGAAGGAAG GCACCATGTG GNGGGTGGTG GGTGTGAAGT TTTCACNTTG	300
GCAGTGGCTG TTCCTGAACC CTCAGGGCCT GATGATNCAG TTCCATNGNC AAACGG	356

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

GACTTTGGAT CCAGCTCAAA ATCTNACCTT NTCCTGAGCC CTTGCCTAGC CCCACCTCC	60
ATCTTCGCTG CTCTGCTGCC TGTGCCGGGN AGGGGCTCTG TTTTCCCCT AGAAATCTAT	120
GCCTTGCGCT GGGGGCCAGG ACACCACAGG GGTAGGCTCG TNTACAGCCT CACTAGCCCA	180
AGGGCCTACG AATGCCCTCT TGGGACAGAG AAGCCTGGAA TGGAAGAAAG CTNATGCCAT	240
TNCCTTGGCT GCTGGTTCTT TTGGCATTGG GAANTCTTCC TTCTCTCTAA TGTCATNCTT	300
GCTGCTGTNC CGCTGCATTA TTTCCCTTTA AATNTTTCNG GGANTTGGGG GTGAACNGNT	360
GTTTGCACCN AACCTGGGG ATGTGCTTGG GGGAGGAAGG GGAGGGGGAA GGTCTGGGAA	420
NTTTNTNTN TTTGGCCCAG TTNAGGTTGN AGGNCAGGGG GGNCCCCGTT CTGGAGGAAG	480

GAGAGCNTCC

490

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

GGNAGAGGTG GCTTGAACCC GGAAGTTTAA GGCTGCAGTA AGCTATCATG GCACCCACTG	60
CACTCCAGCC TGCNTAACCC AAAGAGACCT TACCTCTAAA AAACAAAAAA ACGGAATCCC	120
CAAGTAGTTA GTGTTGCATT GTCTGCTGCC GTCCAGAGCC CAGAACGCTT CCTCCAGCTT	180
GGCGCCAAGG TCCCAAAGGG CGCACTGCTG CTCGGCCCCC CCGGCTGTGG GAAGACGCTG	240
NTGGCCAAGG CGGTGGCCAC GGAGGCTTCA GGTGCCCTTN CTGGNGATGG CCGGCCANA	300
NTTTCGTGGA GGTCAATTGGA GGCCTCGG	328

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

NAGAGCACAT CAAGGAAGAN CACAACATGT GGGCACTATC TNTNCTTCAT CGTCCTGGTG	60
AAAGTNAAAG GAACTCCACC GAATATACTG GGCCTGAGAA GTTACGTGGC AGAAATGAAT	120
CAAGGAAAGA AACCTTGACT GGTTCCTCCAG GATGAGAAGC CATGTNATTG GTCAGCAGTG	180
AATTCTGAAA GGAGNACAGT NTGNGCCTGN GGAAACCTG	219

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

CAGAGGACCA CCCGACGAG GAGATGGGGT TCACTATCGA CATCAAGAGT TTCCTCAAGC	60
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CGGGCGAGAA GACGTACACG CAGCGCTGCC GCCTNTTCGT GGGAAATCTG CCCACCGACA	120
TCACGGAGGA GGTACTTGAA GAGGCTCTTC GAACGCTATG GNGAGCCCAG CGAAGTCTTT	180
CATCAACCGG GACCGTGGGT TCGGCTTCAT CCGCTTGGGA ATCCAGAACC CTGGCTGGAA	240
ATTGGCAAAA GCAGAGCTGG GACGGGCACC ATTTCTTCAA GAGNNAGACC TCTTACGGNA	300
TTTCGCTTTC GTTAACAACA TGGGNGTNAG	330

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

TGCTGGAGAA CCAGACCCCA GAGTTCTTNC AGGACGTCTG CAAGCCNAAG TACAGCGGCA	60
CCCTGAACCT GGACAGGGTG ACCCNAGAGG CGTGCCCTGA GCTGGACTAC TTTGTGGTCT	120
TCTTCTCTGT GAAGCTGCGG GNGTGGCAAT GCGGGACAGA GCAACTACGG CTTTGCCAAT	180
TCCGNCATGG GAGCGTATCT NTGAAGAAAC GCCGGTACGA AGGCCTCCNA GGCTGGNCCG	240
TGCAGTNGGG GCGCCATCGG GACGGTGGGG CAATTTTGGG TNGAGACGAT TGAGNAACCA	300
A	301

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

GGCACGAGCC CAATNGGGNT CCCTNCNCA GCCTCTACCT CTCCTNAANC CTNTGANANC	60
CNCCTACACA CACACACAGG CATACTCAGN CCCACTCAA GCTGAGAATG ATCCAACCTCA	120
GCCCTACTTT NCGGATGGAC ATATTAAGGC CANGAGGGG GGNCTTNCC CCAGGTCGTA	180
TGGCAGNGGG G	191

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

GGCACGAGCA GGTCTGGGCG GGGCACGTTT CCACGGTCTG ACCCGCCTTT CCCGCTGGTG	60
CCAGGTTGTN TCCAGCGGTT CAAGTGCTGC CAGGTCAACA TCGAGGAAGG GCTAGGCAAG	120
TNTTGGTGGA TCCTGCGGAA AACCTGCTTC CTCATCGTGG AGCACAACTG GTTTNAGACC	180
TTCATCATCT TCATGATTTT CTTGAGNANT GGCGCCCTGN TNAGNNCCAG GGTNAGAGTT	240
TAGAGGAGGG ATTGGCTGGG GAAGGGTGTT AGGAGAAAGC CANTNGGGAA AAGGCTNAGG	300
CCAAAGCCCA GTGGGCTTNT TNAACACAGA TTTGGCTGTG GGTCCCAAGA AGAATGATCC	360
TGTTAAAGTG CTTTTAGGCT TGNTTGCTTT GAGCCTTTGG GATTAGAATT CCATACTTTT	420
TCACATTGTG ATNCCTTTNA GCAATTTNCC NA	452

(2) INFORMATION FOR SEQ ID NO:263:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 398 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

GGCACGAGCC CCTATCAACT CTTTGGTCGA TCGGCTGGCC CTTCTCCAGG TCAGGAGGAT	60
TCTNCAGCAG CTGGGACTGG ACAGCACGTG TNAGGACAGC ATCGTGGTGA AGGAGGTGTG	120
CGGACCGTGT CCCGGCGGGC GGCCACGCTC TGNGGTGCTG GCCTGGCCGC TATAGTGGA	180
AAAAGGAGAG AAGACCAGGG GCTAGAGCAC CTGAGGATCA CTGTGGGTGT GGACGGCACC	240
CTGTACAAGC TGCACCTCA CTTTCTAGG AATATTGCAG GAACTNTNN AAGGAACTTA	300
GGCCCTCGNA TGGTGATGTG GACATTTTCA TCTGTCANAA GATGGNCANT GGGAAAAGGG	360
GCAGCACTGA TTTACTGNTG TGGGCAAGA GGTTTACA	398

(2) INFORMATION FOR SEQ ID NO:264:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 201 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

GGCAGAGGG TAAATCCTAG CTTCTCGGGA AACTAAGGCA AGAGGATCAC TTGAGCCCAG	60
GAAGGTGGAG GCTNCAGTNA GCTGTGATTG CACCACTGNA CTTTAGCCTG TNTGAACAAA	120
TTTGTGGGCA TAGGAATTCT TCATAATGTT CCTTTATTAA TCCTTTNTTT TTTTTTTTTT	180
TNAAAAGGGN GGCCNCTGAC C	201

(2) INFORMATION FOR SEQ ID NO:265:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 301 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

GGCAGAGGTC AATGTACATT TNATATTAAA AAAAGCCAAA ATAACAATGG GGTGAGANCA	60
GGAGGCCACT ATACCAGTGG CCAAGNAGTT CANATCCTTG GAGGCCGTCT TTGGAGAGGC	120
TCANTGGGAC TCGTATTCTG GGCAGCAGCA CAGCACCGTN TGGGAACAAG GTACACCCTC	180
CCCACACCTG NGCCTTTTCA CCCACAGGGC AAGGGATGTG GCGAGAACTG NNGGGCACAC	240
GTGGAAAACA GTTCAGCCCT GCCCGGGCGN TCTTTTAAAG GNNGAGCTCT AAGGGATCAC	300
	301

A

(2) INFORMATION FOR SEQ ID NO:266:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 507 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

GGGAGGCGGG NGGCCATGCG GNTTNCAGCC CTGAAATCTC CCAGCCGCAG AAGGGCCGGA	60
AGCNCCGGGA ACCTAGAGCT TCCACTCAGT CCGAGCCTGC NAGGTGGGCC GGGAACCCGA	120
ACGGACCCCA GGATCGGGAA GTGGCTCCGG CCTCCAGGCT CCGGGGCCGG CGNCTGAACC	180
CCATCCCTGC TTCCTACGGC ATGACATTGA ACCCCGGTGN TTGCTGACAC CCAGCTCGCT	240
GCCTCCTAAG CATTNCACTT CTGGAGCACC CTGAGTCCCA TTNCGNCCCC GTAGCCCGGC	300
CAAGTTTTC TTTCCATTTC CATCCAGTGG GCAGNGCCAG GTGCACATNC TTTTNTAAG	360
GTGGATGGGC TTTTGACCCC GTGGGTGGTT TTNCCCAGGG NNCCAAAANN CTGATTATTA	420
ANCANCAACA ANAACAACCT TTTNGGGTNA ATTTNNAGCC AGTTTTTTTN CAGCAAGCAT	480

507

TTTAAGGGGG AAANTAGTTN AATTGAA

(2) INFORMATION FOR SEQ ID NO:267:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 122 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

CCACCTGGGA GCAGGTACAG GNTCTCTGAC ATATCTCNAT GGGNTACAAA ATGAAGNTGT	60
ACTNCCAGAC TAACCCCTAC TTCACAAACA TGGTGATTGT CAAGGGGTTT CAGCGCAACC	120
GN	122

(2) INFORMATION FOR SEQ ID NO:268:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 181 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

CGGCGGCCAT TCGGAAAAAC TTCCCCACGG CTACTGCGTC CACGTGGNGG TGGCGTGGGG	60
NACTCCCTGT AAAGNAGAGN GAGCATGGCG CCCGGAANGT CGTGAGTCGA GTCTTTCCCG	120
GGCTAATCCA TGCCNGNGTG GAGGCTTCTG ACGCAAGTTG GNGCCANGT GCTGGATCGA	180
C	181

(2) INFORMATION FOR SEQ ID NO:269:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 296 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

GGCACAGGTC TTTTGCCACG GCTCTCTGGT AATGCAGAAT CTGGGTGAGA CTTCCACCNC	60
CACACAAGGC TCGGTGCTCT TCGGCACGGT CAACGGCATG ATAGGGCTGG TGACCTCACT	120
GTCAGAGAGC TGGTACAACC TCCTGACTGG ACATGCAGAA TCGACTCAAT AAAGTCATCA	180
AAAGTGTTGG GAAGATCGAG CACTCCTTCT GGAGATNCTT TCACACCGGA GCGGTAAGAC	240



AGGAACCAGC CACAGGTTTG CATNGACGGT NNACTTTGAT TGNAGAAGTT TCCTGG

296

(2) INFORMATION FOR SEQ ID NO:270:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 62 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

GGCANAGGTG GCATATTCCT GTAATCTCAG NCTCCTNGGT AGCTGGGACT ACAGNNACAT

60

62

GC

(2) INFORMATION FOR SEQ ID NO:271:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 431 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

GGCAGAGTNT TTTATTTAAC ATGATTTTTTC TATATCGTTA CTGTCGAATG CTAGANGAAG  
 GCTCTTTCCG AGGTCGGACA GCAGACTTTG TATTTATGTT CCTTTTGGT GGATTCTTAA  
 TGACCCTTTT TGGTCTGTTT GTGAAGCTTA GTTTTCTTGG GCCAGGCCTT TACAATAATG  
 CTCGTCTATG TGTGGAGCCG AAGGAACCCC TATGTCCGCA TGGAACTTCT TCGGCCTTCT  
 CAACTTCCAG GCCCCCTTTC TGCCCTGGGT GCTCANGGGA TTTNCCCTG TTGTTGGGGA  
 ACTCAATCAT TGTGGGACCN TTTTGGGNAA TTGCAATTTG GACAACAAAT AATNTTTCCT  
 TGGAAGATGT AATTTCCCAA TCAAACCGGG NGGNATAAGA ATNTTGAAAA AAACCAATTN  
 TTTTGAAAAG G

60

120

180

240

300

360

420

431

(2) INFORMATION FOR SEQ ID NO:272:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 101 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

TGAATGGTGG GCATGGNTCA GAAGGATTCC TATNTGGGCG AACGAGGCCC AGAGCAAGAG

60

101

AAGGCATCCT TCACCTTGAA GTAACCCNAT NGNAGCACGG T

(2) INFORMATION FOR SEQ ID NO:273:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 480 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

GGCAGAGNCA GGCCTTCTCA GGAAGAAAGT GGAGGTCCTG GCTGAGGCCT GCACAGACCT	60
GCTTTCGCAC CAGAAGCAGC TCACCGTGGG CCTGCCGCCC GAGCCCCGGG AAGAAGATCA	120
TCTCTGNGNC CCCTTCCCCC AGAGGAGCTT CANAAAACTN CATCTACGNA GGCCAGTGGG	180
CAGGACATCA GCATTGCCGT CCTTCACGCA GGAGGATTGT GGTTTACCTG GCCATGTTAT	240
GTTTCAGGGNC GCACAGACCT NCTTTTNTGG GAGATTGCTT GAGACTNCGG ATTGGGANTG	300
ATCATTCAGG TTGTTGGGCC ACGGGAGCNT NGGCACGGAG CCTTGAAANT GNTTCAAGGA	360
GGAAGAGGNT TTTTNGAAAN TTTTGATGGA ACCTTCAGNC CTTTGGATT ATGNAAAAAT	420
TTTCTGNAA CCATATTTTT AAGTGGGGGA AAAAGTTTGG GGGTTTGAAA GAAGTTTNCN	480
	480

(2) INFORMATION FOR SEQ ID NO:274:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 418 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

TTGGCTGGGA CTGTCTCCAC GCTGGGGTAC AAGTTCTTCA CGCNCATCCT TGAATCAAAA	60
TTCAAAGTCC AAGACACATG TGGAGTNCAC AACCTCCATG GGATGCCGGG GGTCTGGGG	120
GGCCTCCTGG GGGTCCTTGT GGCTGGACTT GCCACCCATG AAGCTTACGG AGATGGCCTG	180
GAGAGTGTGT TTCCACTCAT AGCCGAGGGC CAGCGCATGC CCACGTCACA GGCCATGCAC	240
CAGCTCTTCG GGCTGTTTGT NAACTGATG TTTGCCTCTG TGGGGCGGGG GGCTTGGAGG	300
CATCATATTG GTNTTATGCC TCCTAGANCC CTGTGCCCTT TGGGATTGGG TNGGCAACCT	360
TCTTCCAAGG TGGGGGGGCA AAGAAGNCTT NAAAAATTCT TCCCTTAACC ANCAACCA	418

(2) INFORMATION FOR SEQ ID NO:275:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 340 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

GGCACGAGCC GGTGTTATCC TCCAGTGCTG AGACAGGCCG TCTCCCTGGC CCGGCGCATC	60
CAGGACCCTC TGATTGAATT TGCCCAGGTG TGCAGTTCCG ATGAAGACAT CCTGTGTCTC	120
AAGTTTCACC CCTTGCAGGA GCATGTGGTG AAAGAGGAGC TGCTCAACGC CTTGTACTGT	180
GTAATTTATC AACCGAGTCA ATGAGGTCGG GGTGATGTC AACCGTGCCA TTNGCCCACC	240
CTTACAGCCA GGCCTTGATC CAGTATGTTT TNTGGCCTNG GACCTTGGA AGGGACCCAC	300
CTACTGAAGA TCCTGGAAGC AGAACAACAA CCNGGTTNNG	340

(2) INFORMATION FOR SEQ ID NO:276:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 303 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

TACACACTTT TAAACAACCA GCTTTCACAG GAATTCACCTC ACTATCATAG GAACAGCACC	60
AAGGGGGAAG GTGTTAAACC ATTCAGGAGA AACTGCCCCC ATGCATTGGN TAATNATCTT	120
CCACCAGGCC CTACCTCCAA CGTTGGAGAT TNCAATTCGA CATGAGATTT GGGCAGGGAC	180
ACAGATCCAA AACATATCAG ACCTAAAAGC AGTTCATGGG AGACCACTGA ACAAGCGCAA	240
AGTCNCCTGA GAATGTGCGT TCAGGGTGTT NCACANAAGA GGCANAGNGG TCGATGTGGT	300
TTG	303

(2) INFORMATION FOR SEQ ID NO:277:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 378 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

GGCACGAGCT CGTGCGTTC TAAGTCACTA GGAGATGGTA AAAGCAATAC CATGAGACTT	60
--	----

CCGAGGCTAG GGTACGAAAG GATGGCTTCT GCGTGGTGCT CANTCTCTCC CAGATCCCTT	120
GCTCTGTAGG AAACCAACCC CCTAAGGCCT AAAGATGGAA GTGACCCAGG TGTCTACTGA	180
TGGATGAACA GATCAACAAA GTGGGATGTA TTCACACAAA GGAATATTAT TCAGGGGGGA	240
AANGGAAGNA AATTCTTGAC ACATGGNTAC AACATGTAAT GAACCTTNGA AAGACATGAA	300
TGCTGGAGTG AAAATAAAAC TTAGTCACAA AAAGGACCCA ATTAAGTNGC ATTGAGNATC	360
CCANTTTNT TATTGGAA	378

(2) INFORMATION FOR SEQ ID NO:278:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 480 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

GGCAGAGGAT TTTATTTACT ATTATTTTAG AAAAAGTAGG CAGTAATTC GAGTCAACTG	60
CTTTTTCTAA ATCATTTAAC GTGTAAATG AGGAACCTA CTGCACAAAT GTAGGGTTAA	120
GTATCACTTT TGAAGGTTA CTTCAAAGTA AGTGNAATTA AGGCTATCAA GGGAAGAATG	180
TTTTTGGCTA TAACTGGCA TAAAGAAAAN GAAGAACTGG GNGAAATTAC TGAAC TAGAG	240
GAAGTNCATC GGAAC TAGAG GTGTTGAACT AAATTATTTG TAGACGTGAA TCCGGCTTTC	300
CATTGTNCCG GGGGAAAATT TCCCATGGT TTNGTTTGGT CTTCTTCGNC CCAGGTTCCA	360
TTAATGGGCC ANGNCCACA CATTTGGGGG TGGGTTTAAG GGNACCGGN AAATTTAAAC	420
CCGTTTAAAA AGGGGGGGGG GGGGGGNCCA AGGNTTCCCC CCNTTTGGGG AAAGTGGGTT	480
	480

(2) INFORMATION FOR SEQ ID NO:279:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 154 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

GGCAGGAGGC AAACANCTCA GCAAGCTCCT TCTGTCCAT GGACACTGGT GTTATACACG	60
GGTTTCCAAC ATGATTCTCT ATTTTTCCTA TAAGAATGTG GNCTATGTGA AACCNCCTTT	120
TCTGGTACCA CNNCCTTTTG NGGGATTTTC AGGG	154

(2) INFORMATION FOR SEQ ID NO:280:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 237 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

```
GGCANAGGGA AAAAGCCATT CTACTAAGTC CTGTCCTTGG ACAATAACAC CAGTAGGNNA      60
ATGCTGAGTT GGAAAAATTA GCAAATCTAG AGTCTTCTCT GGTTCATTTC TATTNATTTA      120
AGCTTTATGG GACTTGCTTT NCGATTAGCT GCAGCTCCTG CCCTTAGCTT CTTTNGTTNA      180
ATTGCCCAAG GGCTAGTGAA GACTTAGGTT CTCCTCCAAG GTTAGAAAAT TNGNTAA        237
```

(2) INFORMATION FOR SEQ ID NO:281:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 435 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

```
GGCAGAGCAC AGATGCTGTC CTGAGCAGAT GGCATGTAAT GCCCGCACCA NCCGTTCTGG      60
GGTCACGTGC AAGAGGCTGG CTGGAAATNA TGCCAGGCAT GCTCTTGCCA CCAGAGAACC      120
TCTTGCCCTG TTCTNATGTG CCCAGAGCC CAGTNTTGGG CCTCCCCTTG AACGCTCCCC      180
TTCGTGCCCC CTACCTGTGG GAAGGTCTCT TCTGAACTGC CCCTGTCCTG TTCCCAACAG      240
GTTCAGGCCA ACAAGGTGAA GAAACTCTCC ATCGTTGTCT CCCTGGGGAC AGGGGGGTTC      300
CCCACAAGTG CCCTGTGAAC CTGTNTGGGA TGTTTTTCGT TCCCAGNAAA NCCTTGGGGA      360
GGTTGGGCCA AAATTGTTTT TTGGGGGCCA AGGNAATGGG GGAANATGGT TGGTGGGATT      420
TTTTNAATTT TGGGG                                           435
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(2) INFORMATION FOR SEQ ID NO:282:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 446 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

GGCAGAGCTT TTGACCCTCA TTTCAAGATC AACAATGCAG TTTCCAATAT CATTTGCTCC	60
ATCACCTTCG GAGAACGCTT TGAGTACCAG GATAGTTGGT TTCAGCAGCT GCTGAAGTTA	120
CTAGATGAAG TCACATACTT GGGAGGCTTC AAAGACATGC CAGCTCTACA ATGTCTTTCC	180
ATGGATAATG AAATTCCTGC CTGGACCCCA CCAAACCTCTC TTCAGCAACT GGGAAAAAAC	240
TGAAATTGTT TGTTCCTCAT ATGATTGACA AACACAGAAA GGNTTGGGAT CCTGCCAGAA	300
ACAAGAGACT TTATTGATGC TTACCTTAAG GAATGTNCAA GGCACACAGG CAATCCTACT	360
TCAAGTTTTC CTGGAGGAAA ACNTCNTTGC GGCACCTGGA CNTTTTTTTTG CCGGANC GGG	420
ACAATTCCCA ATTGGGGTTG GGTNG	446

(2) INFORMATION FOR SEQ ID NO:283:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 319 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

GAGCCGGCCG TNCTGCCAGC TGCNTGTAAT GCAGGAACCT GGCTGCACCA TGGGTATCTC	60
CTCCANCTGC AATTTTCCTT TCTNACTTT NTGCAGGTN ACCTACCATG GGGTCTCCCC	120
ATGTTAAGGT GACTGCAGAG AAAATTAATG GACTTACGAA ATGATTACCT GCANNCGGAT	180
GAGGCTAATA AAGATTTTTG GTTCAAAGGT ATGGTAAGAG AGTGAATTCA GAAAGGCACT	240
GGNAAGAGAA TGGNAAAGTT AGGGTGTGGC TAGAGANGGA NCTTCAAAGA GNCTGCCCCAT	300
GTTGTGGAAC TTCCCATAG	319

(2) INFORMATION FOR SEQ ID NO:284:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 309 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

GGCACGAGGA AAAGAATTAG AGTTCTTGAA AAACTTAAT GATGCTGATC CTGATGACAA	60
ATTTCAATTGT CTGAGAACTC TTCAGGCACT TCTATCACAA GCAGCATCTT TGTCTGGTAT	120
TCGAGCCTCT CAGCATGAAC TTACGAGAGG TGTTAAAAA ATATGGTAAA GATGTTGGTC	180
TTCAATATTAA AGCTGTAAGA TCCTATAGTT CAGCAGTTGT TCCTGGCATT GAAACTCCTT	240

AAAAGATGCA TATNGTACAT GCCGATATCA AGCNAGACAA TATTCTGGGT TAATGGNATN 300  
CCAAAACNT 309

(2) INFORMATION FOR SEQ ID NO:285:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 368 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

GGCANAGGGC AAAGTCCACA CTGGGGAACG GCCCTATGAA TGTAGCCTGT NTGGGAAAAC 60  
CTTCACTACC AGATCCTACC GCAATCGGCA CCAGCAGTTC CACACTGAAG AGAGGTCTTA 120  
TGAAATGTAC AGAGTGTGGG AAGGCCTTCA AACATAGTTC CACCCTCCTT CAGCACAAGA 180  
AAGTCCATAC TCCAGAAAGG CGTCAGGAGG ACAGGGCACA TGGGGAAGGT CGTTAGCTGC 240  
TTAGCACCGT GTTCCATCAG GAAAGGTCTT ATTNCCAGAA AGGNGGTAA GGAGAGTTGG 300  
CCCTTNAGAN TTCCCTTCCG AAAGGGGTTA AAACCTTGGC AAATTCCCAA CAACCCACCC 360  
CCAGGGNG 368

(2) INFORMATION FOR SEQ ID NO:286:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 387 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

GGCAGGAGCG GCACGAGGGA AGATCCTAAT GAGGACATTG TGGAGAGAAA CATCCGAATT 60  
ATTGTTCCCTC TGAACAACAG GGAGAATATC TCTGAATCCC ACCTCACCAT TGANAACCAG 120  
ATTTGTGTAC CATTTGTCTG AACCTCTGTG AAAAAATGTG AATCCTACAG AAGTGGAGCT 180  
GGATGAATCA GATAGTTACT GCTTACCCAG AGCAATATCT GTGAATGGAA GNCAGTGCTT 240  
ACAGAGACCT GCTTACACTT ATGNACAGAA ACAAGTGCTT ACACAGCTGT GGGTTCCCCA 300  
CTTCGTNATT ATGGGTTGGT GAGGACCCAA AATTGGGTGG GGAAAACAGG CCTTTAAANC 360  
CCCCAGATTG GCCTTGTTTA TTCCCTG 387

(2) INFORMATION FOR SEQ ID NO:287:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

TGGGGGCTCT TGGGTTCCCTC GTCTGCTACA CAGAAGTGAG GAGATTCCCC TGACTGATCT	60
CATGTTGTTA AGTGTTCCTAT CCATCCCCAC CACACCCCAA CTTCTTCATG NAAGCAGGTN	120
TCCATCCTTA TAACTTGAGA GGCTGTGAAT CATTCCATAG ATGTNGGTCT TCTGCTACCG	180
NTCTTCACAT TGCCTCTACA TACCAGGTCT TCAGCTGCAT TCTAGGAAAC ATCATATACT	240
ATTGGATTGC AAATCTATAA ATAATATAAG ACAATGGACT GACAGGGGAA AAAAGTTTTT	300
TTTTAAGTTT ACAAACNTCA ATCCCACTTG TTGGCATTTC NAAGGGGGCN ATACTTTTTC	360
CTTNATTCCA CCGTTTAAAG AAGTTTNGGA ATT	393

(2) INFORMATION FOR SEQ ID NO:288:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 508 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

GGCACGAGTG GNAATTTTAA GGGAATGAAA ATTAAACCTG GCTCAATGGG NAAACCTTCT	60
CCTGCTTTTCG ATGTTAAGNT TGTAGATGTA AATGGCAATG TTCTACCTCC TGGACAAGAA	120
GGTGATATTG GCATTCAAGT TCTACCCAAC CGACCATTG GCCTTTTTTAC TCATTACGTG	180
GATAATCCTT CAAAAACAGC TTCAACTCTA CGAGGCAATT CTATATCACT GGGGACAGAG	240
GATATATGGA TAAAGATGGG TATTTCTNGT TTNTTTGCAA GNGCAGATGT TGGCANATAT	300
NCCCTGGTTN TCGATTGCGC CCCTTTGGGT GGNAAATCCC CCATTNNCAC CCCTTANTTT	360
AGAGTNCCCT TTTTCAAANG CCCNACCCCT TCAAGGGGGG NGGTNAAAGT TTTNGGNTTT	420
AAAACCCNTT TCNANGNCCA NTTCAAGGCC CCTTTTAAGG GGTTCGGGGG CTTTTAAAAA	480
CTCCGGGCCT TNAATTCCC CAGGGGGG	508

(2) INFORMATION FOR SEQ ID NO:289:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 402 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

GGCAGAGNCA GAAGCCAAAT CAGGGACTGC TACTCCACAG AGATCGGGAT CAGTTAGCAA	60
CTATCGATCT TGCCAAAGGA GTGATTCAGA TGCTGAGGCT CAAGGAAAAT CCTCAGAAGT	120
TTCTCTTACC TCATCTGTGA ACCTCACTTG ACTCTTCTCC TGTGACCTA ACTCCAAGAC	180
CTGGAAGTCA CACAATAGAA TTTTTTGAGA TGTGTGCAAA TCTAATTAAA ATTCTTGCAC	240
AATAACAGA AAACCTTGCT TATTTCTTTT GCAGCAATAA GCATGCATAA TAAGTCACAG	300
CCCAATGCTT CCCATTGTAA TCCAAGTTAT ACCTAATTTT TAACCGGGGG TTNGGGNTTT	360
NGGATTGCAA TTTGNCACCG GGGTTTGGGA CCAGGTTTTT TN	402

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

GGCANAGCNG AAACCGNGTG CGCANCGATN AAGCAACCTN AAGGACCCCA GGAACCCNGG	60
NCTGNGANGG AACGTGCTCA GTGGGGCCAT CTCCGCAGGC TTATAGCCAA GATGACGGNA	120
GAGGAAATGG CCAGTGAATG AACTGAGGGA GTTGAGGAAT GCCATGACCC AGGAGGCCAT	180
CCGTGAGCAC CAGTGGCCAA GANTGGCGGN ACCACCACTG ACCTNNTCCA TGNAGCAAAT	240
GCAGGAAGAG GANTGCAC	258

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

GGCAGAGCA GATGTTTACA GCAGCACTAT CCATAATAGC CAGAAAGCAG AAGCAGCCCA	60
GATGCCCACC AGCAGGTGNA TGGATGGACA GACTGTGGTC TGTCAGTGAA TGGAATATTA	120
TTCAGCCCTT AAAAGGAATG AGGGACTGAC ACAGCACACA TGAGTNTGGG AAACAGGATG	180
CTGAGTAAAN GAAGTCAGAC ACAAAGGCC ACACATTGTG TACTGTGTGA TTCCATTTCT	240

GTGNAATGCC CAGATTAGCA ANTCCGTAGA AACAGAAGTA GATGAGTGGT TGCCAGGAGA	300
TGGGGGAGAA GGAGCGGGGA GTATGTTTCAT TCAGNCTGGA TTCNTTAAAC AAATGCCACA	360
GANGTTGTTT TAAACAACAG ACATTATTTT TCANGTTTTG GAGGTGGAGT TCTAGGCGNG	420
GTGCCTTCAA TTTCATTCCC ATGAGGCTTG TTCNTGGTTG CAGAGGCCAC CTTTTATTTG	480
TTCCACANAN TTTTCC	496

(2) INFORMATION FOR SEQ ID NO:292:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 238 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

ACGNNTNAGT NGCCAACTAC GTGGTCCAGA AGATGATTGA CGTGGCGGAC AGGACCAGCG	60
GAAGATCGTC ATNGCATAAG ATCCGGCCCC ACATCGCAAC TCTTCGTAAG TACACCTATG	120
GCAAGCACAT TCTGGCCAAG CTGGAGAAGT ACTACATGAA GAACGGTGTT GACTTAGGGC	180
CCATCTNTGG CCCCCCTAAA TGGTATCATC TGAGGCAGTG TTCACCCGNT GTTNNCNT	238

(2) INFORMATION FOR SEQ ID NO:293:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 397 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

GGCAGAGGGA AATGGATCAN AGGATTCAGG CTGCAGAACA TAAGACACGG AAAGACGAAA	60
AACGCAAAGC TGAGGAAGCC CTCAGTGACC TCAGACGTCA TATGAANCTG NAAGTAGGAG	120
ATCTGCAGGT GAACCATTA AAGCTAAGA AAGCTCGAAG AACAAATCAA ACGCGTAAGT	180
CCAAAAGGAA GATGTGGCTG CATTGAAAAA ACAAATTTAT GATTTATCCA ATGGGNAAC	240
CAGAAGTTAA GAAAGACCTT TTAGAAGCAC AGACAAACAT AGCCTTTCTT CAGAGTGAGT	300
TAGATGCTTT TGAAAAGTGG TTATGCTGAT CCGAGTCTGA TTACTIONAGG GNTCTTGGA	360
TTATTCCGGG CTTACCCCNAG AGGTTCGAAT TNGTNTT	397

(2) INFORMATION FOR SEQ ID NO:294:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

GGCAGAGTTT CAAACAGGTA TCTAAGAACT TCAGTGAAGT ATTCCAGAAG TTAGTACCTG	60
GTGGCAAAGC TACTTTGGTG ATGAAGAAAAG GAGATGTGGA GGGCAGTCAG TCTCAAGATG	120
AAGGAGAAGG GAGTGGTGAG AGTGAAGAGG GGTTCCTGGCT CACAAAGCAG TGTCCCATCA	180
NTTGACCAGT TTACTGNAGT TGGAATTAGG GTGTCATTTA CAGGAAAACA AGGTGAAATG	240
AGAGAAATGC AACANCTTTC AGGTGGACAG AAATCCTTGG TAGCCCTTGC TCTGATTTTT	300
GCCATTNCAG AATGTGACCC GGCTCCTTTT ACTTGTTTGA TGAATTGACC AGGTCTNGGT	360
GTTCCAGCAC AGAAAGGCTG TTTTCAGTTT GGTTTTGGAA CTTGCTGTAC AGTTCATTTT	420
TTACACTANT TTTNGGCNGA ACTGTTGGGT CANTGNCATT T	461

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

GGCAGAGCC AGTATTTGGT ATCTNTNTCT AGAGCGAGCA AGAGAGGGAG AGAGGAGGAA	60
AAAATACACA TANTACAAAC ATACATGCAT GCACACATAC ATACACATGT ATACACACAC	120
ATAATTTGAA AACTGNTTGG CACTTCAACG NTGCTGAAAT TGTTTTTAAA TTGAAGTTTC	180
TTTCTTCCAC AAAGCAGCCG TTTCTATTCA AATGGANATT CAGTACCAGA GNNTAAATGT	240
CTATGTAGTC ATACTGATTT TAGATAGNTA AGGGCTACAG CATACTANNT CGACAACCAA	300
NTTTGTCATG TGAATAAACC GTTTACTTTC AGTTGGGGCT TACCATTACT GGTTTTCCGC	360
TTGGGGGNNT TTTT	374

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

GGCANAGCCA GACGGA	ACTG GAAA	ACCAGC TGGAGT	TACAA TAAGAGG	CGA GAAAGAGA	AC	60
TGCACAGAAA GCATGT	CATG GAACTT	CGGC AACAGC	CAAA AACTTAA	AG GCCATGG	NAA	120
ATGCAAATTA AAAAAC	AGTT TCAGGA	CACT TGCAAGT	TACA GACCAA	ACAG TATAAAG	CAC	180
TCAAGANTCA CCAGTT	TGGTA AGTTACT	TCCA AAGATT	GAGC ACAAAC	ANT CTAAAG	AACA	240
CTGAAGGATG AGGCAG	ACAA GAAAACTT	TGC CATT	TTTGGCA GAGCAGT	TATG AACAGGG	TAT	300
AATTGNNATG ATGGCT	TCTT CAAGCN	TTAC GGCTAGT	TGA GGCTCCAG	GA GGCAGTT	GCC	360
CGGGCCTTGN GGNTAC	CG					378

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

GGNAATGGTT ACAAAG	CAAC CATTGATT	AG AAGTATG	CGA ACTGTAAAA	GGGGA	ACTTT	60
AAAGTTAATA TCTGGT	TGGG TGAGCC	GGTC CANTGAN	CCA CAGATGGT	CG CTGAAA	ATTT	120
TGTTCCCCCT CTGTTG	GATG CAGTTCT	CAT TGTTTAT	CAG AGAAATNT	CC CAGNTGG	TAG	180
AGAACCAGGA AGTGNT	NAGT ACTATGG	CCA TAANTTG	TCA			220

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

TTTTTTTNTT TTTTTTTTTT	TTTTTTTTTT TTTTTTTTTT	TTTNNTTTN	50
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(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

GTAATGCTCC TTTNNCCCC CGGCAAGNTC TCAACGNCCC TAAACCTCTA TATCCCCACG	60
ATGGCCTTCA TTA CT TACGT NCTCCTGGCT GGAATGGCAC TGGGCATTCA NAAAAGGTTC	120
TCCCCTGGNA GGTNNTGGGC CT	142

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

GGCANAGTTG GCACCCCTG GCAAGGCNGG TGGGGGCNCC GGGCCCANCC TCCCCAGGC	60
TTGGTGTACC CATGTGGTGC CTGTCCGAGT AAGGTGAACN ATGATNAGGA ATGCNAGNCT	120
GTGTAAGGCC TCCTGCCAGA AATGGTTCCA CCGTGAAGTG CCACAGGCAT GGACTAAAAG	180
CGCCTATGGG CTGCTGNACC ACTGTNAGCT TCTNCCGTCT GGGCCTGCAA TCTCTGCCTC	240
AAGACCAAGG AGATCCAGTT CTGTCTACAT CCGTNAAGNG GCATGGNGGC AGCTNGTGGC	300
TNCTAAACGA ATGGG	315

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

TGCCCTGGGC CTGNA CTGNG GGTTC TGGTG GGACATNATT TATTGGGAAC CATGTTGCAT	60
GCATNAAGGG AGTGNCGCAA AAGCAATGCA GCAGAACGCA GGGNGCCTCT GTGAGGNCAC	120
ATTGTGGNGG ATGGTGTGT CTTAGNTGAG AAGATCACTG NTGGAACTT CCTGGCT	177

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

CCAGCTGAAT TTTAAAAAANT ATTTAATAGT GACAGGTCTN ACTGTNTTGC CCAGGCTCGT	60
TTTGAACCCC TGGGNCCAGG CGCTCCTCCN ACCTTGAACC TCCCAAAGTT CTGGGAGTTA	120
CACATGTGAG GCCANCACAC CAGGNCCAGA CTGGGTGAAT TTATGAANGA AATTTAACTT	180
CTGCCCACAC CGNCCNGCCT CCCC GCGAGA	210

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

GGCACAGCGG GCTGAGAGGA GCGTGGCTGT CTCCTCTNTN CGNCATGGNT GTGCTCGGCC	60
ACNGATATCG GTGTACTCCG AAAAGGGGGG AGTCATTTGG CAAAAATGTC ACTTTGCCTG	120
GCTGTATTCA AGGCTCCTAT TCGACCAGAT ATNGTGAAC TGTTCATCG CGNACTNTGC	180
GNCAAAAACA ACAGNCAG	198

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

CACATGAAGT GTTACAAGTG TTGAGGACTG CGGGAAGCCC CTGTNCGNTT GAGGCAGATG	60
ACAATNGCTG CTTCCCCCTG GGACGNTCAN TGCTGTGTGCG	100

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

GGCAGAGCGA AAAA ACTTCC ACTTCCACGA CTGGAGTGTG TGCCAGCCTG TGGTGAGGGC	60
--	----

TTCTACCCAG AAAGAGATGC CGGGCTTGCC CCACAAAGTG TGTTTGAAGG TGTGAACGAG	120
AACTGCTTGT AGCTGTGCAG GCTCCAGCAG GNAACTGTGA GCAGGTGTGA ANACGGGCTT	180
CACACAGCTG GGGNACCTNC CTGCATCACC AACCACACGT GNCAGCAACG CTGACGAAGA	240
ACATTCTGCA AGAATGGTGT AAGTNCCAAC CGGCTGTGCG AAACGNTAAG CTNCTTGCAT	300
TCCAGTTTCT GGCTGGCCNG CACGTTGACC TCCTGGGNCC GGGGT	345

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

CATGCACTTT GCCTTCGGA ATGGCTGTAC ATTCAAGATA CTTGTCCAAT GTGCCATCAG	60
AAAGTATACA TCGAAGANAT NATCAAGGAT AATTCAAATG TATCTAACAA CAATGGATTT	120
ATTCCACCCA ATGAAACTCC AGAGGAAGCT GTAAGAGAAG CTGCTGCTGA ATCTGACAGG	180
GAATTGAACG ANGATGACAG TACAGATTGT GAATGATGAT GTTCAAAGAG AAAGAAATGG	240
GAGTGATTCA GCACACAGGC GCANAGCTGA AGANTTTAAT GATGGATTAC TGACTGATGA	300
AATTAGCTTT TATTAATGGT TGAGGTATTT GTTTNAAATT CCAGTTCCNT CCAAATGGGG	360
TAATATCCCT TCACCTTCAT GTGTAACCAG GCACAAAAAC AGTTTCATGT GGATCCGTGG	420
ATGGGTTTTN CNTTTACNGT NGATGTGNTA C	451

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

GGCACGAGGC CAACGGTACC TGTTTATGCG AGGAGGGCTA CGTTGGTGAG GACTGCGGCC	60
AGCGGCAGTN TCTGANTGCC TGCAGTGGGC GAGGACAATN TGAGGAGGGG CTCTGCGTCT	120
NTNAAAGAGG GCTACCAGGG CCCTGACTGC TCAGCATTGC CCCTCCAGAG GACTTGCGAG	180
TGGCTGGTAT CACGAACAGG TCCATTGAGC TGGAATGGGA CGGGCCGATG GCAGTNACGG	240
AATATGTGAT CTCTTACCAG CCGACGGCCC TGGGGGGTNT CCCAGNTCCA GCANCGGGTG	300

CCTGGAGATT TGAGTGGTGT CACCATGANG GAGCTGGAGC CAGATCTTTC CATNCTCAAG 360  
GGCTACAATT TAAGACGTTC ACAGNGACCA CCTTGGAGTG CAANGGGNGC CTTTT 415

(2) INFORMATION FOR SEQ ID NO:308:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 312 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

GGCANAGGGT AGACGGAGCC GCCATCCGCA CTGCAGTCCC CTCTCGGCTG CTTGCTCAGC 60  
CTGCTCCGGC CCCGGTCTGC CCCCACGGAG CTCCGGGCAC TTGTGGCAGA CGAGCCCGAG 120  
GACCTGGACA CGGAGGACGA GGGCCTCATC AGCTTCGAGG AGGAGCGGGC CCAGCTGTCC 180  
TTCAACACGG ACACGCTCTG CTGACCACCC AGAGCTGGGC CANGGAGGAC ACGCTCCACT 240  
GACCACCCAG AGCTNGGCCA AGGACTTAAC AATGGGGGAC ANAAGTTCCC CANTTGCCTG 300  
GCNAAGGGCT GG 312

(2) INFORMATION FOR SEQ ID NO:309:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 210 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

ACAGGAACCT NGTGTCTNGT GGCTNGCCCG NGTGCGTGAT NATGAAGGGA GATTCTATG 60  
TCATTGAATA TGCTGCCTGT AATGCCACCT ACAATGGAAA TTGTTNACCC TGGGAGCGAC 120  
TTCGGCCAGN TAATCCCAAT CCCCTTGGCA ACCAAAGGNC AGCTTCTTGA AGGTTACCAT 180  
GGGCTGTGCC CGNGGGATCT NGAGAGNAAG 210

(2) INFORMATION FOR SEQ ID NO:310:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 118 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:



GAAAGNGGAC GCCCAGGGGT GCTGCATNGC ACAACCAAGT TTTTGTGACAG CGGGAGNGGN 60  
 CCCGGGNGCA GAGGTAGTAC GCTCAACAAG ATGTGTTAAA GAAATCTTAC TCCAAGGN 118

(2) INFORMATION FOR SEQ ID NO:311:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 104 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

CACCTCCGAG AGCCTGGATG TNATGGCGTC ACAGAAGAGA CCCTTCCCAG NGGCACGGNT 60  
 CCAAGTACCT GGNCCACAGC AAGTGACCAT NGGACCATGC CAGG 104

(2) INFORMATION FOR SEQ ID NO:312:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 270 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

ACTTTGGACG TTCAATGTCT GTGGAGAAGA TAGACATTAG TCCGGTTTTN CTTCAAAAAG 60  
 GAAGCACAAA GATTGCNCTA TATGGTTTAG GATCCATTCC AGATGAAAGG CTCTATCGAA 120  
 TGTTTGTNAN TAAAAAAGTA ACAATGTTGA GACCAAAGGN AAGATGAGAA CTCTTGTTTT 180  
 AACTTNTTTT TGAATTCATC AGAACAGGTG TAAACATGG GAGTACTAAC TTNNTTCCAG 240  
 AACAATTTTT GTTGANTTC ATTGANTCTT 270

(2) INFORMATION FOR SEQ ID NO:313:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 453 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

GGCACGAGGT ATTTTNACT GGATATTGCC TTTNTNCTTT TNCTTGGTGC TGCCTTGTTA 60  
 TACTTNCTCT TGTCTGGGT GANAAAATTT ATCTACAGAN NAATCAAAAG TTTGTGGTCT 120  
 AGAAATAAGC ATAGCACAGT TAATGGNCAT TACCACAATG GAATCCTCAA TGGCAAGTAC 180

ANAAGAAATG GCCATATTAA ACATGAAAAG AAAGTGAAAT GAGCCAACAG CCCAGGTGAT	240
AGAAATAAAT TGGTTCACCTC ATTGAATTTT TATTGCTATT ATTTAGTCTA ACAGCTTACT	300
TAAAAGTAAA ACATCAGTAA ACAATTCTTA ACATGCCCTT ATGAGANCTA CTTAATGAAA	360
TTCCTGTGGG ATTNAAGGTG GCTGTAAAAA GCACAAACCT AAAATNGCAG AAATGTNNTT	420
NATTTCAAAT ACTGATGTAG GGGGTTTTTG GCA	453

(2) INFORMATION FOR SEQ ID NO:314:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 323 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

TTACAGAGAA CATATGCACA CTANNNGAT CTCACAATTA TCAACAATGA AATTNATGAG	60
ACAATCAGAC ATCTGGNGGA AGCTGTTGAG CTCGTGTGCA CAGCCCCACA GTGGGTCCCT	120
GTCTCCTGGG NCTATTAGGN CTNTCCCCAG ATATCTGGGG CATAACTGGG AGCACCTCAT	180
TTGTGGAAAA GCCTCTTTGT TATCGGGCTT GTGTCAGCAG GTCATGGTCC CTAGAGACTA	240
CCTAGTTGTT AGTGTTGACC TACATTTGAT AATTAATTGT CAGTTNCNAN TAGTTANGGG	300
GGGGGAAAAA NCATTTACAC ACT	323

(2) INFORMATION FOR SEQ ID NO:315:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 391 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

GGCANGAGGN GCCCGCGGGA TTGTTCAACC GCGCCGTGAG CCGGCTGAGC AGGAAGCGGC	60
CGCCGTCAGA CATCCACGAC AGCGATGGCA GTTCCAGCAG CAGCCACCAG AGCCTCAAGA	120
GCACAGCCAA ATGGGCGGNC ATCCCTGGAG AATCTGCTGG AAGACCCAGA AGGCGTGAAA	180
AGATTTAGGG AATTTTAAA AAAGGAATTC AGTGAAGAAA ATNTTTTGT TTGGCTAGCA	240
TGTGAAGATT TTAAGGAAAA TNNCAAGGTT AAGACGCNGA TGCAGGAAAA GGCAAAGNG	300
GTTCTACATG ACCTTTTNT TCCAGCAAGG GCCTTCNTCA CAGGTCAACG TTGTAGGGGG	360
CCAATTTTCG GGTTCACNG GAAAGNTTCC T	391

(2) INFORMATION FOR SEQ ID NO:316:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 355 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

AAACAGGCTG AGGAGGTTCC GAGGCTCAAA GGAGGGGAAG GAGCCCCGAG GAGGCTCTGN	60
ANTTGATGTC ACTTAGGTCC AGGGCATCCN TGGGAAGGAG AGAGTAGTGA CACTCAGGAT	120
CCAAAAGCTA GCCCTGCCCA CCCAGCCCC TGGACCTGCT TACCTGGGTG TGCNACCTGC	180
TCCGGGGGGT GGAGGTGCTC CCCACAGTCC GGGCCAGGAC AGCCTCAGGG GAGAGTNAAG	240
GCCTGCAAGA GGGNAAGCGG AGACAAGGAG GGTGTCCAGG GCTAGGGAGT NCCGGTTGAA	300
ACCAGTTTTG TCCCTGTTGC AAGNTTCCAG GTTNCCGNTN GACAAAACAA GCAGG	355

(2) INFORMATION FOR SEQ ID NO:317:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 465 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

AAACAGGCTG AGGAGGTTCC GAGGCTCAAA GGAGGGGAAG GAGCCCCGAG GAGGCTCTGN	60
ANTTGATGTC ACTTAGGTCC AGGGCATCCN TGGGAAGGAGA GAGTAGTGAC ACTCAGGATC	120
CAAAANCTAG CCCTGCCCAC CCCAGCCCCT GGNACCTGCT TACCTGGGTG TGCACCTGCT	180
CCGGGGGGTG GAGGTGCTCC CCACAGTCCG GGCCAGGACA GCCTCAGGGG AGAGTNAAGG	240
CCTGCAGNAG GGNAGCGGAG ACAAGGAGGG TGTCCAGGGC TAGGGAGTNC CGGATGAAAC	300
CAGTTTGTTT CCTGTGCAAG TTCCAGGNTC CCGTTGACAA ACAGCAAGGT GCCACATTCA	360
GGNCATTAAA AATTNGTGCA TTTGAAGCAG CATTTGACAG TTTNAAATTC TTCCTTTGNT	420
GNATTCCAGG CCCTTTTTCT TTAAACAAN GGATTGGGG CATT	465

(2) INFORMATION FOR SEQ ID NO:318:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 336 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

TGACCAAGCT TCGGGANGAT GGGCAGGGAG AAATGCCACC ANTACTGGCC AGCAAAGCGC	60
TTCTGCTCGC TAACCANTAC TTTTGTGTTA ACCCGATGGC TGANTACAAC ATGCCCCATT	120
ATATCCTGCT TGANTTTCCA AGGTCACGGG ATGCCCCGGA ATGGGCAGTG CAAGGAACAA	180
TCCGGGCAGT TCCANTTGCA NAGACTGGCC AGAGCAGGGC GTGCCCAAGA ANAGGCGAAG	240
GGAATTGCAT TGANCTTCAT CGGGGCAGGT GCNATAAGAN CCCAAGGAGC CAGTTTGGG	300
ACCAGGATGG GGCCTATNCA CGGGTGGCAC TGCANT	336

(2) INFORMATION FOR SEQ ID NO:319:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 354 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

GGCAGGAGGT TATTTTTTAC TGGATATTGC CTTTNTNCTT TTNCTTGGTG CTGCCTTGTT	60
ATACTTTCTC TTGTCTTGGG TGACAAAATT TATCTACAGA NNAATCAAAA GTTTGTGGTC	120
TAGAAATAAG CATAGCACAG TTAATGGGAC ATTACCACAA TGAATCCTC AATGGCAAGT	180
ACANAAGAAA TGGCCATATT AAACATGAAA AGAAAGTGGA AATGAGCCAA CAGCCCAGGT	240
GATAGNATAA ATTGGTTCAC TCATTGAATT TTTATTGCCC ATTATTNGT CTAACAGCTA	300
CTTAAAGGTA AAACCATCCG TNAAACCATT CTNACCAGGC CCTTTNGGGG TCCN	354

(2) INFORMATION FOR SEQ ID NO:320:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 345 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

GTGTTTCGANT GGAACATGCT CAAATTTGGT GCCAGCCGGG CCGCCGATGA CGCCGAGCGG	60
GAAGNCCAGG GACCGAAAGG AGCGGCTGAA AACTCGCGG AACCCGGCTA CCCGNGGCCT	120
CCCTTCCACA GCCTCCGGCC GCCTGCGGGG GAACGCAGAA GTGGCTCCCC NCANACCCCT	180
TNACCCCTAC CTTCANACAC GGNTTAACAN CTTCCCCCG GCCCGTTTTT CGGCATNGGA	240

GAGAGAGCGG AAAGTGAAGT TATGCGGGNT GCAACCGGGG GGGGCCCCCG TTAAACATT 300  
TTCCTTGGTT NCGAACCTTA ANAGGNCCGA CAAAGATTAN CTTTT 345

(2) INFORMATION FOR SEQ ID NO:321:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 376 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

GGCACGAGGG AAGGTGAAGA AAACGGAGAT AATACTATTT CCACTGGTCT GTTGACAGT 60  
GAGGCTGACA GATGCCCAAT ATGTCTTAAT TGTCTATTAG AAAAGGAAGT TGGTTTTCCA 120  
GAAAGCTGTA ATCATGTCTT CTGTATGACT TGTATTCTTA AATGGGCAGA GACACTGGCT 180  
TCATGTCCTA TTGACCGTNA AACCTTTTCA GGCAGTGTTT AAATTCAGTG CATTGGGAAG 240  
GTTATGTTAA GGTTCCAAGT AAAAAACAG CTGAGGGGAA ACAAAGNCC AGGAAAAATG 300  
GAAACTCCT TTGGGGAAAC AGGTCTCCNG TCCNGGAAAA TTTCTTAAAA GGCTGTTTTA 360  
GGGNGGAAAA GNCCCT 376

(2) INFORMATION FOR SEQ ID NO:322:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 437 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

AATGATGAGT TCTATACTAA ACAAGATGTA ATTATTACAG CATTAGATAA TGTGGAAGCC 60  
AGGAGATACG TNGACAGTCG TTGCTTAGCA AATCTAAGGC CTCTTTTAGA TTCTGGAACA 120  
ATGGGCACTA AGGGACACAC TGAAGTTATT GTACCGCATT TGAAGTGAAG CTTACAATAG 180  
TCATCGGGAT CCCCCAGAAG AGGAAATACC ATTTGTACTC TAAATCCTT TCCAGCTGCT 240  
ATTGAACATA CCATACAGTG GGGCAAGAGA TAAGTTTGA AAGTNCCTT TTCCCACAAA 300  
CCTTCATGTT TAACAAATTT TGGGCAANCN NTTTCATCTGC AGGAGGAGTC TTACAGAGGT 360  
TCCGGGTGGG NCANATTTGG GANGGNTTTT TCAAGTTTAA AAGGTNCCTT GGCCGGGGCC 420  
CGGGAATTGG TCCCCGT 437

(2) INFORMATION FOR SEQ ID NO:323:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 320 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

AATGNTGAGA TCTATACTAA ACAAGATGTA ATTATTACAG CATTAGNTAA TGTGGNAGCC	60
AGGNGATACG TAGACAGTNG TTGCTTAGCA AATCTAAGGC CTCTTTTAGA ATCTGGANCA	120
ATGGGCACTA AGGGACACAC TNCAAGTTAT TGTCCCNCA TTNCTGGNG TCTTCNCAAN	180
AGTCCATCGG GNTCCCCCAG AAGCGGGANA TCACNTTGG GTACTCTAAA AATCCTTTTC	240
CAGGTGCTTT TNGAACNTGN CCCTAACATG GGGCAAGAGA TAAGTTTNAAGTTCCTTTT	300
TCCCACAAAC CTTNTTTTTT	320

(2) INFORMATION FOR SEQ ID NO:324:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 409 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

GGCAGGAGCT GTCCTGACCC TNAGGCCTAT GCTCAGTCCA TCGCAGACGN CCGGNTCGTG	60
TTTGAAATGG GCACCGAGCT GGGTCACAAG ATGCACGTNC TGGGACCTTG GTGGTGGCTT	120
CCCTGGNCAC AAAAGGGGCC AAAGTGAAGA TTTGAAGAGA TTGCTTCCGT GAATCAACTC	180
AGCCTTGGAC CTGTACTTCC CAGAGGGCTG TGGCGTGGGA CATCTTTGCT GAGCTGGGGC	240
GCTTACTACG TGAACCTCGG CCTTCACTGT GGGCAGTCAG CATCATTGCC AAGAAAGGAG	300
GTTCTGCTTA GACCAGCCTG GGCAGGGAGG AGGNAAAATG GTTCCANCT CCAAGACCAT	360
CGTGTTACCA CCTTGNATGA GGGCGTGTAT GGGATCTTTC AANTCATNC	409

(2) INFORMATION FOR SEQ ID NO:325:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

AATGTGATGG TGTATGTTGG GATTCCCATC GGGGAGGGTG CTCATNAATG AAGAGGTACT	60
CAAGACAATT NACGAGGGAG ATGCCGATGA GGTGACGAAG CAGAGGATTC ATGATGGAAA	120
AAAGAAGCCA GGTGCTTTNT NGCACATCTT TNCAGCCAAG GATGCAGAGA AGATCCNNGA	180
GCTGCTCCGA AA	192

(2) INFORMATION FOR SEQ ID NO:326:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 408 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

AGCTCCGCAG GCACTNCANT AAAAGCCTGA CCCAAACATT TGGAGATGAC AAGTACTCAC	60
TGGCCCGCAA GNGGTGCTCA CCAACATGTG CTCCCGGNCC ATGCAGATGG CACTGTACTT	120
CTGCTCGGGG CTGCTGCAGG GACCCAGCGC ATTCCGGCAC TACGCGCTCA ATGTGCCCCCT	180
GTACACACAC TTCACCTCGC CCATCCGCCG CTTTGCCGAC GTCCTGGTGC ACCGCCTCCT	240
GGCTGCCGCG TTANGCTTTT AGGGGAGCGA TTAGACATGG TCGCCTGGTN ACCCTGCAGA	300
AACAGGCGGG ACCATGTTAA CGGACCGTCG GCATGGGTNC CCAAGCGNGT GCAGGAGTTT	360
CAGTTACCAT TTTNTTNTTT GGTGTTTTT GGGTTCAAGG ANGAGTGG	408

(2) INFORMATION FOR SEQ ID NO:327:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 392 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

GGCACCAGTA CATGGCTACA TTTTATGAAT TCTTCAATGA GCAGAAATAT GCTGATGCGG	60
TGAAGAACTT CTTGGATCTG ATTTCTGCTT CGGGGAGAAG AGACCCCAAG AGTGTTGAGC	120
AGCCCATCGT GCTTAAAGAA GGGTTCATGA ATCAAGAAGG GCCCAAGGAC GGAAGCGCTT	180
TGGGATGAAG AATTTTAAAG AAGAGATGGT TTCGCTTGAC CAACCATGGA ATTTACCTAC	240
CACAAAAGCA AAGGGGACCA GCCTCTCTAC AGCATTCCCA TCGAGGAACA TCCTGGGCAG	300
TGGAGGAAGC TNGAGGAGGG AGTGTTTTCA AAATGGAAAA ACNTGTTTCC AGGTNCATTC	360
CAGTCCAGAG CGTTGNNCTG TTACATCCAG GG	392

(2) INFORMATION FOR SEQ ID NO:328:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 505 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

GGCANAGGGG AGCTGCCTGG ACCAGCCCAA TGGTTATAAC TCCCACTGCC CGCATGGTTG	60
GGTGGGAGCA AACTGTGAGA TCCACCTCCA ATGGAAGTCC GGGCACATGG CGGAGAGCCT	120
CACCAACATG CCACGGCACT CCCTCTACAT CATCATTGGA GCCCTCTGCG TGGCCTTCAT	180
CCTTATGCTG ATCATCCTGA TCGTGGGGAT TTGCCGCATC AGCCGCATTG AATACCAGGG	240
TTTTTCCAGG GCCAGCCTAT AAGGAGTTCT ACAACTGCCG CAGCATTCTGA CAGCGAGTTT	300
CAGCAATGCC CATTGCATTC CATTCCGGCA TGCCCAGGTT TTGGAAAGAA AATCCCGGGC	360
CTGCAANTGT ATGATGTTGA GNCCCCATNG GCNTNTNAAG GTTTACAGTN CCTGNTTGAC	420
AAAANCCTTG GTCANAATGN TTNAAAANTA AAGGTTTGTA AAACTTTTTT TGGGTTATTT	480
TTTCAAAAGG TGGGGTTTTT CACCC	505

(2) INFORMATION FOR SEQ ID NO:329:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 455 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

GGCAGAGCCA GAACCTACTG GACCGGGATG TTACCTCCAA GTCCGACCCC TTCTGTGTCC	60
TCTTTACAGA GAACAATGGC AGATGGNTCG AGTACGACAG GACAGAAACC GCGATCAACA	120
ACCTCAACCC CGCCTTCTCC AAGAAGTTCG TGCTTGACTA CCACTTCGAG GAGGTACAGA	180
AGCTCAAGTT CGCGCTCTTT GACCAGGACA AGTCCAGTAT GCGGCTGGAC GAGCATGAAC	240
TTCTTGGGCC AGTTCTCCTG CAGCCTGGGN ACGATTGCTT TCCAGCAAGA AGATCANTAG	300
GCCTCTGCTG CTGCTGAATG ACAAGCCTGC GGGGAAGGG CTTTGATTAA GATTGTTGC	360
CCCAGGAGTT GTTCCGACAA ACCGGGTTC TACATTAAG NCTGGGGGGG CAAGAAGGTT	420
TGNNCAAGNA AGGGACCCTT TTTGGGAAGT TCANA	455

(2) INFORMATION FOR SEQ ID NO:330:



- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 434 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

CCTTTNAGGA TGCTCCTACA GCAGCTGCCT AATACTTTNA GTTGCAGTNA GATGTTGGCT	60
GGGACCACAG TCATCTAAGG NTACTGCTCA AGATGGCTGT TGTNTNGNAA ACTCAGCTGG	120
GGCTACTGAT CAGAGCACCT GNCATGTGGC TGTCNAGCAA GGCAATGTTA AGGAACATGG	180
GTGACATTTG GAGGTCAAAT TTCAGATGAG GTTGCTGAAC GGCTGATGAC CATCGCCTAT	240
GAAAGTGGTG TTAACCTCTT TGAATACTGC CGAAGTNTTA TGCTGCTGGG AAAGGCTGAA	300
GTGATTTCTG GGGAGCCATC CTTCAGGAGG AAAGGCTGGA GGAGGTTCCA TTTGGTTCAT	360
AAACAACCAA ACTTTACTGG GGTGGNAAA GCNTGNAACC NGAAGAGGGG TTNTTAAGAA	420
AGCCTTTTTT TTGA	434

(2) INFORMATION FOR SEQ ID NO:331:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 242 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

GANAGACCCT TTAAGTNTCC TGANTNTGGA AAAGNCTTCA AAGAAAAGTC AACTGTCATC	60
ATACATTACA GGA CTCACAC AGGTGAAAAA CCTTATGAAT GTAATGATTG TGGAAAAGCC	120
TTCAC TCA GT AAGTCCAACC TCATTGGTCC ATCCAGAAAA CCCACACTGG TGAGAAAACC	180
TATGGTTGCN CTTAAATNTG GAGTNTCTTT ACATTACAGA AGCTTGATCC TTAGTTGATN	240
NC	242

(2) INFORMATION FOR SEQ ID NO:332:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 351 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

TTATTGAGAA TCTCTTTGCA TTAGCTGGTG ATGAAGAACC AGAGGTACGG AAAAATGTGT	60
GCCGAGCACT TGTAATGTTG CTCGAAGTTC GAATGGATNG CCTGCTTCCT CACATGACAT	120
AATATAGTTG AGTACATGCT ACAGAGGACT GAAGATCAAG ATGAAAATGT GGCTTTAGNA	180
GNCTGTGAAA TTTTGGCTAA CTTTAGCTGA ACAGCCANTA TGCAAAGATG TACTAGTAAG	240
GCATCTTCCT AAGTTTGATT CCTGTGTTNA GTGAATGGGC ATGAAGTAAC TTNGGACATN	300
GATATTTATC CCTACTTAAA GGGTNGATGT TTNGAAGGAA GTCGGAAACG G	351

(2) INFORMATION FOR SEQ ID NO:333:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 501 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

GGCACGAGCT ATGCCTTAAA ACTNCCGAGC CCCACTCCAT GTAATAGGAT TCCTGGGCTT	60
CCTCAATGGG GGTTTCATGTN CTTGGACTGC GGGCCCTCAG TCCTTAACTG GAAAGTGAAC	120
CGTCCACTGC CCCATGGAGC CCATCTGGAC ACAGCACAGC CCCAAAACCG TTAGCAGCTG	180
GCTCTGTTTC CAAGCCTGGG GAGGGGTTCC TCAGTGCCAG GAGTTGGGGA CAGGCTGGGG	240
ATCCAAGCTG CTTGAGGGGG TCAACCTTGG GACCAAATTG CCTTAAAGCC TGTGGTTAAA	300
AGGGCTTNAG GGAAGGTTA ATGGGGCCAC NTGCTGGGAA GTTGGCCAGT TGCCCCGGTTG	360
GCAATGGTGT GAATNTTTTG GGCCNTGTTC CCTGCCCTGG GGTTCANCA AGTTNATCCC	420
TCCTTNTTNT NTNTNCTTTG GGGTTTGTTC CNGTNGTCAT NGGTTAATNT CCCCTAGTTT	480
CAAGTTTTAC ATAGGCCTC C	501

(2) INFORMATION FOR SEQ ID NO:334:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 271 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

GGCACAGTAG AAATGGAAAG AAGGNGGGGA TTGTGGTGGC TTGTGCCAG ACTGGAGCCT	60
GGANTAATGG CAGCTCAGTC AAGGAGCAGA CCTGGNACTG GAACAGNTTG AAAACCAGNG	120
TTTTGTACTT TGAGAGGAGA GATTCCANGC TGCTTCTTGA ATCAATCCAA NTTTCATTTA	180

CAGCTCTNGG AACACTTTGG GNGCTGATTT GTCTCTTTAG GGGGNCATCC CCAACATGGT 240  
TGAATTCCAA CTNCTTCAGA TCTTGNGGCT T 271

(2) INFORMATION FOR SEQ ID NO:335:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 203 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

TGTAAATTTA TTGTGATATT TTANGGTTTT CCCCCCTTA TTNCCGTAG TTGTATTTTA 60  
AAAGATTCCG CTCTGTATTA TTTGAATCAG TCTGCCGAGA ATCCATGTAT ATATTTGNAA 120  
CTAATATCAT CCTTATGAAC AGGTACANTT TCAACTTAAG TTTNNACTCC ATTATGNCAC 180  
AGTTTGAGGA TAAATGAAAT TTT 203

(2) INFORMATION FOR SEQ ID NO:336:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 304 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

GGCAGGAGNG CAGACTATTG CCTCAAGGAA CAGTCATTTT TGNAGATATC AGCATTGGAC 60  
ATTTTGAAGG AACTNGAACC AAAGTTATCC CAAAAGTACC CAGTAAAAAC CAGAATGAAC 120  
CCATTGGGCA GGACGCATCA AAGTTGACTT TGTGAATCCC TAAAGAACTT CCCTTTGGAG 180  
ACAAAGATGA CGAAATCCAA GGTGGACCTT GCTGGGAAGG TGACCATGTT AGGTTTAAAT 240  
NATTTNCAAC AGACCGACGT GGNCAAATTT AGGAGCGGGG CANCCCAATA TAGNAAGTTT 300  
CTGT 304

(2) INFORMATION FOR SEQ ID NO:337:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 459 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

GGCACGAGCT GGGGCCACGC TGGTCTGGGA ATAGTTGGGC AGGGAGGCTG TCTACCTGGT	60
CTCCAGAATG GACGGCCCTG TGGCAGAGCA TGCNANGCAG GAGCCCTTTN ACGTGGTNAC	120
ACCTCTTTTG GAGAGNTGGG CGCTGTCCCA GGTGGCGGGC ATGCCTGTTT TCCTCAAGTN	180
TGAAGAATGT GCAGCCCAGC GGCTCCTTCA AGATTGCGGG CATTGGGCAT TTCTGCCAGG	240
AGATGGCCAA GAAGGGATGC AGACACCTGG TGTGCCTTCT TNAGGGGGTA ATGCGGGCAT	300
CGCTGCTGCC TATGCNTGCT AGGAAGTTGG GCATTCTGTC CACCATCGTG CTTCCCCGAA	360
AGCACCTTCC CTGCCANGTG GGTGCCAGAG GCTTGCAAGG GGGAGGGGN CCNAGGGTTC	420
CAGTTGACTG GNAAAGGTTT TTGGAACGAG GNCCATTTT	459

(2) INFORMATION FOR SEQ ID NO:338:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 415 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

GGCACGAGNA AAATTGGAAG AGAAAATACT ATTCTGGGTT GGGTATCCTT AAGGATTAGA	60
ACCGCAGGAC TCCTCCAAGT CTGTAGGCCT ACTTTCTCTA TGAGAATCGT NATGTTAGTC	120
CATCTAACTG AACCTCATCT CTCTTTCAAT GCAGGTATCA CTACCATTAA AGTTAACATT	180
CGTAAATGCC AATTCCCTGG GNNGAGGCTT CCATTGCTGG ACCTGCGATG TCCGGTGNTG	240
NGGCACCCTA CAGTCCTANT TGGACTGAAC AGGCCTGATG GAGGTTGTGG CTGGNCTCAG	300
TTACACCTAA GAAGNTTTGG GGCAAGGTTT ATTCTNNTGC TTTTAAAAAG TGGCATGGAA	360
CTGTAGTGGT TTNAACATT CATNTNGTTT AACAGGGGTC GTAAGCCTGG TTTGG	415

(2) INFORMATION FOR SEQ ID NO:339:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 162 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

TGGNCTNATT CCCCAGCATG AAGGCCCTGA GCCCGGTNCC CGGNTGCAAC NAAGGCGGTG	60
TCCTGCCTGT GGGAAAGCAT CTGGCCATCG CCCGGGGCCG AGGGAAAGGG CCCGGNAAGC	120
TNAGGAGCCG CTGAANCTTG CTGGGACGAN ATGNAACCAC TG	162

(2) INFORMATION FOR SEQ ID NO:340:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 373 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

CGGCATTGCG NCANAANGNC CNAAGGAGGA GTCCTTCGGG CCTGTAATGA TCATCTCTCG	60
GTTTGCTGAT GGGGACTTGG AATGCCGTGC TGTTTCGGGC CAATGCCACG GAANTTTGGC	120
CTGGNTTNTG GTGTCTTCAC NAGGAACATT NNCAAGGCCC TGTANTNAGT GAACAAGCTC	180
CAGGNAGGCA CTGTGTTTGT NAAACACGTA CAACAAGACC GACGTNGCCG NTTCCCTTTC	240
GGAAGGGATT CAAACAGTCT GGGATTTGGG CAAAGATTCT TAGGGAGAGG CGGGNTCTGA	300
AACGAGTNAC CTGNNGGGTT AAAGACCAGT GAACCTTTCG GAATACTTNA AGNAAAGGTC	360
TTTGTGAAGG AAG	373

(2) INFORMATION FOR SEQ ID NO:341:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 298 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

GGCAGGAGCA ACCCGGGNGG TCGCCACGCA CCGCATGCNA CCTNANCCCC AGCCCCGATG	60
GTNAGGCCTA CACACTGGCT TCGAGACCAC CCGTCCGCCT CAATNATGTC ATGCTCAGGC	120
TGGTGACGGA GCTGCGCTGG CAGAAGTNCG TNATNTTCTA CGACAGCAAG TATGGTGAGT	180
TGTCCGGCAG GCGAAGCTGG GGCTGCTTGG GGACAGGGAT GGCCAGATGC TGGGAGACCT	240
GAGAAGTGGG TGGGGCCCTG GACCGGTNGG GGGTGGTCTG TGCTGAGTGG GCCTCCAG	298

(2) INFORMATION FOR SEQ ID NO:342:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 506 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

TTAAGTGTAG AATCAATGAA AAGACTTAAC AGCCTTCTCA ATATCCCAGA AAAGTGCCT	60
GAACAGGGAG GGATGATTTG GAAGATATCT GAAGATAAAC AGCTAGCAGT TTGCCTGAAA	120
TATGCTGGAG TATTTNAGA AAATGCAGAA GATGCTGATG GAAAAGATGT ATTTANTACC	180
AAATCTGTTG GGCTTTCTAT TAAAGAGGCA ATGACTTATC ACCCCAACCA GGTAGTAGAA	240
GGCTGTTGTT CAGATATGGC TGTTACTTTT AATGGACTGA CTCCAAATCA GATGCATGTG	300
CTTGATGTAT GGGGTATACC GCCTTAGGGC ATTTGGGNCA TATTTTCCAN TGATGCATTG	360
GTTTTCTTAC CTCCAANGGT TCNGCACATG NANTGAGANT GGTAGAAAGC GTGATATGAN	420
NTTGTNTAGG ACTGTGTTGT NCATANTTGT GGTAGTAACC ACANNTCCAT TACAGCTGTA	480
NGTTTCTCTT CCTTTCNAAT TTGGTG	506

(2) INFORMATION FOR SEQ ID NO:343:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 515 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

GGCAGAGTNG AAGATGGGGA CCACGGTCTC ATTCAGGGGA TCCTTGTTTT TTTCCAGCCA	60
GCCCACAATG CTGTANGGCA CCTGGAGAGA CAAGTCAGGT GCTGAGCCCG NGTGGGAGAC	120
CTGGAGCAGG GCGNGAGGAG ACNGGCCGAG GGCTGGGGTT CNAGNAAGCA CCTACCACGC	180
CTGCTTAGTG GACCACCTCG AAAGTGGGCC TGGTACTTGC GCCTTCTTGT CAGGCCGAGG	240
CTGCTGGAAT TTGGGTGACT TCCCCGCGTG GTTNTGCGTA GAGCTTGGCC CGGAAAGCTG	300
GCGTCTGAGG CCTTNGGGAA CATGCATTCC TNCTACCAGG TTGGACAGGT TGCCAGTGG	360
CTGGGCAACA GAACGAGCTT GAAAACCACC ATTCAAGCCA TNCCATNGTA AAGTACTGT	420
AACCCTGGTT CCCCAGTCCA ANTTNCTTTT GGGAGCNTNC CNAAATCCC CAGTTTCAGC	480
ANTNTCCCCG GNTGGTTCAG ACAACACAAC CATTC	515

(2) INFORMATION FOR SEQ ID NO:344:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 300 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

AGAACTAGTG GATCCCCCGG NCTGCAGGAA TTCGGCANAG GGNAGCGTGC NGNATTCAAA	60
GCTTACCGAG ATGCTGATGG CCTGGTTATT GACCAGCATG AAATATTTTT GGACTIONAG	120
CTGGAAAGGA CTCTCAAAGG GTGGATCCCT TGGNCGACTT GGAGGCGGTC TTGGGGGAAA	180
AAAGGAGTGC TGGGNCAACT GAAAATTTGG GGGACGGGAC CGGCCTTTTC GAAAACCTAT	240
TAAACTTGCC CGTTGTTNAN AAACGACCTC TATAGAGAGG GAAAACGGNG NAAGGCGGGN	300
	300

(2) INFORMATION FOR SEQ ID NO:345:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 319 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

AGGGAGCACC GGAATGCCC AAGGGGATCG TCCATACCCA GGCAGGCTAC CTGCTCTATG	60
CCGCCCTGAC TCACAAGCTT GTGTTTAANC ACCAGCCAGG TGACATCTTT GGCTGTNTGG	120
CNGGACATCG GNTGGATTAC AGGGACACAG CTNACGTGGT GTATGGGCCT CTCTGCAATG	180
GTGCCACCAG CGTCCTTTTT GAAAAGCACC CCAGTTTATC CCAATGACTG GTNCGGTACT	240
GGGAAGACAG TAGAGAAGGT TGGAAGATCC ANTCNAGTTT CTGATGNNGC GGNCGCAACG	300
GTCTGTTCCG GGCTGGTTG	319

(2) INFORMATION FOR SEQ ID NO:346:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 412 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

GGCAGGAGCT CGTCCTTGNA AACTNATCCA ACAGCCTCAA AATGCGAGCN TGTTTGTNAA	60
CAGACCCGCC CTCGGAATCC TGCCTCCGGA GAACTTTGTG GNAGAAGCTC CGGCAGTCCT	120
TGCTCTCGGT GGCTCCCCAA GGGATGTTCC CAGCTCATCA CCATGGCCTG CGGCTCCTGC	180
TCCAATGAAA ACGCCTTAAA GACCATCTTC ATGTGGTACC GGAGNAAGGA AAGAGGGCAG	240
AGGGGCTTTT TCCCAGGAGG NGCTGGAGAC GTGCATGNTT AAACCAGGCC CCTGGNTGCC	300
CCGATTACAG TATCCTTTNC TTCATGGGGG GGNTTNCCTT GGGAGGACCC TGGGTTTGTT	360

TAGNGGCCCA GGAAATTTTA AAGCCCTTCA AAAGGTTGGG NAATCCCTTT CC

412

(2) INFORMATION FOR SEQ ID NO:347:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 506 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

GGCACGAGNA CACCCTGGGC CTCACACCCC TGCATCACGC CTCTCGGGAA GGCCACGTGG	60
AGGTTGCCCG CTGCCTGCTG GACAGGGGTG CCCAGGTGGA TGCTACCGGC TGGCTCCGAA	120
AGACCCCCCT ACACCTGGCT GCAGAGCGAG GGCATGGGCC TACCGTGGGG CTTCTGCTGA	180
GCCGAGGGGC CAGCCCCACT CTGCGGACGC ATGGNGCCGA GGTGGCCCAA ATGCCTGAGG	240
GGGACCTGCC CCAAGCGGTT GCCTGAACTT GGAGGGGGGG AGAAGGAGTT TNAAGGCATA	300
GAGTNCAAGG GGGTTTTAGC CAAACAAGCA AGGTTTCCAA GGTTTCCAAC NGGCCCAATT	360
GANTTTTCCA AGGTTTTTTT GGGTTTNAAG GTTNNCCTTG CNTTGAAGG GGGACAATTA	420
AAGGNAAGAG GGTTTTCCG GAGGAAGGGG NTGGGGGAA AATTAAAGG GTTTTTGGGT	480
TTNACTTTN AATTAAAAA NGGCTT	506

(2) INFORMATION FOR SEQ ID NO:348:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 322 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

GAAATACGTN TTGCTTTNAT AACTCTNATT GCTTCTTGC TGTTGGGGTG TGTAAGTAA	60
GCATTGATTT NAGTGCTGAG NAATGTGAAA CGGGACTTAC AGGNATGCTT GGATTAGTNC	120
ATCACAGGTT CTNATGAACT TTNCCTACCA CAGTTGANTA ATATTTNTCC TCAAACCTGT	180
GTGCCCTAAG GANTNTGTTA NAATAATTGT TGGATAATTT CTAGGTGGGT GTTTATCCAA	240
GGCGCNAGAA ATTCCCTGCC CTTGGACCAG ATGTGTGGGG GCCNTCTGAC AAAATGGTAT	300
GNTNTGGTTT ANTTTACCAC AC	322

(2) INFORMATION FOR SEQ ID NO:349:

- (i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

GTCTGGTCGC NAGCAACCTA ANTCTAAAAC CTGGAGAGTC CCTTCAANTG CAAGGCGNGG	60
TGGCTCCTAA CGCTAAGAGC TTCGTCCTGN AACCTGGGCA AAGACAGCAA CANCCTGTGC	120
CCTGCCCTTN	130

(2) INFORMATION FOR SEQ ID NO:350:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 396 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

GGCAGGAGCC TCANTCCTTA ACTGAAAAGT AACCGTCCAC TGCCCCATGG AGCCCATCTG	60
GACACAGCAC AGCCCCAAAA CCGTTAGCAG CTGGCTCTGT TTCCAAGCCT GGGGAGGGGT	120
TCCTCAGTGN CAGGAGTTGG GGACAGGCTG GGGATCCAAG CTGCTTGAGG GGGTCAACCT	180
TGGGACCAAA GTTGCCCTTNA AGCCTGTGGT AAAAGGGCTT CAGGGGAAGG TAAGTGGGCC	240
ACCTGCTGGA AAGTTGCCAG CTGCCCCGTT GGCAATGGTG TGAAGTTTTT TGGGCCCTGT	300
TCCCTGGCCC TGGGGGTTCC AGCAGGTGCA NTCCCTTCCC TTGCTTACTN TNCTNCTTTT	360
GGGGGTTTTG TTCCCTGTNA GTTCACTGGG GGTAA	396

(2) INFORMATION FOR SEQ ID NO:351:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 102 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

GGCTATTGTA GGGCACCTNA CATTGCACAA GAAATGCCCC TTGCACTGGT GAATNTGTGC	60
CATTTCGTAG GGTCCGNATC CTCTGNTNAG CGTGGTTTAC CA	102

(2) INFORMATION FOR SEQ ID NO:352:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

GGCATNGTGN CAGGTNTGCA GCAAGTTGTT TCTTAGTGTC CCAACGGAGG AACCACTGAA	60
GCAAAGCTTT ACCTGTGCTC TACAGAANGA AATACTATAC CAAGGAAAGC TGTTTGTATC	120
AGAAAACCTGG ATTTNTTTTC ATTCCAAAGT CTTTGGAAGA GACACAAAGA TCTCTATTCC	180
AGCTTTCTCG GTAACCCTAA TAAAGAAANC CAAACTGCT CTTCTAGTGC CAAACGCCCT	240
GATCATAGCA NCAGTCACAG ACAGGTACAT ATTTGTTCTN CCTTNACTTT TCCAGAGATT	300
NCAACTT	307

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

GGCAGGAGGN AATCATCTTT AANATCACTT TCTNCTTCTT TGTNATTGTN ATTCTCTTGG	60
CCATAATACA AGGTCTAATT ATTGATGCTT TTGGAGAACT AAGAGACCAA CAGGAACAAG	120
TCAAAGAAGA CATGGAGACC AAATGCTTCA TCTGTGGGAT AGGCAATGAA TTA CTTCGAT	180
NACAGTGCCA CATGGCTTTG AAAACCCACA CTTTACAGGA GCACAACTTG GCTAAATTAC	240
TTGTTTTTTC CTGGATGTAT CTTATNGACA AAGNTGGAAA CAGNNCACAC AGGGNCAGGA	300
ATCTTATGTT CTGGGAGGAT GTTATT	326

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

TAGGAGGATA TNACGGCTTG AATATCTNAA ATNCAGTTGA GAAATACGAC CCNCATACAG	60
GACATTGGAC TAATGTNACA CCAATGGCCA CCAAGCGTTC TGGTGCAGGA GTAGCCCTGN	120

TGAATGACCA TATTTATGTG GTGGGGGGAT TTGAATGGTG ACAGCCCACC TTTNTTCCGT 180

TGGAAGCATA CACCATTCGN ACTGNTTCCT GGGACAACTG TN 222

(2) INFORMATION FOR SEQ ID NO:355:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 156 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

TGATATTCAC CTTCTGGTC TGTNGGNTTG CCTTATATCG TNATCTNCTT CTNGGTGGTT 60

AATGGTCATG GTCACCTGGT CACTCCAACA ATATCTGTTG TTTCGTACCT CTTTNNTAAA 120

TNGAACACTG TNTACAATCC GGTGATTTAT GNCTTC 156

(2) INFORMATION FOR SEQ ID NO:356:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 239 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

GGCAGGAGCA ACATATTAAG ACTCTGTCTC TACCAAAAAT ACAAATAAGT NAGCTGGGCA 60

TGGTGATGCA CTCCTATAAT CCCAGCTACT CAGGAGGCTG AGGTGGGAGG ATCACTTGAG 120

CTCTAGAGGC CAAGGCTGCA GTNAGCCGTG ATCATGCCTC TNCACCCTAG TCTGGGTGAC 180

AGAAGGAGAC CCTGTCTCAA AAAAAAAAAA AAAAAAAAAA AACNNNGGGG GGGGCCCCG 239

(2) INFORMATION FOR SEQ ID NO:357:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 293 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

AATCAAAATT GAATATCATT ACTTTTTATA GATCTATTCA GATTTATTCT TTGTNCTTGA 60

GTCAACTTTG TTGGATTTGT ATGTTTCTAG GAATTTGTCT GTTTCATCTA GGTTATCCAA 120

TTTTTTGAAC ATATAGCTCT TATACTAATT CTCTTACAAT CCTTTTTATT CCTATAAATC 180

AGTAGTAGTG TCTTTCATTT CTGAATTTTA GTAGTTGAGT ATTCTTTTNC CNTAATCTAG 240  
TTAAAGCTTT GTTCAACTTT GTGGANCTCT TNCAAAGAAC TAAATTTTNG GTT 293

(2) INFORMATION FOR SEQ ID NO:358:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 289 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

CGCACTCAAG GTCGACACTA GTGGNTCCAA AGANTTCGGN AGAGGAAACA GCGGTTAACN 60  
CCCGGTCCCC AGGGCCAGTC CCTCACCNGG CCCAGAGCAA GGCCACTAAG GATGGGCCGT 120  
GGAAACCAAA GTGGTCATCT ATTNANNCAT CATNNNCNGC AATTTNCCTN TTATCGGNGT 180  
NGAAAGNGNA AGACATTCGA GCCAACTTCA CAAGAAATGT CTAGANAAGA AAGTNCTTTA 240  
TGTGGACCNT GAGTTCCAC NGGATGAGAC CTGTCTCTTT TATAGCNAG 289

(2) INFORMATION FOR SEQ ID NO:359:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 138 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

CTANTCCNAG CACTTGGAAG GCNAAGGNAG GAGGATTNCT TGAGGCCAAG AATTTAAAC 60  
CAGCCTGGGC AACATAGCAA GATCCCGTCT CTATAGAAAA NCTGTNAANT TAGCTGGGCA 120  
TGGNGCCATA TGCCTNAC 138

(2) INFORMATION FOR SEQ ID NO:360:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 138 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

GGCACGAGTG GTGGCTCATG NATGTAATCC CAGCACCTTG GGAGGCTGAG ACAGAAGGAT 60  
TGCTTCAGCC CAGGAGTTCC TGA CTCAAAA AAAAAAAAAA AAAAAAAAAA AAAAAANNCN 120

GGGGGANTTT TTNGGGGG

(2) INFORMATION FOR SEQ ID NO:361:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 176 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

GGCACGAGGT GGCGAGCNCC TGTAGTCCCA GCTGCTGGGG AGGCTGAGGC ACGAAAATCA	60
CCTGANCCCC GGAAGCGGAG GTTGCAGTAA GCCGAGATTN CCCCACGGCA CTTNAGCCTG	120
GGTGACAGAG CGAGAACTCT GTCTCAAAAA AAAAAAAAAA AAAAAAACNN GGGGGN	176

(2) INFORMATION FOR SEQ ID NO:362:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 495 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

ATTAAAACT CCTCTGGTTG CCGTATTTNA TGATCTGGAT ATAGAAGCGG ATGAAGAAGA	60
TGAACTTAGG GCAAGAGGTC TTACAGGTTT GAAAAATATT GGAAATACTT GTNACATGAN	120
TGCAGCTTTG CAGGCTCTTT CTAATTGCCC ACCTTTGAAC ACAGTTTTTN CTTGATTGTG	180
GGAGGGACTT AGCTCGNAAC AGGATTAAGN AAACCTGGCC ATTTGTGAAA AGTTAATCTN	240
CAAACCTAAT GGACAGNGCC TGTGGGCATT AAAAGCCAGG GCCAGGTTTC TGTTTGTGGC	300
CTACTTACTC TGTTTTCAAG GGATTTAAAA ACTGTTAAAT CCCAACATTT CGGGGGGGTT	360
TTTCTNCAGC CAGGGTGGNT CCAGGAATTN CCNTTCGGTG TTTAATGGG NTTTGNCTTC	420
CAGGAGGGAT TTGAAAGGGG CCAGTTCCTG GGAGTTGGAA GGAGGNTCCC CGNAANCCTT	480
AACCCTTGGG GGGGG	495

(2) INFORMATION FOR SEQ ID NO:363:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 376 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

GGCAGAGGAG NATGACCTTG TGCCACAGC ACCTTCTCTG GGCACCAAAG AAGGTTACCT	60
CACCAAACAG GGAGGCCTGG TCAAGACCTG GAAAACAAGA TGGTTTACTC TGCACAGGAA	120
TGAACTGAAA TACTTCAAAG ACCAGATGTC ACCAGAACCA ATTCGGATCC TAGACCTAAC	180
AGAATGTTCA GCTGTACAAT TCGGATTATT TCACAAGAAA GGGTAAACTG TTTTGTGTTG	240
GTATTTCCAT TNCAGGACAT TTTATCTCTG TGCAAAGGAC CGGAGTAGAA GCTGTTGAGT	300
GGGNTCAAGG TATTTACGGN TGGGNAAATT TGTTCACCAN ATTAAGGAAA AACCAGGTTT	360
CCAAACCCAG GGGGGN	376

(2) INFORMATION FOR SEQ ID NO:364:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 204 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

GGCAGAGGGG TAAATTAAGT ATTGAAAAAA TGCTATGGGG CAGAGGAAGA AATGCTAAGC	60
TTCTGTGAGA AGAGAAGACA GCTTGTTACA CAGGTGAAAA GAACAAGCTG CAGCTGAGAG	120
AAGAAAAGTA TAAGAGTTGC TAGGTGTGAC AATCTCAAGA CTTTTCACC ACTACAAATT	180
TAAACAGCCA CCCTAAATCA CCCC	204

(2) INFORMATION FOR SEQ ID NO:365:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 332 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

GGCAGAGNAT TTAGACATTA TTA CTCAAAA TATTCCAGAA AAGGTAAGTT TGTTTGTAAG	60
ANTTTAAACT TGACTGTAAA AAAAGAATTG TATGTATTTG TACCAATTTT TTATATGTNG	120
AGCATTCCTG TGAAATGTTT GCAATTTTNC CCTTTCCTTT CCACTGCCCT GCTAAATGTG	180
CACATGTATT AGNACACAAA TACCCAGTAA ATGGGGAATT ACCCATTTAC ATGGCATACA	240
CACTGAGGTG GGCTTGNGGT ACATACCAA TTTT TAGGAC AACTTACTG GGGTAAGTTT	300
TTGTGGGATA CTTGTNTNAN AANTGATTAA TT	332

(2) INFORMATION FOR SEQ ID NO:366:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

GGCANAGNAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AANAAN

56

(2) INFORMATION FOR SEQ ID NO:367:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 114 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

AGACCTTAAN CCCAGGAGGC GGAGGTTNCA GTAAACCNAN ATTAACCCAC TACTCTCCAG

60

CCTGGGCCAA CAAGAGCAAA ACTCNGTCTC AAAAAAAAAA AAAAAAAAAA AANC

114

(2) INFORMATION FOR SEQ ID NO:368:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 93 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

GGCANAGCGG CCACNCCAAA GTTTTGGGAA TTACAGGCAT GACCCACCGC CCCTGGNTGG

60

ATTCCTTTG AAAAAGNNAA AAGAAAAAAA AAA

93

(2) INFORMATION FOR SEQ ID NO:369:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 111 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

GGTGAACCCT GGCCGCCAC CTCCCCGCGC AAGTTCACCC CTGNGATGCA CGNTTCNTG

60

GAACAAGTTC CTGGTTTCTN TGANGCACCG TGCTGACCTC CAAATACCGT T

111

(2) INFORMATION FOR SEQ ID NO:370:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 362 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

TGTAATCAGC ATCANTAATA ACTGTGAAGT CCTTCATTGG CTTAGGTTGC ACTTNTNGGT	60
AGAGGCTGGG GCAAGGNTTT NTTGGGATCA GGGACACTAG GCAGCCACTC CTCAGGCACC	120
AGTAGTGGTG GGCANTGAAG TCAAATGTGC CAGTNTTCAC ATGCCTGGNT AGCATACACA	180
GATTACCACT GGTGGCTGGT NTGGNTGGGC TGGTCCTTGA ANCCTNCAGG TGGGCATGGC	240
TCCAGGTGCC TGGTGGTGGC CAGTGGTAGG CTTAGGGCAG GTGAGGTGCC TTGGGCCCNT	300
TGGAACAGTG TGGCATGGAA TTGGTGTTG ACAGGNTTGG NAACTNTGCC TTGGCAAAAT	360
TN	362

(2) INFORMATION FOR SEQ ID NO:371:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 173 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

AGAAGCAAGT TNCTTAGCTG GGTGAAGTGG CTCATGCCTA TAATCCGGCA CTTTGGGAGC	60
CTGNGACAGG TGGCATTGNT TGAAGCCAGG AGTTCAAGGC CAGCCTGGGC AATAAAGTGA	120
GAACCTGTCN GTNATAGACA AAAAAAAAAA AAAAAAACA AAAANCNGGG GGG	173

(2) INFORMATION FOR SEQ ID NO:372:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 436 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

GGCAGAGCTG GCGCATCGGT TCATTTCTTA CCTCAACGGC CAGATCATGG CGTGCNACAA	60
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GCGGTGCAGA TCTTCGACAC CTGGGGTGGC AACCTGTCGT CGGCGGCGTA CCAGGAGTTC	120
TCCCTGGGCC TACATGCGCA ANATCGTCAG CGGCCTGATC CGTGAACAGA AGGGCGCAAA	180
GTGCCGGTGA TCATGTTTAC CAAGGGCGGC GGCCTTTGGC TGGNAGAGCA TTNCCGACGC	240
CGGCGCAGAN CGCTNGGGCC TGGATTGGAC CTGCGACCTG GGCAGAGCCC GTCAGCGCGT	300
GGGTAACCGG TTGGGCTGCA AGGTTNACAT GGACCCAACGT GTGCTTTACG NCAAGCCGGA	360
AGCGATTTGC AACGAATTTG GGCCGNATNC TTGGCCAGTT NTGGCAAGGG CAAGGGGCNT	420
TTTTTTCAAA CTTGGG	436

(2) INFORMATION FOR SEQ ID NO:373:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 366 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

GGCAGAGGNA GTGGTATGNG CTGGATCTGG TGAAAAACCA GGATGGCGCG GTGGTGGGTT	60
GTACCGCACT GTGCATCGAA ACCGGTGAAG TGTTTTATTT CAAAGCCCGC GCTACCGTGC	120
TGGCGACTGG TGGACAGGGN CGTNATTTAT CAGTCCACCA CCAACGCCCA CATTAACACC	180
GGCGACGTTT GNGNCATGGN TATCCGTGCC GNCGTACCGT GCAGGATATG GAAATNTGGC	240
AGTTCCNNCC GACCGGGCAT TGGNTGACGG GNNATACTGG TCCACCGAAN TTGNCCGTGG	300
TGAAGGCGGT TATCTGCTTG AACAAACATG GGCGAACGTT TTTTATGGGA GCGTTAATTT	360
TTTTNT	366

(2) INFORMATION FOR SEQ ID NO:374:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 57 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

GGCAGAGTNA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAAAT NNNGGGG	57
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(2) INFORMATION FOR SEQ ID NO:375:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 78 base pairs
  - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

AGGTAGAACC CACCATGGTG CTGTCTCCTG CCGACAAGAC CAACGTTAAG GGGGGGNTTT	60
TNTAAGGTCTG GTGNAC	78

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 506 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

AGGGTACCGT ACGTCGTCGC TGNTGAGTGG GCGAAAAGCT GCAAATGAAA CAGCACTGCC	60
CACATCCGGA TCTGTTACAG GTCGATCCGT TCGAAGCCAT CATCGATGAA GAGCTGGAGC	120
CTGGTGATAT TCTTTATATT GGGNTGGGAT TCCCGGCATG AAGGCTACGC GCTGGGAAAA	180
TGCGATGGAA CTATTCCGTG GGCTTTCGCG CGCCAAATAC GCGGGAAC TG ATTAGTGGAT	240
TTGCCGATTA TGTGCTGCAA CGTGAAC TNG GCGGCAACTA CTACAGCGGA TCCGGATGTT	300
TCCACCTCGC GNTTCATCCT GCGGGATGTT TCTGNCCGCA AGNGAATGGN TNAACTGCG	360
TGAGAATGGA TGCNTCGGAA TTGNTTCANC CAGCCNGTNA CAATTTTAAG CAATGGTTTT	420
GGCGAGTTTT ATNTCCAGT CAAGTCATGG AANNTGGGTT ATTGGGGCNG CCAANGCCGG	480
CTTTTCAGCC GGTGNAATTT ACGGTG	506

(2) INFORMATION FOR SEQ ID NO:377:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 236 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

GGCAGAGCAT GNTTATGGGN TACAAAGNGA TGTTATATTT TATGAATATT TAGCTGGGCA	60
TGGAAGCTCA TGCCTGTAAT CCCAGCACTT TGAGAGGCTG NGGCAGGTGG AGTGCTNGAA	120
GCTCAGGGGT TNAAGATTAG CCTGGGCAAC ATGGTGGGAA CCTATCTCTA CAAAAAAN	180
AAAAAANC TGGGGGGGAA TTTTGNAGT GTTCNGGGN CCTATGGGTT TTACCC	236

(2) INFORMATION FOR SEQ ID NO:378:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 316 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

TTGGCTATGG GACTATATGT NATCTANTGA CTTTTTAAAA ACAGATTACA AACTGTAGGC	60
CTTAGATNGG TAAGTAATTT TTCAGCTGGG CATGGTGGCT NATGCCNGTG GTCCCGGGGC	120
TTTGGGAAGG CCGAGGCAGG CGGATCACGA GGTCGGGGGT TCGGGAACCA TNCTGGTCGA	180
TGTGGCGGGN CCNCGTGTTT TGA CTGAAAA AAGTGCAGAA ATTGGGCTGG GACATGGTGG	240
CGTGACNTG TGGTNCCGGN TGCTTGGGGG TGCTTGGGGG CGGGGGGGGT CGCTTTGGGC	300
CTNNGGAAGG AGGAGG	316

(2) INFORMATION FOR SEQ ID NO:379:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 356 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

GGCAGAGCNG AAAGCGGGCT GCACTACAAC CGACATCGNT ACTACAATCC GGATGTTGGT	60
CGCTATCTGA CGCCTGATCC GGTGAAGCTG GNNGGTGGGC TGAACGGATA CCAATACGTG	120
CCCAACCCGA CGGGTGGNTG GTATCCGTTG GGATTAGTTT GTACACCTGG GGCAGTGCCG	180
GGNCTTCANC AAATAACACA GCAGTTAGCA AAGTCCCTGG AGGGGGATTA GCCGCGCATG	240
AAGCAGCTGG GGGTCATCTA ATTGAAAGGC ACGTTCGGTC AGACAACGGC GCAGTAAGCT	300
TTNAAGGCTT GTAGGCAGAG CCAANTATT TCCAGNNGCA TCCACGGTTT CAGANT	356

(2) INFORMATION FOR SEQ ID NO:380:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 405 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

GGCAGAGCTG NTTGACCGAA CCGTTGAAGC GGTTCGAT ACGACGCAGC TNACCGTAGC	60
GCTCGCCCGG GGAGATGTTG CAACCGCTGG AGCAGNCATG GCAGATGCTC GGCGCAAATT	120
GCATGTCCCA CTTACGGTTG TAGCGCTCGG TAGTGGGTCT TGTCGGTGAA CACACCGATC	180
GGGTCAGACC TTCGGNGAAG GTTNCCGGAG AACTCGCTT CTCCAGCACG CCGTACTTTC	240
AACGCGAACC GAAGTACACG TTGTCGTGGG ACGCCGAACA CGCCGAGGTC GGTGCCGNCG	300
GGNTAAGTCT TTATAGAAGC GCACGNANCG GTAGCAGGCC GATGNCAGCG GTTTCATTTT	360
CGTGGGGAAA TGAACGGGGC CCNAGGTTCC NGGTTTCTGG TTGGT	405

(2) INFORMATION FOR SEQ ID NO:381:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 251 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

GGCAGAGNGT TTTNCGGGCT CAGTTCGTGG TGCCAGCTGC CGTGGGTGCG GTCAATGAAA	60
CGAGTTTCAC AGAACTCCCA GANGCGCCGG TACCAGGTTT CGTAATGCAG CTCCCCCGTC	120
CTTTTNANCA GCGCCTGGGC CAGCGGGCAC TGGCTTCGCA ATGGGTCCAG TGCAGGCGCC	180
TCGCGCCACC ACGGGGCGCT GGCTTCCANT CGAGGGTTTA GACAATNCCN GGGGGGGCCN	240
TTGAAGGGCC N	251

(2) INFORMATION FOR SEQ ID NO:382:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 183 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

CCCTGGCTCT CTTGATAGAG GCGNGAGAGT NNGNTTCCAG ACCAGAATTT ATCTTCAAAC	60
GCTTCGGCTT CGCGCGCCGC TCGTTAAGA ATACGGGTCC GCTGGATAAT AATGGCCCAA	120
GATGCGATTG AAAAACCAAT CAAAATCAAC ATGATAAGTT TAACCAGAAG GCTAGCCTTC	180
AGG	183

(2) INFORMATION FOR SEQ ID NO:383:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

GAGTTGGCGG TCAGGTCACC GCGGCTTCC AGGGGCGAAA TCAGGAAGAT CACCGCCACC	60
GGGATAAACG CCACCCAGTC GAACGAAAAA CCGTACTTGA ACGGCACCGG TAGGCTGATC	120
AGTGGCAGCT GGGGCAGGGC GCCCAGGTTT GACGCGGCCC ATCCACCAAG CCACCACAAA	180
ACCCAGGGTC AGGCCGATCA CGATCGAACC CAGGCGCAGG NAACGCGTTG TTGAAGCGGT	240
TGAGCACCAC GNATGGTCAG CAGCACCAGG GCCGCCACAT GGTTCGTCCG GNGGNGTCCA	300
GGTCGTTGGT GNCATTAAC CGCNGGT	327

(2) INFORMATION FOR SEQ ID NO:384:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 430 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

GGCAGAAAAT AAAACCACCG GGGCCTCCCT TTAAACTTTN GTTCTCAAAG GGCCCCCTCCA	60
CCTGGCCCTG TTCTGGCCCC CAAGGATTCT ATGGGAAGCA GTGGAGTCCC ACAGATCTCG	120
CTCCANACTC TGCTCCCTGA ATCCCGGGGC TCCTCCTAACT CCCCCTGGCC TCTAANACTC	180
CTTCCCATCC TCCCCTCCCA CTCAGAAAAC TCTTTGTGGT CCCCCTGGAT GAGGCCCAGG	240
CTCGAATCCC ATATGCCCGT GTNAACCACA ACAAGTACAT GGTGACTGAA CGCGCCACCT	300
ACATCGGTGA GTGTTTTGAG GCACCACGGG GCGCTTGAAG AAGAGGGGGT TTCAGACACC	360
AGGGCGGNCC CCCGAGGGTG NCCTTATGTT NCACCTTTN CTTTTTAGGA ACTTCCAATG	420
GTTTGATNGA	430

(2) INFORMATION FOR SEQ ID NO:385:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 501 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

GCTTCGCTGG TTTTCGGCTG TTCCAGNATG GTGCTGACCT TGTGTAGGT NAGGCGGGCC	60
TGGGAGTGNA TCACCGCTTC GTAGAACTGG TAGTCGGTCA TTTCGNCGGT TTTCGAGATG	120
GTCATCTCGC ACACCATGGC CAAACGGTCG ACTTTTCGGGT TCAGGGAGCA CAAGCCGTTG	180
GACAGNTGCT CAGGCAGCAT AGGGATGACG CGCTCGGGGA AGTACACCGN GTTGCCGCGC	240
ACCTGGGCTT CGTTGTCCAG GGCCGAACCG ATCTTNACGT AGCTGGGACA CGTCGGCAAT	300
CGCGAACGNA ACAANTTTCC AGCCGCCGGA GGAACAGGCG CATTTGCCAG GCTTGGNTTT	360
CGCATTAGNC CGCATNTNNC GAATTCGCGG GCANTTTTCGG CTTTCATGGTG ACGAACGNCA	420
GTNNANGCAG TTCGATGNGG TTNTNTTTGT NNTTTTNTTC GATTTCCGNT TGAGTTGGGG	480
GTTTTTTGAG CACAGNNTGA G	501

(2) INFORMATION FOR SEQ ID NO:386:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 427 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

GGCANAGGNC TGTACGTGCG CCATTGCTCG TGCATGGGGT TTTTANTGAT TAAGCCTGNG	60
TATGCAACAT CAGCATTAAG NAGCTCGTGT AAANCAGAAT AAACGGCATT TGCGAGCATG	120
ATTGGCTTCT GTCTGCTTGG ATCAGTTGTA TAAATTGGAG TTTTTCAGCTC GAAAAATGCA	180
TGTAATCGTC CGTTTTGAGG ATTTTCAGCA ACAAATTCG GCATTGGTAC GCCATCAAGT	240
GGAATATAAA ATTTCACTTC AGGGCTGGAT TTCATNAGTC GAGTTTCAAG CACAAAGTAA	300
TACTGGATAA AACGGACTAT TTTGGGCTGA ATGTACTTGA ATGCCAGTGC TGGTATTCTC	360
TCGGGACGTA TTTTTCAGAC CCGTGNTCAG NTCCNTCCGT ACATTNGGNT TTGGGTCCGT	420
TAAGTTA	427

(2) INFORMATION FOR SEQ ID NO:387:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 356 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

GGCANAGGTC TCTGTNGCTG TAATTAAGGA TCTTGAGATG AGGAGGCAAT CCTGAATTAT	60
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CCGGGTGGGA CCTGTACCCA GTGACACATC AGGAGAAATT TTTTATATG AGAAAATGTG	120
GAAGGGGAAT TTGAGACAGA CAGAGGAGGA GCAGCCCGAG GGGAGGCGTT GTGTGCAGGC	180
GGAGGCAGGG ACGGGGCGAT GCACCACCGG CTGAGGAAGG ACCGCGGCCA CCGGGTAGCT	240
GGAAGACGCA GNTGGAGCCT CCCCTAGAGC TTTTGGNAAG GGACACAGCC CTGCCAGCAT	300
CTTCGTTTTN GTCTTTGGGC CTNCAAAGAC NAAAATCAAG GCTTTTNGA ACAAAT	356

(2) INFORMATION FOR SEQ ID NO:388:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 326 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

NGCAGAGCGC GAAGTGGTGT GCGGTACTCC TTGAGCGAGC TGCCTTCCGG CGCCACATCG	60
GTGTCGTGGA AGCTGTAGTA GTCGATGCCC AGCTTGGAGA AAAACTCAAA GGCCGCGTCA	120
NCTTGACCGA TGGCCACTTC CATCGCTTTA CCGCTGCGTT GCCACGGGCG CTTGAAGGTG	180
CCCATGCCAA ACATATCCGC CCCC GGCCAC ACAAAGGTGT GCCAGTAACA GGCGGNCATG	240
CGCAGGTGCT CGCGCATCGG TTNCCGAGG ATCAGCTTGT TTGCGTCGTA ATGGCGGAAG	300
NCGAGTGNTA GAGTCGCTNG TCAAGG	326

(2) INFORMATION FOR SEQ ID NO:389:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 382 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

GGCAGAGCCA CGGTCAGGCC GNCATCGGTA CCGTTCTTGA AACCCACGGC CGAGGACAGG	60
CCGAAGCCAT TTCGCGGTGA GTCTGGGATT CCGTGGTGCG TGCACAATNT GCCGACCAGN	120
TGGTCAGGTC TTGCAGGTAC TGGNGGGAAA TCGTGTCCAG GGTTCGGTT GNCGTNGNAG	180
GCCCATTTC GNCAAGTCCA GNAGTAATTG NACGACCGAT GTGCAGGCCG TCCTGGATCT	240
TGAACGAGTC GTCCAGNTAC GGGTCGTTGA TCANGNCTTT NNAGCCGACG GTGGTACGCG	300
GCTTGTTTCA AATAGACACG GATCACCAGG TTTTNAAGGT GTTCGGACAT TTTNGTNGGT	360
CAGCACTTTT CAGGTGGTTN GG	382

(2) INFORMATION FOR SEQ ID NO:390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

GGCANAGGCT GATCGGNACC CAGNTCGAGC ACGTTCCGGC CATGCTGGAA ACCATCTTCA	60
AGAGCGCCTT CGGCCTCGAC CCGGTATTTG GCGGCCTGNT CGGCAGCGCC ATTGTNATGG	120
GTGTGAANGA GGTGTGTTCT CCAACGANGC TGGCCTGGGC AGTGCGCCCA ACGTCGCCGC	180
CGTAGGGCGN TTNAACACC CCGGTGCNCA AGGCGTGGTC CAGGCCTTCA GCGTGTTCCT	240
CGATACCTTC GTGGATTNNN CACCTGCACC GCGTTGCGNN TTNCTGCTGT CGGGCTTTTT	300
ACACCCCAGG NTTTGAAGG TGAATNGAT CGGGCCTGNA CCCAGAACTT CGGTTGGGCC	360
GCCCTGGGTT CGGTTGAANT GGGGGNCCG	389

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

GGCAGAGCTT NGCTTCGCTG GTTTTCGGCT GTTCCAGGCA TGGTGCTGAC CTTGTTGTAG	60
GTNAGGCGGG CCTGGGAGNG NATCACCGCT TCGTAGAACT GGTAGTCGGT CATTTGNCNG	120
GTTCGAGAGA TGGTCATCTN GCACACCATG GCCAAACGGT CGACTTTCGG GTTCAGGGAG	180
CACAAGCCGT TGGACAGNTG CTCAGGCACA TTAGGGATGA CGCGCTCGGG GAAGTACACC	240
CNGTTGCCGC GCACCTGGGC TTCGTTGTCC CAGGGCCGAA CCGATTCTTC ACGTAGCTGG	300
ACACGTCGGC AATCGCGAAG GAACAACTTT CCAGCCGCCG GAGNAACAGG CGCATTTTGC	360
CAGGCTTGGT TTCGCATTAG ACCGCATCGT CGAAGTCGCG GGCATTTTGC CTCATGGTGA	420
CGAACGGCAA TGACGCAGTC GATGGGTTCC TTTGGNCTTT TTTTNGATTT CCGGTTTNN	480
TTTGGGGTTT TTTTtagGCN A	501

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

GGCAGAGNAA GACATCCCAT GTTTATGAGT CTGAAGACTT AACATTGTTA AGATAATACT	60
CTCCAAATTG ATTAAGAGGA TAATACTCTC CAAATTGATC TACAGATTCA ACATGATCCC	120
TATCAAAATC TCAGCTGGCT TCTTTGTAGA AACTGACAAA TTGATTCCAA AATTCATATG	180
AAATTGCAAG GGATGCAGAA CATCAGAACA ATCTTGTAAG AGANCAAAAC TGGAGTACTC	240
CCACTTCTCA AAAACTTACT GCAANGCAAA AGTAATCAAG ATAGGTTGGG CATGGTGGCT	300
CATGGACTGT NAATNCCAGC ACTTTTGAAA GTTCCGAGGC GAGTGGGTTT ACTTGAGGGT	360
CCGGGGTTTC AAANCCAGCC TNGGCCAACT TGGTGGAAAC CCCTTTTTTA TTAAACTTTT	420
AAANAATTG GNTGGGCTGG TGGGCGGGN CCTNAATCCC GGTTTTTCGG GGGTTTGGGC	480
NGGGCATTCTG	490

(2) INFORMATION FOR SEQ ID NO:393:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 230 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

GGCNCTAGAT GTNGTTAAG GTGTAAAACA GACCAACCCA CAGCGGCCGT ACCTTAACTT	60
CANTCGTCAG GAAGAGGCTC AGCGTCGGGG CCAATAGCGC TCCGGCAATG CCAGAAAGGT	120
AACGCAATCA GCAGGTAAAG CGGTCAAAAA TGGGGATTAA AGCGGCGTGG TNAACCCGTA	180
CAGACGTTTC ATATTGTTN TCCCTGTNCC CTNAACGTNT GAAGTGAGGA	230

(2) INFORMATION FOR SEQ ID NO:394:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 293 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

GGCANAGTGA ACAGCGTAGG NACTGTAAAG CATGTNTTGG GGTAAACTT TCCTTTGATA	60
--	----

AAGAGAAACA GGTTCCTTG GATGAATAGA AGGNACAGAG AAGGCAGATC CAGGCTTATC	120
CTTCTCGTGT AAGGGTATAG TAAAGAAAGG TCTATGCCGG GCGCAATGGC TCACGGCTGT	180
GAATCCCAGC ACTTTGGGAG GCCGAGGTGG GTGGGATTCA TGAGGTGCAG GNGATCAAGA	240
CCATCCTGCC TAACATGGTG AAACCCGTCT TTNACTAAAA NTGACAAAAT NNA	293

(2) INFORMATION FOR SEQ ID NO:395:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 254 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

GGCACAGNAG AAAACAGGCA AAAGAGACAC TTCAGGTGGC ATTGATCTGG GAGAAGAGCA	60
GCATCCCTTG GGCACACCCA CTCCAGGACG CAAGCGANNA AGGAAGGGAG GAGACAGTGN	120
ATTATGAACG ATGATGATGA CGGATGACAG TGAATGGACC AAGGGGATGA AGATGATGGA	180
GGATGAAGNA AGGATAAAGT AAGGACAAAA AAAAAAAAAA AAACCNCGG GGGTNNCTTT	240
TGGGAGCGCC CGTG	254

(2) INFORMATION FOR SEQ ID NO:396:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 401 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

GGCANAGNAG AAAACTGAGC TCGTTGGCTG GTTCTCAAA AATCCACTCA TTTGATGATT	60
GTGGTGGTGT TCACTGACTT TATCCCAAAC CTACATGGAA GGGTGTCCG GACAGACAGC	120
TCTTCCCCAA AGAAAATGTC CTCTTAGCTA AGAGTCCATG TTTCTTTTC TAAGTAAGAT	180
TTTGACAGAG AATGGCATAT GTATATGTGN AGGGCTGGGT CGTGTCGTTT CAAATGGAAG	240
CAACAGAAAA GCAGAGCAGG TGTGTCTGGG GAGTATAGAG ACTGAAGGCT GAANGGTGGT	300
TGAGTTTCTG GGTAAATTGG TGGATGGTTA GTATGTATTG ACTTTGAACT TNCCNTTCTG	360
GAGCATTTGT TAGAAGGCAG NNAATCCACA ANGACAGGGA G	401

(2) INFORMATION FOR SEQ ID NO:397:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

GGNAGAGNCG TTGAGGNGCG CGGNGCCGAG GCATAGAGCG TGTCGATCGT GTNGCTCGAT	60
TTGCCACTGC CGCTGACCCC GGTGTATGCA GGTGAAGGTG CCGAGCGGCA GGCTGGCCGT	120
CACGCCCTTC AGATTGTTGG CGGTGGCGTT GTGGACGGTC AGTTTCTTGC CATTGCCCTT	180
GCGATGGGTG GTNGGTACCG CGAACTGCCN NCCTGTNCCG ACAGATAATC GGTGGTTGAT	240
GCTGTTGGGG TTGGTCGAAG TGACTTNCCT TCGTAACGTG GCCCTNCGCG ATNGGATTCG	300
GCCCCACCCA TGGGAACGGC GGGNAACCCG GACCCATGTT CGATGNACAT GAA	353

(2) INFORMATION FOR SEQ ID NO:398:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 304 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

GGCANAGCTG GNAATGGTTC GCTGAAGAGC CTGGCTGGCA ACTNTTCGCG AAATGGCGAG	60
AGCTGGCAGC CACTCGCTGC CTTCCGGTAT GCCGACCGCG GCGGAATTCG CTGTTGGGGT	120
AGTAGCTTTC GCTGCGCTGG NTAGGCGGTG TAGGAACAAT GCCCGGTTGG TCCATTCGAA	180
ATCGAACAGC ATGCCCAATG CTTACGCAC GCGCCTGGTC GGCGGAACGC NGNCGCCGGT	240
TNATTCATGG AACAGCGCCT GGGTGTGCT GGGGAATCCG GTGNAGGTAT CTCGGNCCGG	300
GATG	304

(2) INFORMATION FOR SEQ ID NO:399:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 317 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

GGCAGAGTGA ATTTTNGCCA GTGAACACTT CAGCCACCAC GGTGTATTTCG CTAAAGGTTG	60
AACAGCCCAT GTAGTGAAG ATTGGCTGGC CGTTGTAAGA AAAACGCGTT GTCCTATCAG	120

GCATAACCCC TTTGACCCTG CGTGGCGCGA ACGGCGACAA ACAGATTGGT TTTACCTGGA	180
TTTACAGAAC AGGCATTTCGC CACATTCTGC AGTGTAAGC GGAATTAACG TGATCGCCTG	240
GCACAACGCT GGTCACAACT TTGGCCCACT TNTACCACTA TGNCCGGNAC CTTTNGTGTT	300
CCCAGCAAGG TTTTGTN	317

(2) INFORMATION FOR SEQ ID NO:400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

GGCANAGGGA GTGGTATGNG CTGGATCTGG TGAAAAACCA GGATGGCGCG GTGGTGGGTT	60
GTACCGCACT GTGCATCGAA ACCGGTGAAG TGGTTTATTT CAAAGCCCGN GCTACCGTGC	120
TGGCGACTGG CGGACAGGGG CGTTATTTAT CAGTCCACCA CCAACGNCCA CATTAAACACC	180
GGCGACGTTT CNGGCATGGN TATCCGTNCC NG	212

(2) INFORMATION FOR SEQ ID NO:401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

GGCANAGCAG CCCTCAGGCA GCTCCAGCAG CAGATATTTA GCCCGCCGCT GCACGCTAAG	60
CACTGGTTGG TCGCTTAAAC GGTAGATCTC TTCTGAAACC GGCCAGCGCA ANTNCCGTTG	120
CGCACCCTG CATGAAGAAT GGTTCACCA ACGAAGATGC GGTTCCTATGC CGCGGCGGCT	180
GGTTTCAACT TCGGGGTAAT TCAGGCATAG CATCTCCAGG TAATGGAACA GAATGACAGT	240
CAATATGGGG GTCAGGCAGA TNNTCCAAAA AACCCCGGCG GAGGCGAGGT TTTTTTTTNA	300
ACATCAAAGG CGAGGANTTN TTTGATT	327

(2) INFORMATION FOR SEQ ID NO:402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

TGCACGTTNN TTGATCATGA CGTGCATGNT GTGTCTTGGG CATTGACANC AACCATGAGG	60
TTGCCACACG GTGCTTGTTG GACAATNGCC ATGTAGGAGT CCACAAGGTT CTGGGTGGTT	120
TCCATTTGCC GNTCCAGCTA TGGGTCCATG GAGTTTTATN AAGCTGTCNN TGCCAT	176

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

ACAGAGTTTG TCAACCTCAN NNCTACTGAC ATTTGNGCT GTGGTGTGGG GCCGCCCTGT	60
CCCTGGGNAG GAGGTTGAAA AGCATCCATC GTCTTCACCC ACTTGGTGNC AGGAGCGCCC	120
TCTAGCTATG AATGGACCAA GTTGCCACGT GTGCCTCTAG TGGCAGGGTA GGAATGCAG	180
TCACCCCCAG GTGAGGGACC ACGGCTTCC CTCAAGTGC CAGGGATAGC CTCTNCCGAA	240
TTGGTGACAT TGGGAATCCA GATGTGGAGG AGGTGGGGAA AAGGGNCCTG TGGGATAAGG	300
TTAGGGGAAG AGTTTTTTCC AGGTTCGTTA GGTGGGGAAA GGT'TTNCCAA GGGCANGGAA	360
TNTNCCCCC CGGGGCAANC AGAAAAGGGC CATT	394

(2) INFORMATION FOR SEQ ID NO:404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

GGCAGAGCAG GTCCAAGGCC TCGCAGAACC GCAACATACC TGTAAGCACC TGGGCGCCTT	60
TAGGGTCATG CTGGGCAACC ACAAACCTGC GGTCGATCTT GATGAAATCC ACAGGAAACT	120
GGTGCAGATA GCTCAACGCA GAAAACCCAG TGCCAAAATC ATCCAGATAG ACCTTGGCGC	180
CCATGGCCTG CAACTTCTGG ATGGTCTGGC GGGTGGCCGG GATGTCGCTG ACCAGGGCGT	240
CTTCGGTAAT TTCCACTGAA ACTTGCCCAC GGGCCTGGCG AAGAATTTNC ACCAGGCGGT	300
CGCCATAGGG GCGTCCTTTG NAGCGTGGTG CTGGAAATNT TGATGGGTCA TCGGCAGTTT	360

CAAAACCCAN CTTTTGNCCA TTTCTGATAA TTGGNGGCAA CAACCTGGGG ATTGCCACCC 420

ACAAGTTTAN GTNCCGGGA 439

(2) INFORMATION FOR SEQ ID NO:405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

GGCAGAGACT TGAACCAGGG AGGTGGAGGT TGTAGTAAGC CGAGGTCGTG TNACCACACT 60

CCAGCCTGGG CGACGGAGTG NGGACTTTGT CTAAAAA AAAAANNTC 120

GGGNGAA 127

(2) INFORMATION FOR SEQ ID NO:406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

AAGACTGNAN CANCCNAACA GGNCCAGGAA GTACACGAGA AGCTCTGTAG GATGGCTTAA 60

GTCCAACGTC TCTGAATGCG GTGGCTCAGA GCACCCGTAT CATTTATGGA GGCTCTGTGN 120

ACTNGGGCAA CCTGGAAGNA GCTGGCCAGC CACCTNNTGT GGATGGCTTC CTTGTGGGT 179

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

GGCACAGCGA ATACGTACAC CGTATCGGTC GTACCGGGNG GGCCGGCAAC GATGGCCTGG 60

CGATCTCGNT GATCTGCCAT GGCGACTGGN ACCTGATGTC GAGCATCGAG CGCTACTTGA 120

AGCAGTCGTT CGAGCGCCGC ACCATCAAGG AAGTCAAAGG CACCTACGGC GGGCCGAAGA 180

AAGGTCAAGG CGTCGGGCAA GGCTGTTGGC GTGAAGAAGA AAAAGGTCGA CGCCAAGGGG 240

GACAAGAAGA AGGCCGGTGC CAAGTCGCCG ACCAAACGCA AGATTGCCAA CCGTCCGTAG	300
ACCGACAACC TGTCGTTGG TTCAGCAAGG TTGGGCATGG GGNCTTTGAA AGCGNCGNAA	360
AGCCNGNAAG CA	372

(2) INFORMATION FOR SEQ ID NO:408:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 214 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

GGTCACGAGG TACCCAGTGT GGTCCCTGCC TGGACCCAGC CTCTNCTGTT GTCCCCAGAC	60
CACAACGAGT NTNCCACCAG CACCATGTCTG TNCTAACGGC GTGTGTCTCA ACGAGGATGG	120
CAGCTNCTCC TGCCTCTGCA AACCCGGCTT NCTGTTNGCG CCTGGCGGCC ACTAACTGCA	180
TGGGTAAGCC TGGAGCCAGA NTGGCCAGCG GTNG	214

(2) INFORMATION FOR SEQ ID NO:409:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 512 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

GGCAGGAGCG GAGATGCCGG TGGTCAGCC GGTGGNGCTT TCGATGGACA CGGTAAACGC	60
GGTGCTGAAC ACGCTGCCAT TGCTCGGCAC CATCTGCTGC AGGCCGAGGC GCTGGCAGTG	120
TTCGTCGGTG AGGGTCAGGC AAATCAGGCC ACGCGCTTCC CGGGCCATGA AGCTGATAGT	180
CTCGGCGGTG CAGCACACCC GGGNCAGCAA CAGGTCGCCT TCGTTCTCCC GATCCTCGTC	240
GTCCACCAGG AGCACCATTT TGCCCTTGGC GGTAGTCTTC GATGGTGTCT GCGANTGTTG	300
TTGAAAGACA TGGTGGNTGN TCCGATTTAT TGTTGTNAT GTATTNTGGT NTTACCACAA	360
AACCAAGCAA GAGGATGTTT ACGATGGAAG GTTTNANTGG GTTTNCCCNT GTGAANGTGT	420
TCCGTTGNCA GAGCAGTAAC ACGCATTACA CCCAGCGNG GGCCTGGGGC CTTTCGGGAA	480
TTTTGGCGGG CGTTTCCTGG GCCANGGGN TN	512

(2) INFORMATION FOR SEQ ID NO:410:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

```
GGCACGAGGT AAGCCCCCCC GTCGNTGTAG TGGAACAGAA ACGGCGGAAG TTTACTTTTTT      60
GCCGCCGTCC GGTAGTCCGT TGAAGCAGAA ATAATCATCG TAGTTTCTCG TNATTNTTGT      120
TTTGGTAAAC GGTGTAGTGG TAAAGGTTGT CCCCAGCAAG TGTAGTTTAG ATAAATCAAG      180
GTGATGGAAA TTAAACCAAC GAGATCGCCA TAAACAGACT AAGCTCCAGA AGAGACGCTC      240
GCTTCAGGTG TCCTGCGCGN AATGCCTNCG NNGCCTTGGA CCN                        283
```

(2) INFORMATION FOR SEQ ID NO:411:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 346 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

```
GGCACAGGCC GGTTGCCGNT AATCCGCAGC NACTGGTGCG CGGCACTGCT TTACCGCCTG      60
CGAGGCACCC TGCGGAAAAC AACCTGNACG GCAAGACCGG CTCCATGAGC GGCGTGTCGT      120
CNTTAACTGG GTATGTNACC GATGCCAATG GCGGCAACTG GTGTTTTCAA TGGTGACCAA      180
CANTTACGTG GTCGCAGGCG CGCGGNTCAA GCGGCTGGGA AAACCGCCTG GCCACGGCAC      240
TGGGCCAACA GCACGGACTT ATTGAGCACC GAAGATCAAA TTGTACGNGG GGCTTGCTCC      300
GGAATGGGGT NGTGACANTC CAACACNTGT TACTGATTGG NTCCCA                        346
```

(2) INFORMATION FOR SEQ ID NO:412:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 282 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

```
GAGTGCAGTG GTCTGATCAT GGCTCACTAT AGCTTCANTN TCTAATCCTC CCGCCTCANC      60
CTTCCGGTAG CTGGAACCTAC AGGCGGACAC GCATGCGCAT ATTTTAAGTA GAGACGGGTT      120
TCGCCATGTT GCCCAGGCTA GTCTCTCCAA CTCCTGGCCT CAAGCGAATC CTGCCGCTTT      180
```



GGCCTCCTAA AGTGCTTGGC TTACAGGCGA GCCACCACGC CTGGCTCCAG ACTTTTTTTTT 240  
TTTTTTTTTT TTTTTTTNAA AAAAGGGNTT TTTNTAANN AG 282

(2) INFORMATION FOR SEQ ID NO:413:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 313 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

GGCAGAGCGC CNATCCAGCT ATTCATNGGG TGCGGTTCN CCGGGTTTCG ATNATGTTTCG 60  
GCAACTGGGA AATCCGCCCC AGCAACCGTC CCANTGCGTC CAACCCCGGA ATCTCGATGG 120  
TCAGGGACAT CAACGCATTN TGNTCTTCCT TGTTCAACG GGTGTTGACC GNCAGCACGT 180  
TGATCCGCTN GTTGAGCAGG CACTTGTGAA GAACGTCACG CAGCAAGCCG GGAACGTTTCG 240  
TTAGGCACGG TTGGATAATG TGCCACCGGG ATACGTGAGT NACCGGCANC GGCCCCCAGC 300  
TGNACCTGNG NTG 313

(2) INFORMATION FOR SEQ ID NO:414:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 455 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

GGCANAGTTG GAAACTTACT TGAAAATCGG NCAAGGCAAA ANTTTTTTTT GTTTTGTTTT 60  
GTTTTGT TTTT TAGTTCCATG TATACTTCAA AAAGAACTT GTNTTCGGAA GTTGAGAATG 120  
CCACTGGGCG CGGTGGCTCA TCCCTATAAT TCCAACACTT TGGGAAGGCT GGAGTGGGCG 180  
GATCACTGGG AGCCCAGGAG TTCCAGATCA GCTTGGGCAA CATAGTGAAA ACTCCTCTCT 240  
ACAAAAAAT TAGCCGGGTA TGGTGGCAGG CGCCTGTNTT CCCAGCTACT CCGGAGGCTG 300  
AGGCGGGGAG GATCACTTGA GCCCCGGGA GGTGAGGCT GCCATNCAGC CATGATTCCC 360  
ACCATTACAT TCCANNCCGG GGNAACAGGT TTAAAAAAA AAAACNCGG GGGTATTTTT 420  
AGGGGGCCCCG GGGGCCCCCTG CGTTTTNCCC CCCGG 455

(2) INFORMATION FOR SEQ ID NO:415:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

ACTTTTNAAA CCCGAACTG AAGACACTCA TCATCAACCG AAATGTCGAC TGNCGTTCCG	60
TCTCTCGGGG AAATCAACGC CCTCAACGTG CCCTCCCTTC CGGGCAACCT GAACAAGCCC	120
AATCAGACCC CCGCCTGGAC CAGCAACCCT CTGTTTGTNT ATNTNACCGA GACGTACAAC	180
ACCATTGCNT CGAAGCGNAG TGGNCCTGAA CCTCCTTAAA CCCCGBAACC CTGGAGAACC	240
TCAACAAGGA GGTGTNCAAG GACGTGTTCC TCACCAACTA CTTCTTTCAC CGGTTTGCGG	300
GCCGAGATCT TCCAAGACAT TTCAGCATGA ACCCNGNCTT TCCAGTGTTT CCATTCTTTT	360
TTTTGGGGGT TCCAAGGTGT TNCCCCCTTA GGNNTTTN	398

(2) INFORMATION FOR SEQ ID NO:416:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 111 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

TCANCATATG CATTTTTTGG TGCAACTTTN CGGGAGGNGC ATAAGAAGGA AGTCACCCCG	60
ATGCTTCANT CAACTTGCTC ANAGGTTTCT AAGAAGTGGC TCAGAGNGGT T	111

(2) INFORMATION FOR SEQ ID NO:417:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 353 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

GGCACAGGTG ATCGGNACCC AGNTCGAGCA CGTNCCGGCC ATGCTGGAAA CCATCTTCAA	60
GAGCGCCTTC GGCCTCGACC CGGCATTCCG CGGCCTGGTC GGCACNCCAT TGTNATGGGT	120
GTAAANGAGG TGTGTTGCGC AACGANNCAG GCCTGGGGCA GTGCGCCCAA CGTCGCCGCC	180
GTANGCCGAT TNAAACACCC CGGTGCNCAA GGCCTGGTCC AGGCCTTCAG CGTGTTCCTC	240
GATACCTTCG TGNATCGGCA CCTGCACCGC GTTGNCTGAT CCTGNTGTCG GGGTTCTAAC	300

ACCNCAGGNT TTCGAAGGTG AATGGGNATC GTGCTGGACC CAGAATTGGG TGG

353

(2) INFORMATION FOR SEQ ID NO:418:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 481 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

CGGGAACAGG TTGGNATCAA TATTCTCCNC TGGCGTNAAG ATCANCCCGT NATCCGNCGC	60
AAACTNTTAT TACAAACCAC GCAGGAATCG ATTGAGAACC ATTGGCCGTT TCGTCGGCTA	120
TGAANGATCA GCTGTATTTT TGGCGGGTAT TCCGCAAGCG GGTGGAGTG AAGCCCGANT	180
AATTTTGGTC GCCGCACGTG GNAGATTAAT TATCCTGCTA AACCGTATAA AGCGCCGGCG	240
GGATAAATGC GAATTGCATA CCATTTTAA GGCTTTGTTA AGCCTGAGAG TTTTTTTTGC	300
AAGGGAACCG CTTGCTAAGG GCGGTTTNC CACCTTTTCC CTCGNGTGG ATTTTTTGAA	360
ACGGGAACCA CAGGNTTTTT AAGGGTCCAC AAATTTNCCC CGGGTTCAGG GTTCCTTTTT	420
AAAAAAGGC GAGATTGGTG CGNATCCAAA AATTNCNCTT GAACGGATTG GNCAGGGTTT	480
	481

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(2) INFORMATION FOR SEQ ID NO:419:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 132 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

TCGAATTCCT GGAATCAAGC AATCCTCCCG TNTNAGCTC CCAAATTGCT AGGGTTNTAG	60
GTGTAAGCCA GCCCTGGCAA CAAAGTGTGA AGACCCTGNT TCTGACCAAA AAAAAAAAAA	120
AAATTNAAAN CA	132

(2) INFORMATION FOR SEQ ID NO:420:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 357 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

CNGNGCTTCC ATCGGNTNAC CGCTGCGTTG CCACGGGCGC TTGAAGGTGC CCATGCCAAA	60
CATATCCGNC CCCGGCCACA CAAAGGTGTG CCACTGAACA GGCGGCCATG CGCAGGTGCT	120
CGNGCCATCG GTTTGCCGAG GGATCAGCTT GTTTGCNTCG TAAATGGCGG AAGGCGAGGG	180
GAGAGTCGCT GGCAAGGCCT TCGAAGCGCA CCTGATTCTA CAACGGGGAN NTTACGGGCA	240
TGGGNGTTTT CTTATTGTT CTTGGGCGAT GTTTGGGTTA TTAGCAAAGG NACCTGGGGT	300
TGCTGNTTTT TGGAAATTAA CCAAGGTGTA NTNGCGGTTT TGAGTTGGNG AGGGTTA	357

(2) INFORMATION FOR SEQ ID NO:421:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 517 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

GGCACAGCAG CNCTCAGGCA GCTCCAGCAG CAGATATTTA GCGCGCCGCT GCACGCTAAG	60
CACTGGTTGG TCGCTTAAAC GGTAGATCTC TTCTGAAACC GGCCAGCGCA ATTGCCGTTG	120
CGCACCACTG CATGAAGAAT GGTGACCA ACNAGNATGC GGTCTATGC CGCGCGGCT	180
GGTTTCAACT TCGGGTAATT CAGGCATAGC ATCTCCAGGG ATGAACAGAT GGAGTCAATA	240
TGGGGGCAAG CAGNTATCAA AAAACCCCGC CGGAGCGAGG TTTTTTTTTT ACATGCAAAG	300
CGGAGAATTA TTTGATTTTG CGCTTCTTTG TAGATNCACG TGGCTGGGCG GAACAACCTGG	360
GNCCGAATTT TTTNANTTNC CAATTTTTTC CGGCTTNANN ACGTTGTTN CCTTCGTAGT	420
GGNTNTAGAA GNGNCCANT ACCNGNAGGA GGAACCCACT TTGNTTTTTT CAAGGATAAC	480
CTTTAGNCCA GGNTTTTTTC CCNTAAGNAT TNAGACT	517

(2) INFORMATION FOR SEQ ID NO:422:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 459 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

GGCAGAGCAG CCCTCAGGCA GCTCCAGCAG CAGATATTTA GCGCGCCGCT GCACGCTAAG	60
CNCTGGTTGG TCGCTTAAAC GGTAGATCTC TTCTGAAACC GGCCAGCGCA ATTTNCGTT	120

GCGCACCACT GCATGAAGAA TGGTTGCACC AACGAGATGC GGTCTATGC CGCGCGGCT	180
GGTTTCAACT TCGGGTAATT CAGGCATAGC ATCTCCAGGA ATGAACAGAT GCAGTCAATA	240
TGGGGGCAAG CATNTAACAA AAAACCCCGC CGGAGCGAGG TTTTTTTTTT ACATCAAAGC	300
GAGATTATTT GATTTTCCGC TTCTTTGTAG ATCACGTGCT NGCGAACAAAC TGGATCGATT	360
TTTTTCAGTT CCCATTTTTC CGGTTTAGTA CGTTTTNCCN TCGTAGTGGT ATAGAAGTGA	420
CCCATTANCC GCAGAGGAAA CCATTTGATT TTNTCANGG	459

(2) INFORMATION FOR SEQ ID NO:423:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 391 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

GGCACAGGTT TTTNGGGCTC AGTTCGTGGT GCCAGCTGCC GTGGGTGCGG TGAATGAAAC	60
GAGTTTCACA GAACTCCCAG AAGCGCCGGT ACCAGGTTTC GTAATGCAGC TCCCCCGTGC	120
NTTTGAGCAG CGCCTGGGCA GCGGCACTGG CTTCGCAATG GGTCCAGTGC AGGCGCTCGC	180
GCACNANGGG GCCTGGCTCC AGTCGAGGGT GTAGACAATG CCGGGGGCGC CGTCGACGGC	240
CCAGGCGTAT TCACAGGCGC TGGCGAACAG GCCCTTGGCG TCGGTCACTA ACCACTCAGG	300
GGTGACGAGC CCGGCATCCA GCGCGCACT TCAGGGTGCA AACCANTCGN GCCCATTGAA	360
ACCNTGGCCC GGGGGTGATN CCNTAGGGAC G	391

(2) INFORMATION FOR SEQ ID NO:424:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 452 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

GANTTGGCGG TCAGGTCACC GCGGCTTCC ANGGGCGAAA TCAGGAAGAT CACCGCCACC	60
GGGATAAACG CCACCCAGTC GAACGAAAAA CCGTACTTGA ACGGCACCGG TACGCTGATC	120
AGTGGCAGCT GGGGCAAGGC GCCCAGGTCG ACGCGGCCCA TCCACCAAGC CACCACAAAA	180
CCCAGGGTCA GGCCGATCAC GATCGAACCC AGGCGCAGGA ACGCTTTGTT GGAAGCGGTT	240
GAGCACCACG ATGGTCAGCA GCACCAGGNT CGCCACCATN NTTTTNCCGG CGGNGCCAG	300

GTCGTTGGCG CCATNAACCG CCGGNCATGT TCGGTGACGG NCACTTGNTC AGGGACAAAC 360  
CCTTCAAGGT AATGATGGTG CCCGTGAACC ACCGGGGTGT TTAATTTGGC CATTTNCCCG 420  
TTGAAATGTT TGNGNACCNT TTGNTTAAAA GC 452

(2) INFORMATION FOR SEQ ID NO:425:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 342 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

ACACCAACTA CCAGTATCAC CGGCAGTTGT NCCTGTNTTA CCCANTCTGC ANAAGTGAAA 60  
GTNTCAGAAA GCGGCGTAAA CCAGCCGCCA GCACCTTCCA CTAACACCCA GTCAGCCTGT 120  
TGTNCAAGCG CCGCGTAAAT CCGGCGCTCA TTACCAATGA ATTCTATCGG TCTGCCCTCT 180  
TGCGCCGCTG GATGATGTGC GGCGNAGTGG GTTCTGCGAA NGTGTGAAGG NTTTACTGTT 240  
GCGTAATCCA GCTGCAGGCT GCTGTTGCCC TGTGAACGCC AGGCGTCGCT ATTGCGTGAA 300  
CCCTTCCGGG GTNTTTTCCG NTGNCANTGG NGACCGGTTT TT 342

(2) INFORMATION FOR SEQ ID NO:426:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 377 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

GGCACGAGGN CAGCCAGACC TTGCCGGTTC CCGACGGCCT GGACTGGATT CAGGCGGCAC 60  
GAATCCCGGA AACCTTCTTC ACCGTATGGG CCAACCTGTT CGGCATCGGC GGTGCGCATA 120  
AAGGCCAGCG CGTNTTGATC CATGGCGGCA CCAGCGGCAT CGGCACGACC GCGCCTGATG 180  
CTCTGCCGCG AAGTTCCATA TCGAAGCGTT CGCCACCGCC GGCAGCNTGG NAAAAATGCG 240  
CCGNCATCCG CGAAGCTGGN TNCCGAGCCG ATCAACTACC GGGAACAGAA TTTCGCCGAG 300  
GTCATCGCTG ACAAGACCGC AGCGANAGGN TGTCAATGTN GGTCTTCTGA AATCATGGGT 360  
GGCTNCTACC TGANCGG 377

(2) INFORMATION FOR SEQ ID NO:427:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

GGCACGAGGG AAGCACGGCC CANCCNTCCG GAATTCAACA TTGGCTCAGC AGGGAATTCA 60  
GCCCCANCCCA CGGNACCTGN 80

(2) INFORMATION FOR SEQ ID NO:428:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 490 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

CNNCTGCAGG TCGACACTAG TGGATCCAAA GAATACAGCC GAGTTTCACA CCAACTACCA 60  
GTATCACC GG CAGTTGTNCC TGTNTNACCC AATCTGCAAA AGTNAAAGTN TCAGAAAGCG 120  
GCGTAAACCA GCCGCCAGCA CCTTCCACTA ACACCCAGTC AGCCTGTTGT NCAAGCGCGC 180  
GTAATCCGGC GCTCATTACC AATNATTCTA TCGGTCTGCC CTCTTGCGCG CTGATGATGT 240  
GCGGCGAAGT GGGTTCTGCG AAGGTGTAAG GATTTACTGT TCGGTAATCC AGCTTGCAGG 300  
CTGCTGTTGC NCTGTAACGN CAGCNCGTCTG CTATTGCGTA AAACCTTCCG GGGTCTTTTC 360  
GGTTGCCAGA GCGGANCCGG TTTATAAAAC CTGCCGTNCC GGTAGCCTGT NGGCTTTTTC 420  
NGGGTTGGTA AAAAGTNGCA CAATTGGGGG AACAATTTTT CCCCCANTTT GGGGTATCCC 480  
GTTTCCGGTG 490

(2) INFORMATION FOR SEQ ID NO:429:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 359 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

GCTGAATATN ATCGAGTGCT GGGGCGATGA TGTACCTCAG GGGCAGGTNA CCTCNTTTC 60  
CATGGCGGTC AAGCTCAAGG AGGATGAAAC CNTGGTGTTT TCCTGGATCG TNTGGCCGTC 120  
GCGGCAGGTG CGTNTCGNCG GGAATGAGCA AGGTGAATGG NAAGACCCGC GCCCTGAAAG 180

GCAGACGTCA ATCCGATGCC GTTTGATGGG CAACGGGATG GATCTATGGC GGATTTAAGA 240  
TGATCCTCAA CACCTGAGGC CAGGCGTTCA TGGGACGGCG GCTTTANTCC CGATTCTGTCT 300  
NTTCGCANGG TTAGGACCGA CGATAAATTC TGGGTTGCAA GACCANTGNC GAAAAAAGT 359

(2) INFORMATION FOR SEQ ID NO:430:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 357 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

GGCACGAGCA AACTCTGCT AAGGACCATA AGCATATTTN ATCACTTGCA GAGAGGCATC 60  
ACTGTCACCC CAATTTACAG ATGGGAAACT GAGCAGAAAG TTGTTAAAAC ACCCAGCACT 120  
TTGGGAGGCC GAGGTGGATG GATCACTTGG ATCTCTGGAG GTTGAAGCC AGCCTGGGGA 180  
AACATAGCAA AACCCCATCT CTACAAAAA AATCCAGAAA TTAGTTGGGT GTGGTGGCGC 240  
ACGCTGTGAG CCCAGCTGC TTCAGAAGGC TGAGGCTTGC AGTAAAGCTG AGGTTTGCCA 300  
CCCACTGGCA CTTCGNGGCC TGGGGGCAAC AGGNGACCCT GTTTTCAAAA AAAANN 357

(2) INFORMATION FOR SEQ ID NO:431:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 339 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

NCGATATCGC CACGNTCGTT CAAATACTTG AAGTCGACGT TCTGTGAACC GCTGCCATGC 60  
AGATGAATTT NTCCTGTNCG GCCGGCAGTN CGTTGAACGG CACTTCCAGG GCTGAACTTG 120  
TAGTGCGAAA NCAGACGAAA CCCAGCATCT GGAAGTAATA GACGTTACGC CTGTCCCCAG 180  
NCACGTATCG CACCCTTCCG NCAGTNTGNA GGTCACCGTT GAACCAGGCG CTTGATTGTT 240  
CGAAGAATTG CTTTAACCN CAGGNCATCA CAGGTTTCGG CAAGTGNCCG GCCGGGGTTG 300  
TTTNAAGGG AAAACAAGT TTCGGTTTCC AANTTCGCT 339

(2) INFORMATION FOR SEQ ID NO:432:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid



- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

GGCAGAGGNC GNCGGCGGNG GCGGCGGGGN ACTCGGACTC CTGGGACGCC GACGCTTN 58

(2) INFORMATION FOR SEQ ID NO:433:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 367 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

GGCANAGTTT GCATTTAGGA GAAGGGCAGA TGGTGTGTGG TCGAAAGCTC ATGGGACTGT 60  
AAATTGGTAG ACTTTTTTAA AAATCCAGCT TTTGCCCTA ACTTTTGGTC TCGGAGACCT 120  
CTGTCCTTTA ATAAC TAGAA CTGTAGGCCG GCGTGGCGG CTCATGCCT GTAAATCCCA 180  
GCACTTTGGT AGGGTGAGGC GGGCGGATCA CAAGGTCAGG AGTTTCGAGN ACCAGCCTGG 240  
CCCAGCATAG TGAACCCCTG TCTCTAGTAA AATTACAAA TTTAGCCAGG CATGGTGACG 300  
TGCGCCTGTA GTCTTCAGCT ACTTGTTAAG GGNTGGGGGC AGGNGNTTTG CTTTGNAACC 360  
CGGGGNG 367

(2) INFORMATION FOR SEQ ID NO:434:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 287 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

AGCTTCCAGG TTGAAGCCGG NGAGCGCGTG GCGATCATCG GCCCGAACGG TATCGGCAAG 60  
ACCACCCTGC TGCGTACCCT GGTCAACGAA CTGACTCCGG ATGCCGGTAC GTGCAAGTGG 120  
TACCGACGCG GCTGAAACTG GGCTATTAAC GCCCAGAACC ATGCTTCGGA ACTTCAAGGA 180  
CGAAGTCCAA CCTGTTNCGA CTGGGTTGGG CCGCTGGACC AAGGGAAGGG CGAGCAAGTG 240  
NGTTCGCGGT ACCCTGNNGC CGCAAAC TGG TTCTTCCAAC GANGNGG 287

(2) INFORMATION FOR SEQ ID NO:435:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

GGCACAGTAA AAAGGTTGAA AATGGCTTTT TTCCACTAGG AAGGCTGTGG GGACATAAGC	60
TGACAACTAC CCTACATGGA ACAGGCAACC CCGTCATGCA AGTAGGCCTC TCTCCCAAAG	120
GCACCTCCAT CCCTGCTGTC ATGTGGCACA GATGAGCACA CCTACTACGT CACAATGCAG	180
TGTAGCCACG CCAGACTGGA CCAAGGACAC ACTCTTAGCC TTCTCTTCTC TCCAAATTCA	240
CTTTATTAAT CTTTAANCCC ACACATCCGT GGTGCGGAAA GGTGTCCTTT GATTCTTCCA	300
AAATTCAAAA GGGCNTTCCC TGNTATGGNT GTCTGGGATT TATNTT	346

(2) INFORMATION FOR SEQ ID NO:436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

GGCANAGCTA GTNCTTTNTT CCATAAAAAA AAGTCGTGCC TGTGGTTATG AAAAAATGTT	60
CAACTAACCT AGAAGAGTTC AGCTACCAAG TGAAGGATTA TGGGAAAGCA GTATTTTTTC	120
AGACCTGGGT ATGCATGAGT GAATACCCAT GAAAGCTTTA TGAAAAATAT ACATCTCCTG	180
GGCCCCATT AATCAGAATT TCTGTGGGTG TGGCCTCCAA GTTCATACTT TAAAATGGGA	240
TCTCCACATA ATTCCATGTA CACCCAGGCT GGGTAAACA CTGAGTTTCA TGTATTTATT	300
ACTATTCCAG AAACAAACAC AAATCTTGG GGTGGGATTT TAAAGGGNGC AAGGTTTTTN	360
GGNTGGTGTT AAGCAAAGCC ATTTTNAAG TTGGTCTNTT GGCAACTCCA AGG	413

(2) INFORMATION FOR SEQ ID NO:437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

AANCTANCGC NANGNGCGCC TGCAGGTCGT AACTAGTGG ATCCAAAGAA TTCGGCACGA	60
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GGGTGCACCT GGCGATTCCG AAAAGCTCGG TGTTCGTGCG TNATGAACGC AAGCCCAGCG	120
CCTCGGTCCT GGTGGAACCT TTTGCCGGCC GCTCCCTGGA GCCTGGCCAG GTATTGGCGA	180
TCATCAACCT GGTGGTCCAC CNACNTTCCT GAATTGAGCA AGTGCGCAGA TCACCGTAGT	240
CGACCAGAAG GGCAACCTGC TGTNCGGNAC CTTGCGGAGG AACTNTTTNG CTGACCATGG	300
CCGGNCAAGC AGTTCGGACT GACAG	325

(2) INFORMATION FOR SEQ ID NO:438:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 104 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

GGCACGAGGN AGAAAAGGAA GGGTGAAGG AAAAGAAAAG AAAAAAAGGA AAGGAAAGAA	60
AGGGAAAGAC AGGAAAAAAA AAAAAAAAAA NCNCGGGGGN NCTT	104

(2) INFORMATION FOR SEQ ID NO:439:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 158 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

GGCACGAGGC CATGGTGTCTG ACCAGGNGGC TCGGTTTCATC AATGCTGTTG AGCGAAGACA	60
GGACTTCAGC CGGGACTTTN TTGCCCAACT GCACATATTG CTCGAACTGC GACANAGCTT	120
GCGCACGNAC AACTNGGATT NATGATCCCG GGCTTCGA	158

(2) INFORMATION FOR SEQ ID NO:440:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 372 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

NNGTANNGCG CCTGCAGGTC GACACTAGTG GATCCAAAGA ATTCGGCAGC AGCCGNCACC	60
CAGCGTGGCA TGACCTTGGA ACTCAGAGGT CGGCTTTTTG CGTACCAGGT TGATAGTGGC	120

CCCCAGTGAA CCAGCACCGG TCAGCAGGNC ANTCGCGCCC TTGAAGTACT TCAACACGGT 180  
CGTAGATCGC CATGTCGCTC AGCGTGTTCC CCGTCGAGTA AGCCACGTTG CGTGCGGTGG 240  
AAGGGNATCC CGTNATATTN GGAAGTTGTT GATAGAGAAA CCACGAGCGT AGTAGTTGCT 300  
GCCTCAGTA TCGAAGGCTT GAAACGGNAA TGCCCGGCGT NTGGNGCATC AAGTTNGNCG 360  
ACACTGGTCA GG 372

(2) INFORMATION FOR SEQ ID NO:441:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 139 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

GAGTAGGNGC CCATNCATCT TTGCTGTGGA GCATTNGCTC CTTTTNNGG GTGGGAATNT 60  
GCCTTGCCCG GTCTGCCGGA AACCAGCAGG AGCAACCTGC GTNCCCACA AAATTTNNGG 120  
TGTA CTGGAC CCACTNGCA 139

(2) INFORMATION FOR SEQ ID NO:442:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 509 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

GGCAGAGTGN CATNCAGNTC GGACCGAAAA AAGTGGTTTA ATTCGGGCTG GCTTGTGCG 60  
GTGTGAGCGG TCTGTTTTAT GCCATGGCTT TTTGGTTCAC TGGTCTGCCG TTGCTGAGTT 120  
TAATTCTGCT GTGCATTGGC AGGGTGTTTC TCGGCGTCGG CNAAAGCTTT GCCAGTACGG 180  
GGTCTACCTT ATGGGGGATT GGCCTGGTGG GGCCGTTGCA TACCGCCCGG GTTATCTCAT 240  
GGGAATGGGG TGGCGACTTA CGGTGCGATG GCTGCCGGGG CACCGCTTCG GTGTTTTACC 300  
TCAATCAGCA CTGGGGGGTT GGGCTGGGGG TGGCGGCGTT GATCGTGTTG GNCGGTGGNC 360  
GGTTTCGCTG TGGGNTGTG GAATTNCAAA CCAACGTGA ACGATTCNNC GNCGTTAANG 420  
GTAATTGCCC TTANCGAAT TTTNNGGGGC TTATTTGGAC TTAAGGTTTT GGGACTTGCA 480  
ATGGGTACCT GGGTTTTGCC GGNANCGNA 509

(2) INFORMATION FOR SEQ ID NO:443:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 480 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

GGCAGAGCTT GGCTTCGCTG GTTTTCGGCT GTTCCAGGAT GGTGCTGACC TTGTTGTAGG	60
TCANGCGGGC CTGGGAAGTN AATCACCGCT TCGTAGAACT GGTAGTCGGT CATTTGCGCCG	120
GTTTTTCGAGA TGGTCATCTC GCACACCATG GCCAAACGGT CGACTTTCGG GTTCAGGGAG	180
CACAAGCCGT TGGGACAGCT GCTCAGGCAC ATAGGGGATG ACGCGCTTCG GGGAAGTACA	240
CCGGGTTGCC GGGCAACTGG GGCTTCGTTT NTCCAAGGCC CGNACCNGTT CTTTAAGGTA	300
GCTTTGGACA AGTTGGGCAA TCGGGGACGA AACNAATTTT TCCAAGCCNG CNGGAGGAAC	360
AAAGGGGCAA NTTTNCCAA GGTTTTGGGT TTCGCAATTA AAACCCCAT TGTTCGAAA	420
TTCNCGGGG NAATTTTNGG CCNGAANTGG GGGACGGAAC CGGAAATTTT ACCGCAAATT	480
	480

(2) INFORMATION FOR SEQ ID NO:444:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 482 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

GGCAGAGGAA GACATCCCAT GTTTATGAGT CTGAAGACTT AACATTGTTA AGATAATACT	60
CTCCAAATTG ATTAAGAGGA TAATACTCTC CAAATTGATC TACAGATTCA ACATGATCCC	120
TATCAAAATC TCAGCTGGCT TCTTTGTAGA AACTGACAAA TTGATTCCAA AATTCATATG	180
AAATTGCAAG GGATGCAGAA CATCAGAACA ATCTTGTAAG AGANCAAAAC TGGAGTACTC	240
CCACTTCTCA AAAACTTACT GCAANGCAA AGTAATCAAG ATAGGTTGGG GCATGGTGGC	300
TCCTGGACTG TAATCCCAGC ACTTTGGAAG GTCCGGGGCG AGTGGGGTTC ATTTGAGGTT	360
CAGGGGTTCC AAAACCAGNC TGGGCCACCT GGGTGAACC CCCTTTTNTA CTAAACTTTT	420
TAAAAAATTT GGNTGGGGCT TGGTGGGCGG GGNCGTAAT TCCCGGTAC TCNGGGGGGT	480
TT	482

(2) INFORMATION FOR SEQ ID NO:445:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 253 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

GGCAGAGGGC TTCCAGGCAC ACCAGCGCCA GGNAGTAGCG CAATTCGTCA TCGTCCGGGT	60
ATTGCNGCAC GAGGTTGGCG AACTGNACCT TGGCGTCTTC CATGCGGTCC TGTTGACCA	120
GCATGCGGGC ATAGGTCAGC AGCAGGCGTT TGTCGCCC GTACTTCTTG ATGCTTTTTT	180
CCCAGCAACG GGAATCGTTT NCTTGCCNGG GTTTGAGGTT TTNCAACAAG CGGGCGCGCA	240
NANGGATTCG GGG	253

(2) INFORMATION FOR SEQ ID NO:446:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 168 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

GGCACAGGAA GGAAGAAGAA GAAGGAGGAG GAGGAGGAGA AGGAGGAAGA NGAAAGAAGA	60
AGAAAGAAGA GGAAGAAGAA GAAAGGAAGA AGGAAGAAGG AGAAGGNGGA GAAGGNGAAA	120
AAGCGNANAG AGGGAAGGAA GANGAAGGGA AAAAAAAAAA AAAAAACC	168

(2) INFORMATION FOR SEQ ID NO:447:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 340 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

GGCAGAGGNA AAAAGGGAGA TACTATTTTN AGTAAATTTG AGGGCAAGGA ATATACAAAG	60
GAGTTAGGTG GCTTGGAAGA AGATTTTTC TATATATGTA AACTAAGCTG TGTGTGGGTG	120
GGTATTTTGC TTGTTGGTTT TTGAGACAGG CTCTCACTGT AGTCCAGGCT GGAGTGCAGT	180
GTGGCAGTCA TAGCTCACTG TAACCTTGAA CTCCTGCACT CAAGCCATCC TCCCACTTCA	240
GCCTCCTGAG TAGTTAGGAC TACAGGTGCG TGCTACCACA CCCTGCTCAC TTTGGCATTT	300

TTTTNTNTTT TNTGTTTNTT TGATTTTTTT GGGACATAGT

340

(2) INFORMATION FOR SEQ ID NO:448:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 309 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

GGCAGAGTCT GGACCGGNCT GGCCAATATG GTGAAGCCCC CCTCTCTACT GAAAATGCAA	60
AAGTTAGTCG AGTGTGGTGG TGGGCACCTG NTAATCCCGG CTATTTGGAA GGCTGAGGCA	120
GGAGAATTAC TTGACGCTGG GAGGTGGAGG TTGCAGTGAG CCAGGGTCGT GCCGCTGCAT	180
NCCAGCCTGG GNAGACAAGA GTGAGACATT ATCTCAAAAA AAAAAAAAAA AAAAAANAAA	240
AAAAACCCGG GGGGGTTTTT TTTGGGGGGC CCGGGGCCNN TGNTTTTCCC CCCGGGGGGG	300
GTGNCCCCG	309

(2) INFORMATION FOR SEQ ID NO:449:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 317 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

AGCTTCCAGG TTGAAGCCGG TGAGCGCGTG GCGATCATCG GCCCGAACGG TATCGGCAAG	60
ACCACCCTGC TGCGTACCCT GGTCAACGAA CTGACNCCGG ATNNCGGTAC GTNCAAGTGG	120
ACNGACGCGG NTGAACTGG GCTATTACGC CCAGGACCAT GNTTCGGAAC TTCGAAGACG	180
GAGTCCAACC TGTTGACTG GATGGGCCGC TGGACCAAGG NAAGGCGAGC AAGTGGTTTCG	240
CGGTTACCCT GGGCCGCATN GTTGTCTTN CAACGNCGAG NTCCTTTAAT TCGGTTGTAG	300
GTGAATTTCC CCGTTGG	317

(2) INFORMATION FOR SEQ ID NO:450:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 371 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

GGNACAGCTC GCGGGAGCGA TATCGCCACG GTCGTTCAAN TACTTGNAGT CGACGTTGTG	60
TGAACCGCTG CCATGCAGGA TGGAATTTCT GCTGTTTCGGC CGGCAGTTCG TTGAACGGNC	120
ACTTCCAGGN TGAAC TTGTA GTGCGANNCA ACGAAACCCA GCATCTGGGA GTGAATAGAC	180
GTTACGCC TN TCCCAGCCAC GTNATCGCAC CCTNNGGTCA GTNTGTAGGT NANNNTGTGA	240
CCANGCGCTT GGATGTT CNT AGAATTGCTT AACCCCCAGG CCATCACANG TCGGGCAAGC	300
GCCGGCCGGG TTGTTGAAGG AAAACANCTT CNGTTNCCAG CTCGTGAATG GNATGGCCTC	360
AGATTCGTGC A	371

(2) INFORMATION FOR SEQ ID NO:451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

GGCAGAGCAG CNCTCAGGCA GCTCCAGCAG CAGATATTTA GCGCGCCGCT GCACGCTAAG	60
CACTGGTTGG TCGCTTAAAC GGTAGATCTC TTCTGAAACC GGCCAGCGCA ATTGCCGTTG	120
CGCACCACTG CATGAAGAAT GGTTGCACCA ACGAGATGCG GTTCTATGCC GCGGCGGCTG	180
GTTTCAACTT CGGGTAATTC AGGCATAGCA TCTCCAGGGA ATGAACAGAT GNAGTCAATA	240
TGGGGGCAAG CAGATANCAA AAAACCCCGC CGGAGCGAGG TTTTTTTTTT ACATCCAAAG	300
CGGGNATTNT TTGATTTTCG CTTCTTTGTA GATCACGTGC TTGGNGAACA ACTGGTTCNN	360
ATTTTTTT	368

(2) INFORMATION FOR SEQ ID NO:452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

GGCAGAGGNA TGGGTGCCTG TGGTCCCCAG CTGCTCGGNA GGCTGAGGCA GGACAGTCGC	60
TTGAACCCGG GCAGCAGAGG TCGNGGTGAG NCNAGAATTG TGTCGCTGNA CTCCAGCCTG	120
GGCGACAAAG GAAGACTCAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAAC N	171



(2) INFORMATION FOR SEQ ID NO:453:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 508 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

GGCACGAGGC GCTGAATATC ATCGAGTGCT GGGGCGATGA TGTACCTCAG GGGCAGGTGA	60
CCTCGTTTCC CATGGCGGTC AAGCTCAAGG AGGATGAAAC CGTGGTGTTT TCCTGGATCG	120
TCTGGCCGTC GCGGCAGGTG CGTGAACGCC GGTNATGAAG ACAAGGTGAT GGAAGACCCG	180
CGNCCTGAAG GCAGACGTCC AATTCCGATG CCGTTTGATG GGCAACGGGA TGGATTCTTA	240
TGGGCGGATT TGAAGNATGG ATCCCTCCAA CACCTGAGGG CCCAGGCGTT TCATGGGACG	300
GGCGGGTTGT TAGTTCCGAT TCGNCTGTTC GCCAGGGTTA GGGACCCGAC GGATTAAACT	360
TCTGGGTGGC AAAGACCCAT TGCCGNAAAG ANTNNATTCT TAGAGCGGCC CNGGGNCCCA	420
TTCGTTTTTT TCCANCCCGG GTTGGGGTTA CCAGTTAAGT NTTACCCATT TCGGCCTTTT	480
AGTGATCGAA TTTTACAATT TCATTGGC	508

(2) INFORMATION FOR SEQ ID NO:454:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 488 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

GGCACGAGGC CATGCGCAAG GACGTGCTGG CTAAGTGCTA CGGCGGCGAT ATCTCCCGTA	60
AGCGCAACTG CTTGGAAAAG CAGAAGGCCG GCAAGAAGCG CATGAAGACG CTGGGCTCCG	120
TCTCGGTGCC GCAGGAGGCN CTTCGTGGCC GCGCCTGTCT ACCGACGCCG ATGATTAACC	180
CACCCAAGCA CGCCGAACCC TTCTCGCAGC CGCGCCTTGG TTGCGAAGGT TGTCAGCTGC	240
CGGATTCCAC GGCANGCTTG AGCGNCCCGG TCCGCGCAAG AGGGGTTGGG GCTGGGGCTT	300
TAGGCGAGTA NTTAGGTTGA ATCGGCCCAG GGTNGGACCC AGACTATTTCG GTNCTGGTGT	360
TCGTTTCGAGA GTTATTTTTA NAGCGGNCCG GGGGCCCAT TCGATTTTCC ATCCGGGTGG	420
GGGTACCAGG TNAAGNTTAC CCAATTGGNC CTTTAGTGGA TCGTTTTACA AATTNATTGG	480
CCTNGTTT	488

(2) INFORMATION FOR SEQ ID NO:455:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 493 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

GGCAGCAGNA CTGCGGCGTG CTTCTGTCTG CGTTTCGCCA AGANCTTCAA TTGGGCCCCAC	60
CTGGACATCG CCGGNACCGC CTGGTANCAG CGGCGGCAAG GACAAGGGCG CCACTGGCCG	120
TCNGGTTCCA TTGCTGACCC AGTACCTGCT GGAACCGCGC CAAAGCCTGA AAATNAAGAT	180
TNCCGGGCGC TTGTAAACC GCCCGNGCT GCAGGGAACC GCAATGTACC CAAGTNGACT	240
TCTTATATAT TGCCCAGCGC CGATTCTTC CGCGGGCCTG GNACTTTGCC TGCAAGCTTC	300
ACCGNAAAAA GCCTGGCGCA TGGGCCACCG TATCTNACCT GGCATTNGCA ACGGTTGCCG	360
NCCAGNTTNA CGGACCTTGG ACGGNCCGTC TGTGGGGGTT TTCAAGGGGC GAAAGTTTTC	420
GTGMNCCCAG GGTGNCCGCC GAATTCAGAA CCGGAAGGGC TGGTTGGTAC TNGGGTTTTG	480
GGGCGACAAT TGN	493

(2) INFORMATION FOR SEQ ID NO:456:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 396 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

GGCAGGAGCG CGAAGTGGTT GCGGTACTCC TTGAGCGAGC TGCCTTCCGG CGCCACATCG	60
GTGTCGTGGA AGCTGTAGTA GTCGATGCCC AGCTTGAGGA AAAACTCAAA GGCCGCGTCA	120
CCTTGCCGAT GGCCACTTCC ATCGGCTTNA CCGCTGCGTT GCCACGGGCG CTTGAAGGTG	180
CCCATGCCAA ACATATCCGC CCCCAGGCCAC ACAAAGGTGT GCCAGTAACA GGCGGCCATG	240
CGCAGGTGCT CGCGCATCGG TTTGCCGAGG ATCAGNTTGT TTGCGTCGTA AATGGCCGGA	300
AGGCGAGGGG AGAGTCGCTG GCAGGGGCTT CGAAGCGCAN CTNATCGACA ACGGGGAAG	360
TACGGCATGG GGCCTTTTTT CTNATTGTTC NTNGGG	396

(2) INFORMATION FOR SEQ ID NO:457:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

GGCAGAGGCC	GGTTGCCGNT	AATCCGCAGC	GACTGGTGGG	CGGCACTGCN	TTACCGCCTG	60
CGNGGCACCN	TGCGGNAAAA	CAACCTGCAC	GGCAAGACCG	GCTCCATGAG	CGGCGTGTCG	120
TCGTTGAACT	GGGTATGTCA	CCGATGCCAA	TGGGCGCAAC	TGGTGTTTTC	GATGGTGACC	180
AACAATTACG	TGGTCGCAGG	CGCGCGGGTC	AAGGCGCTGG	GAAAACCGCC	TGGCCACGGC	240
ACTGGCCAAC	AGCACGGACT	ATTGAGCACC	GAAGATCAAA	TTTNGACGN	GGTTTGCTCC	300
GGAAATGGGG	TTGTTGACAT	TCAACACATG	TAANTGATTG	ATCCCAGCGT	TTTTCGGGGN	360
AAAANCCC						368

(2) INFORMATION FOR SEQ ID NO:458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

GGCANAGGCC	AGGCCATCGC	CCTCAAATAC	GACGGGCAAC	AAGCGCCGAC	CCTNNNCGCC	60
AAGGGGAGCG	NATGCCCTGG	CCGAAGCCAT	GCCTCAAGCT	GGCCCGGGAA	GAACGANTCC	120
CGATTTACGA	AAATGCCGAG	CTGGTCAAAT	TACTGGCACG	CATGTNGTTG	GGCGACACAT	180
NCCCGGAAGA	NTGTACCGC	ACCGTCGCCG	AGATCCATCG	CGTTTGCNTG	GGACGCTGAA	240
GGGCAATTCC	CGGTGGGCTA	CGACCCGGAA	CGCGGGGCCG	GTGGAGCGTT	TTTTGACGGG	300
AAAGAGGGCG	ACGATTTATT	AAGGTNGGGA	GCCGGTTGAN	NTTCCCAAG	TTTTTGGGGG	360
CCNCCGN						367

(2) INFORMATION FOR SEQ ID NO:459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

GAGCAGACAC CAAGAAGTCC CAGGCCAAAA TTTTAATTGG NCTAGANAAT GTGGCTGGGG	60
TGTNAGTNAC CAGCCTCAAG GATGGGCTCT TNAGCTTGCA TCTAAGTNAG AATGTCATCG	120
GTGGGCTCCA AGGGGGACTT CCTGCTGGTN AGCGAAGCCA TGTGAATTGA CCTGCTGACC	180
AAAATGTACC GGGCTGTGCT GGATGCNACG CNAGGCAGCT TACAGTCACC GTGAACTAAG	240
AAAGTTCTCC AGTGAAGGTT CCAAGGAGAA CAGTGTGGCT GTCNAGGTTT GTNCCAGGGC	300
CCTGCAGTGG TGNACCAGN AAGGTTACGT TACAAAAAAA GGGGGNGTCC TTG	353

(2) INFORMATION FOR SEQ ID NO:460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

TNCNTNTTTT TATTTAGTNC TACATAGTTT TATTGCATGG TTGGGTAAAA CTAACACCAC	60
AGGNAAGCAA TGTAAGATTG TCATGACCAC CATGGTCCCT GGTGCTNNAT TTTAAATTTT	120
TTTGGGGGAT GCGCTCTNAC TTTNTTGCCC AGGGTAGAGT GCAGTGGTGC NATCTCTG	178

(2) INFORMATION FOR SEQ ID NO:461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

GGTGGTGAAT TTCCCCAACT ATNACCAGAC CTNAAAAATC GTGGGTAANA AGCTGGTGGG	60
GGTNTCCACC ATCGNAGGCG TGACCTATGA GCGCNTAANA AGAGAANTGG CCTAAGCAGC	120
CAGGCCCCGGC CCAGGGAAGC TACAAACCCA CCANTAAAC TGAATATAAG GACAAAAAAA	180
AAAAAAANTT TTGGGGGGGG GNCCGGNTCC CN	212

(2) INFORMATION FOR SEQ ID NO:462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

CAAGGATTAC AGAGCTAGTA AGTGGCAGAN CTGGGCTTTA AACCCAGGGA AGCTAGATTC	60
CAAAGTTTTG TTTTCTTAAC TACTAAGCTA CACTGTTGAT CACCCTTGGN GTCGTGGGTT	120
AGGAAGAAAA GGAAGGGGAA ACAATGAAGG TGGGAGAAGA TGAAGGACTT AGGGCTCAAA	180
GCTGATGCTT CANTGAAGGT GGGAAAACCT GTGCCTGTGG GGTTTTCTC AGATTACACA	240
CACGTGGCAC AGTTTTNCAT NATNCAGGTT GCTGAAAAAN AGGT	284

(2) INFORMATION FOR SEQ ID NO:463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

GGCACGAGGC TCTGTGAAG ACGACCACAT CCCCTTCCTC CGCAGAGGGG TACCCGTGNC	60
TCCATCTCAT CTCCACGCCC TTCCCTGCTG TNTGGCACAC CCCTGCGGAC ACCGAGGTCA	120
ATCTCCACCC ACCCACGGTA CACAACTTGT GCCGCATTCT CGCTGTGTTC CTGGCTGAAT	180
ACCTGGGGCT CTAGCGTGCT TGGCCAATGA ACTGTGGAGA GGACTGTGAA GAGAGAAGGT	240
CCCAGCGGGG GCCAGTGAAG GCTCAGGCAG GTTACTGCCT AGGGTGTGCT GGTTTGTCTT	300
TTTCANACCT TTGTTTCCN AATTGTGCTA CANTGGAAGA CNTGTTTGNT TTG	353

(2) INFORMATION FOR SEQ ID NO:464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

GGCACGAGCT CACTTCTGGA GAAATTGTTT ATCTTCTGGA GAAGATAGAT ACAGATTGGT	60
ACAGAGGGAA CTGTAGAAAC CAGATTGGCA TATTTCTGTC CAACTATGTC AAAGTGAATT	120
GTAAGTGGGT TGTGTTTGTT TTAATTGGT CATATACTCA GTGGGTTCTA TGTGACTTGT	180
AGGTTGGAAA AAATAACTAG AAACCCAGAT TCTAGTTCTC TTTCATTGAT TCATTTGGCA	240
TTTGGAAT TCAAAAATAA NGTTTGGTCA ACTAGGTGGT GGTAAATTAT TATNTTATGG	300
GGTGTTAGGA ACTTAATGCC NANANGCTGT TCTGAA	336

(2) INFORMATION FOR SEQ ID NO:465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

GGCACGAGCC AGGCTGGTCT CGAACTCTTG GCCTCAGGTG ATCCTCCCGC CTCAACCTCC	60
CAAAGTNTTA GGATTACAGG CGTGAGTCAC TGCATCTGGC CAATTGGATA CATTCCTGCA	120
GCCAAATTTT AAATTCTTCC TATTGTGCTA TAGTATGGAT GTGCCTTAAT GTATTTAACC	180
CACCCCTTAT TATTGGGCTT ATTATTGAAC TTATTTCCAG CTTAAGTGAT AGAAACAGTG	240
CTGTACATCC TCCTAGCTAA ATCTGTGTAT ACACCCCTAG TGATTTCTT AGCTTCAACT	300
CTTAGAAGTG GGATTNTTGG GTCAAAGGGC ATGCATCTTT TAAAGTNNTT GATGTTTATT	360
GCCAANN	367

(2) INFORMATION FOR SEQ ID NO:466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

GGCANAGTGG TAGCACCTTC AAAGAAATCC CCGTGAAGTG TCTATAGACC CACACTAACA	60
AAAGTNAAAA TTAAAGGTGA ACCTGAAATT CAAACTGATT AAAGAAGGTG NTACCAATGA	120
ACTNGAAGTG GTCCATGGAG AGCCAATTAT TAAAAAATAC ACCAAAATNC ATTGATGGAG	180
TGCCTGTGGA AATANCTGAA AAAGAAGACA CGTGAAGAAC GGNTNCATTA CAGGTCCTGA	240
AATAAATNAC ACT	253

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

GGCAGAGCA GATTTGGAAA AGCAAGGGAT AACATATGCA GTACAAAATA AGTGGTGAGA	60
TGAAAGCTAA AATGAACATC TGGAAGAAAA AAGCATGGCC AGATGGGGTA AAGTCCAGAA	120
AGAAGAGTGA ACAGAGCTGG AGGTACAATG GTAAACTGTG TCTCACTAAA ATCTTCCAGC	180
TCCATGAAAA GGGCTGTGGC TTGACGTTTA TAAATGTNTG GAAGGAAAGA GAAGTCTATA	240
ATAATCTACC TGTTGACACA ATATACATTG GGGAAGTTAC ANCTTAAACA ATTATTTTNA	300
TATCACTTCA TTTTACCCAG GTATTTTCAG GGAAATTTTT AAAACGGTTA CNCTTTTTTC	360
ATGTACCCCN AAAGTTCNTG GGCAGTNTCA TCTTNGGGCC	400

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

GGCAGAGNCT AACCTCATTA AACACCTGAA AGTTNACACT GGAGAAAGGC CTTATNAGTG	60
CAGTGAAATG TGGGAAATCC TTTAGCCAAA GTTCTAGCCT CATTCAACAC CGCAGAGTTC	120
NCACGGGNAA AAAGGCCTTA TCAGTGCCAG TCAATGTGGG AAATCCTTTG GGCTGCAAAT	180
CTGTCCTCAT TGCAACACCA GAGAGTTNCA CATTGGAGAA AAGCCTTAGC TGTACTGNNG	240
AATATGCAAT TTCCCTTTTA GTGTAATTAT ACTGAAGNG TAACANCTNT GAAGNGNGGA	300
CAAGTTACCT GATTTGGGAA GCCCCAACAT NTAGGGTTAT ACAGTGGGGC GGTTTTCCCC	360
TTTAAGTTCC CGGTTATGTG NTTAACATTT TTTNNAACAT GGCCTTTTAG GAAGGGTTAN	420
GACTTTTTTT NAATTG	436

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

GGCAGAGTTA CAGTGGATGA TCTGAAGAAC CTTTTCATAG AAGCTGGATG TTCAGTGAAG	60
GCTTTTAAAT TCTTTCAGAA AGATCGCAAA ATGGCGCTCA TTCAATTGGG ATCTGTGGAA	120
GAAGCAATTC AGGCCCTCAT TGAGCTTCNT GAACCATGNA CCTTGGAGAA AATCACCACC	180

TCAGAGTTTC CTTCTCAAAA TCTTACAATC TGNACTTTNC TGTGAATTTT TCTCCTAAAA	240
CTGGGACCAT AATTTCNAGT AAAAACCTTC AGACATNGGA CTGAAGCAGC TTCAAGACCC	300
AATTTTGCCC TCTTTNCACA AAATAAACTC TTTNCTGAGT TTGATATTNC AAGTATATTT	360
NNAAAAATCA AGGGGTTTTT TTTTTTGGA ATTCCCCC	398

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

CCCAGAGGAC AGATTATCTA CACGTGGAAA GGAGCAAATG CCACACGAGA TGAGCTGACA	60
ACATCTGCGT TCCTGACTGT TCAGTTGGAT CGGTCCCTTG GAGGACAGGC TGTGCAGATC	120
CGAGTCTCCC AAGGmAAAGA GCCTGTTTAC CTA CTGAGTT TGTTCAAAGA CAAACCGCTC	180
ATTATTTACA AGAATGGAAC ATCAAAGAAA GGAGGTCAGG CACCTGCTCC CCCTACACGC	240
CTCTTTCAAG TCCGGAGAAA CCTGGyATCT ATCACCAGAA TTGTGGAGGT TGATGTTGAT	300
GCAAATTCAC TGAWTTCTAA CGATGTTTtk GGTCTGAAA CTGCCACAAA AATAGTGGCT	360
ACATCTGGGG TAGGAAAAGG TGCTTAGCCC AGGAGGAGGA GGAAAGGAGC AGAGTATTGT	420
AGCAAAGTTG TCCCTAAAGG TGCAAAAACC TTAGGGATCC CAAGAAGGcG AGGAGCCAGA	480
GGGAGTTCTT GGAATTCCCC CTTGGAGGG	509

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

TTATCATAGA TTTNCCNGGT TTAGTTCACA TCTATCTCGA TGAGTGCTCT TGCCTGCGCC	60
AGTCTTAAGC CTCCTTGCTT GTTACATTCG TTCAATAGAG CAGATTTGTA TTCTAAATAG	120
GCTCCAGGGA CCAACCTCAC CATCTGACAG AGCTCCTTTT CTTTTTCATT CAGCTTCTCT	180
GTGCCAGGGA GGCCAGTGAG GTTCAAGGGT GGTGCACTCC GTCTACCTGA ATTCGAAGCC	240
ATTGGAATGG AAGGACTCAG GCCGGAATCA ATGTCAGCTT GCCGGCGGAG CCACTGCTGG	300



CAAGCACTAC TGNCTGGAT ATACTGGAGA ACTTCTGAGA GCATAGTGCG TTTAAGGCGC	360
TCTTCCTCCC GTGTCTTCTT GAGGTGATCG TAGGTCTGG CACTACAAA ATTGGTAATG	420
CCTGCTGTCC TGTATTCTTG GAGCCTCTTG ATTTCCCTTC GGAGTTCAAA TTCCAATGCA	480
TGGNTTTCAA TGAATTTGGC ATGTTCCACT GGCCCCACAA TTCTTGCAAA TCGNCTCATT	540
GTTTCATACA GGTCTGGAC CTCCTTGGGA TACCGCCGNT CCATTAATTG AACTTTCTA	600
	600

(2) INFORMATION FOR SEQ ID NO:472:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 497 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

GGCANAGACC TGNATGTAGA TGCCCATCCC AAAAGGAGCA AGATCTGCTC TTGCAGTGGG	60
TGTTGAGAGG GGCTGGGAAG GCTTTTTTCAG TCAAATATGG AGCTGAAAAN NTTCAGAATG	120
TGCNTATGTT GTACATTATC ANTAAGAATC CTAACAGGAG CACAGTGTGA TTTCTCTTCG	180
TAGTGGGCGT ACATGGTCTT GGGTTTCCAT GTGCAGCAGT GAGAGTTGGT CTCCAAAGCA	240
GAACGGTCAG CATTAACTTC AGCCAAGCAA GCATTCTGTA TGGGGTGCTC CCTTTAAAGC	300
CCAAGGGAAG GCAGGCTCTG CTGCTTTTGC CCACCTTTTC AGAGGGAGAG GTGTTGCCCC	360
ACCANGGGTG CCAGGTGTGC TGGGGGCCCTG AAGNTAAAT TAAGTTGTTT TGGGAAAAAA	420
TAATGTCTTT AAGTTTCTGC CAGAGNGAAT NNGTANCCAT TTAAATCCA TTTCATCAGG	480
GGGTTTTTTT AGTCAGT	497

(2) INFORMATION FOR SEQ ID NO:473:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 491 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

GGCAGAGCTG GTGAAGACCC AGAGGAAAGG GGAGTAAAC TTGGATTGGG AGATTTTCATT	60
TTCTACAGTG TTCTGGTTGG TAAAGCCTCA GCAACAGCCA GTGGAGACTG GGAACACAAC	120
CATAGCCTGT TTCGTAGCCA TATTAATTGG TTTGTGCCTT ACATTATTAC TCCTTGCCAT	180

TTTCAAGAAA GCATTGCCAG CTCTTCCAAT CTCCATCACC TTTGGGCTTG TTTTCTACTT	240
TGCCACAGAT TATCTTGAC AGCCTTTTNA TGGGACCAAT TAGCATTCCA TCAATTTTAT	300
ATCTAGCATN NTTGCGGTTA GAATCCCAGG GATGTTTCTT NTTTGACTNT AACAAATCTG	360
GGGAGGACAA GGTGGTTTNC CGTGTNCCAC ATTNACAAGT CAAGNTCCCG TTGGACTTTG	420
CAGTTCCTGC CAGTTTCCGA CCANCTGCAN TTTNGGACTT GGAGGGGGNC CTAGGNAACG	480
GTTTTGACCA A	491

(2) INFORMATION FOR SEQ ID NO:474:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 495 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

GGCAGAGNCA GTGTATAACA TATTACATGG TATGCCATGG AATACTATGC AACAAATAAAA	60
AGGAATAAAC TATTGATACA CACAACAAC TAGATGGATC TCAGGGGAAC TATGCTGAAT	120
GAAAAAGTCC AACAGAAGAA GTTACATAAA TATGAATTCC AGTTAGAAGA CATTCTTGAA	180
ATGGCAAAAT TATAGAGATG GAGAATAGAT TATTGATTG ACAAGTCTCA AGGATGGAGT	240
GGGGAGAGGG GTTGTGTAAG CCAAAGAGAG GTAGCAAGAG GGATCCTTAT GGTTGATGGA	300
TCAGTTCTGT ATTTTAACTG TGGTGGTGGC CNCTATATCT ACACNNTGGN TAAAACTACC	360
CTAACTTTAC AAACACACAA TGGGTACTTT NAANCCGTTG AGTCGGATTA TCTCTNGACC	420
AAGTCATTTT CCATTTNGTA TTNACCTTGG TTGACCGGTT TTTCTGTAA GNATTGCCGT	480
CTGGGGGGTC CACCG	495

(2) INFORMATION FOR SEQ ID NO:475:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 353 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

ATTTTATGTT TTCTTTTAT TAATTTTCT TCTTAAATAC CATGTCTTTC TGGCTGAAAT	60
CCTTGCCAAA ACCAGGAAGG GCCAGTGAC TGTGGGTGAA TTTTNCTAAT TCATTTCTTT	120
GTCATTTGAA GCCTTCTGTG GCTTCATGCT GCTTTATGTG TGTGTAAATA TTCAGTATCT	180

TTTCCTAGTT TGCACCTTTG TCACAACTGC TAATTAAGCC ACCTATGGAC ACATTGTAAT	240
ATAAATTATT TTGGGCCACG GTGGAGTGGG AGGGAAAAGAA TCCAGTTTCA CAGGGGTAA	300
ANTNTGGCAT GTNGTGGAGG TTAATATTTN ANTAAGTTTG CAAAACCAC TTC	353

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

NTTGCTGCCG TCTGCACACG GTCCGCGCGT CGNTGGAAGA CCTGGGNTGG GCCGATTGGN	60
TGCTGTGCC ACCGGAGGTG CAAGTNAACC ATGTGCATCG GCGCGTGCCC GAGCCAGTTT	120
CCGGGCGGCA AACATGCACG CNCNGATCAA GACGAGCCTG CACCGNCTGA AAGCCCGANA	180
CGGTGCCAGG GCCCTGTN	198

(2) INFORMATION FOR SEQ ID NO:477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

GGCAGNNGTG GAACAGGACA TCCAGCCTGA TGGGCAGATG CCAAGTGACA AGACCATTGG	60
GGNGAGGAGA TGATTCCTTC AACACCTTCT TCAGTGAAGA CGGGGGCTGG NNNCATGTGC	120
CGAAGGCAGT GTTTGTGGGA CTTGGAACCC ACAGTNCATT GATGGAAGTT CGCACTGGGN	180
ACCTACCGCC AGCTCTTCCA CCCTGGAGGC ANCTTNATNC ACAGGCAAAG GAAGATGCTG	240
NCAATAAACT TATTGNCCCG AGGGGNACTT ACACCATTG GNCAAGGGAG GATTCATTGG	300
AGCTGGTGGT TTGGGANCCG AA	322

(2) INFORMATION FOR SEQ ID NO:478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

AGCGCAAAGA CAACTTCCAG ACCATCCTCA GCCTCCAGCA GTTCCAAGGG NCGGGCGCAC	60
AGGGACATCC TGGTATGCAT GACCTCGTGT TCTGGTTCGG GGACCTGGAA CTTACCGCAT	120
TGGAGAAGCT NATGAACCTG NCACTTTGGT TCAAGTTTGG NCATGCGTAC AGTNAGTGCA	180
GNT	183

(2) INFORMATION FOR SEQ ID NO:479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

GAAGACCCCA GACATCAAGC TCTTTGGGAA GTGGAGCACC GATGAATGTG CAGATCAATG	60
AACATTTCCC TGACAGGATT ACATTGCAGT GAAAGGAGTN AGTGATGNCC AAGTACCTGC	120
CTCTGCACAG TGCCAGGGNC GGTNATGGCG CATATACGCC TTGCCGCCAA AGTTTCAGTT	180
GTGCCCATTA GTGGTGGCGN CCTGCACTTA ACTACCATGN NTGAATGGCA CGG	233

(2) INFORMATION FOR SEQ ID NO:480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

CACCCTGCAG GTGGACAGCT GGCCGGTCAA CGAGCGGTAC CCGGCAGGCC GCCAGCTGAC	60
CATCTTGAAC AGCCAGGCTG CCATCAAGAT CGGGGGCCGG GAATCAGGGC CGCCCCTTCC	120
AGGGCCAGGT NTCCGGCCTC TACTAACAAT GGGCTCAAGG TGCTGGCGCT GGCCGCCGAA	180
GAAGCAACCC CAATGTGNCG GNACTGAGGG TCACCTGCGN CCTGGTGGGG GAGGNGCCGT	240
CCGTGNTGGC TNCAGTGCGN GGAACCACGG CCACCACNT GGCTGGTTGT ACATGGGCCA	300
CCACCNTTCT GGGAGGACTA CCACCACCAT GGGCCACTTA	340

(2) INFORMATION FOR SEQ ID NO:481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:

GGCACGAGAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	60
AAAAAAAAAA AAANANANAA AAAAAAAAAA AAAAAAAAAA NAGN	104

(2) INFORMATION FOR SEQ ID NO:482:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 352 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

GGCACGAGAA GAATTGAATT TACATGAGCT CTGTGCAGTG TGCCTAGAAG ACTTCAAGCC	60
TCGAAATGAG TTGGGGATTT GCCCATGTAA GCACGCCTTC CACAGAAAGT GCCTTATTAA	120
GTGGCTGGAG GTTCGTAAAG TGTGTCCCCT GTGCCAACAT GCCAGTTCTA CAGCTGGCCC	180
AGTTGCACAG TAAGCAGGAC CGTGGACCCC CTNCAGGGAC CCCTTCCTGG GGCAGAGAAC	240
ATTGTATAGC TTACCGCAAG GATNCAGACT GTTGCTGGAC ACGAACGTCT GTTTGGAGCC	300
AGGAGGAACA CATGTGGTGT TTGTTTGGTT GCTNTNTNAC CTNGGGACAC CA	352

(2) INFORMATION FOR SEQ ID NO:483:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 384 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

GCNTCGNTGT CCAGCNTGGT NTCCAGTCGG TTNTTTCCTC ACATGGTGGC TCCTGNCCAC	60
CCTGGCCTGC CCACCTNAGG GATCCCCCAC CCTGCCATCG TTTCCCCCAT CGTNAAGCAG	120
GAACCGGCAC CCCCCAGCNT GAGCCCTGCA GTGAAGCGTG AAAATCACCA GTTNACCGTG	180
AAAAAAGGAG GAGGAAAAGA AAGCCCCACG TGAAAGAAGC CTCTGATTGC TTTCATGTTG	240
TATTATGAAN GGAGATGAGG GCCAAGGTGG TGGCTGAGTG CACCCTGAAG GGAAAGTGCC	300
AGCCATTTAA CCAGATACCT TGGTAAGNAA AGTGGGCACA ACCTGTTTTC GNGNAGGANC	360
AGGTCCAAGT TATTAGGAGN TTGG	384

(2) INFORMATION FOR SEQ ID NO:484:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

GGCAGAGCTC CGTCCCNNGA GATTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTT 53

(2) INFORMATION FOR SEQ ID NO:485:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 298 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

GGCAGAGGAC CGTCGCAGTC GGACCAACTG CTGGCAGAAT CTTCGTCCGC ACGGCCCCAG 60  
CTGGAGTTGC ACTTGCGGCC GCAACNNCNA GGGGGCGCCG CAGAGNGTGN GNCAAACGGG 120  
GACGACTGTC GCTCGGGNCC GGGCGNTGCT GCCGTCTGCA CACGGTCCGC NCNTCGNTGG 180  
AAGACCTGGG NTGGGCCGAT TGGGTGCTGT CGCCACGGGA GGTGCAAGTN AACCATGTGC 240  
ATCGGGCGCG TGCCCGAGCC ANTTTCCGGG CGGCAAANA TGCACGNNGC NGTTTAAG 298

(2) INFORMATION FOR SEQ ID NO:486:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 490 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

GGCAGAGAGA AAGGTTCTGGT TACTGCCGAA GACTGCTGCC TGGAGGCAAA GGGAAGCGCC 60  
TTCCTGAAGT TTACTGCATT GTGAAGCCGC CTGGGAATGC TTCACCTCTT TTNAAGGGAT 120  
CTTGATGAG GTGGAAAAA GACGAGGCAT CTCTCCTGCC CTGGTTCAGC CACTCATGNG 180  
AAAGTGTCAT GGGAAGCCCC TTTCCCAGCC CTGGGCAAAA CCATCCTTGT NNAAGNAACT 240  
TCCTGCCAGG TTTCAGGAAC TGAGGTTGAT CAACTGTGC CGCCCGNTGG GACTTCCCGG 300  
CTTCGAGCAA GTGGGACTTT GNAGTCTTCT CTTGNTCNTN CCTTCAGGGT TCCGGCAACT 360

GGTNTNGTGT GTTTGNNCTC CCTGNTTTTT GGNAGAGGAG GGTCACTCTC ATTGCAGACA	420
AGNTCAAGTA CCCGCCTTGG GTTAATTTTG GTTAAAGGGT TTTGAATGAC ANTGGGTTNT	480
TGGGACCCNC	490

(2) INFORMATION FOR SEQ ID NO:487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

GGCANAGCTG GGGGTGTCTC TGCAGGGTAC TGGCAGCCTT GCTACACTGT CCTCATTTCCC	60
AGATGGAAAG ACCTGAGTGC CTCTGGCCTT CCTCCGGGAA TGATTTCTCTC ATGAAAATGA	120
NCCAGGCCAC TTCTTCCGAG GGCCAGGCCG CCCCTCCCC GAGAACCTGT CCTGCCGTCC	180
GCGGGTGTNT GGCTGTAGG GGAAGTGAAG GCTGGGCTTG CTGGGCACCT CTGGAAATCT	240
GAACCCTGTG GGGCCAAAGA AAGCACCCT GTAGTTTCTG CAGACCCCCA TGCGGTTCAT	300
TGTGCATTGT TTGGTTTCTT AGGATGTATG TTTTCTAGT TTTTCTAAT GGAAACCCGG	360
GANTAATGTA AATAGCTTTT TTGGGNACGG NTTTTAATGT CAAGTATGTN CCGTGTGGA	420
CTATTTCAAG GTGCTGATGC AACAAATAATT AAACCTGGNG GGGGCCGGNA AAAAAAAAAA	480
AAA	483

(2) INFORMATION FOR SEQ ID NO:488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

GGCAGAGGNC CCGCGGTGCG CGGCCCTACG ACCTGGACCG GCGAGATGAT GCCTATTGGC	60
CGGAAGCCAA GCGGGCCGCC CTGGAATGAG CGCTACCATT CTAACCTTAA CCGCCAGTAC	120
CGCTTCCACG AACTTTNAAC CACAGGGAAC CGCGGCCGCT NACCCCGNAC CACTTCGGTG	180
GNACAGGAGA GAAGGTTCAA GGTTCATGA ATGGGNAGAA CGNAGAAGGN ACAGCATTTA	240
CCCAGAACGC CATGGGAGGN ACCAGAGCGG CCACGGGCCG GGAATTTCCG CGAATGGGTT	300
GGGGGGGGTT ATGGCTCTGA ACAAGGGNTT TAGNCGAGGG CCNGGGGTTG CCTTCTTCCC	360

CCCAGGGGCA GACGTTTATT GGGGGGACCA TTGGCCNAAG AGAAGATGAC CGTTCATGGC	420
AGGNAAGGNC NACGGGGGGN NTNNTGGACA GGNTTACAAG AGTTGGCAAN TNGCGAANAN	480
CATTTCCGTT AATTCCGGC	499

(2) INFORMATION FOR SEQ ID NO:489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

GCGTCGCCTT GTTCTACGAT ATGACCATTT TCCATATACA CCACTCGGCT GGCGGTTTTA	60
CGCGCCACTT CAACTTCGTG GNGTGACGAT CACCTGGGTA ATATTCGTTT CTGCCAGCTC	120
ACGAATGAAT GCTGACGATT TGTGCCGTAA TTTCCGGGTC CAGTGCGGCG GTCGGTTCAT	180
CGAACAGCAG TACCTGCGGT TCCATCATCA ACGCACGGGC AATAGCAACA CGCTGCTGCT	240
GACCACCAGA AAGATGCAGC GGGTAACGAT CGCNATAAGG TTTGAGAACG CAGACGTTNC	300
CAGCAGTTTT TTCTGCACGG GGCCAGCGCC TGATTCTTTA ATTCAANCCC CATTACAAGG	360
GCAGGGCGGT TTCAATTCAA GGTTTTGTTN GCACGGTCAA ANTGGGGCCA CAGGTTNTN	420
TT	422

(2) INFORMATION FOR SEQ ID NO:490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 365 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

GGCAGAGCA GGGCTAGGTA ACCTGTCTTG GGAGTNTGAG ACCGCCCCGC CCTGCCACGC	60
CCCTCACCGC CCTGCCCCGA GGCGCCAGCN NANCTCCTTG GCTTCCTTTC CTAGATAGTG	120
ANGTCCACCA ACCTTGGAGG TGCCTTTTCA AAACACCCGG GAGGCCGTGC CTCAGCATTC	180
TGTTACTCGG CCTGCAGCCC CAGTGCCAGG AGCCACCCCG AACC CGGAAC CCGGCCAGGC	240
TGGTTNCAGG GAGGCCGAGG TGGCGCTGAG GTGGCTTTCA GCACGCTGGG GATTGGNTTC	300
CTGCTNCAGG GATGCTGTTG CATTTCTGCC TGCCACTTTT TGCCNGACAC CAGATNTGTT	360
TTNAA	365



(2) INFORMATION FOR SEQ ID NO:491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

CACAACCTNC TCATGGGTGA CACCAAGGAG CAGCGCATCC TGTAACCACG TNCTNCAGCA	60
TGAGGTAGCC CTGNGAACGN ACAGAGCGTG CTGGAAGGCC ATTGACACCT ACTNGCGAGT	120
CA	122

(2) INFORMATION FOR SEQ ID NO:492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

GGCAGAGGNN CGGGNGCTGC ATCGACGTGA ATNAGTGCTG GGCCTCGCCA GGCCGNCCTG	60
TGCCAGCACA CGTGTGAGAA ACACACTCGG CTCCTACCGC TGTTCCTGCG CCTCCGGGTT	120
CCTGNTAGCA GGGACGGCAA GCGCTGTGAA GACGTGAATN AGTGTAAAGC CCAGCGCTGC	180
AGCCAGGAGT GTGCCAACAT CTATGGCTCC TACCAGTGCT ACTGCCGCCA GGCTTACCAG	240
CTGGCTGAGG ATGGGNCACA CCTGCACAGA CATCGACGAG TGTNCTCAAG GCGGCCGGCA	300
TCCTNTGGCA ACTTTCCGNT GTTTTCAAAG TGGCCAGGGG AGGTTTACCA TTGTGCATGC	360
CCTGAGCAAG GTTACAACAT GTACGGGCCA ACGGTAGGTT CTGCAAGGTT GNGATNAAGT	420
TTTGCNANCT TNT	433

(2) INFORMATION FOR SEQ ID NO:493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

GGCAGAGTGG GAACCTCTTT CTGGGCTGGC GANGCCTGAG GCCACTCCCT CAGCTTGCAG	60
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GGAGGTGTGG AGGGAGAGGC GCGACGGGNA ACAGGGGCTG CGTGCGGCTC TTGCGGGCCA	120
GCTGGAGTTC TGGGTGGGCA TGGGCTTGGC GGGCCCCGNA CTCGGANTNA GNCGGCTGGC	180
CCT	183

(2) INFORMATION FOR SEQ ID NO:494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

GGCAGAGGNN AAAGTTGTNT TGGCTTTGGC TTGCAACTCT TTGGCAGGAA TTCAGCGAGA	60
GAATTTACAG AAAGCCATGG GAACTGGTGA CAATCAACTA TTCCTCTGAA CCTGAAGAAT	120
CTGANTTTTG TATTTGTTGA CTGACCAAAA CAGGATGCGA GTGTAAATGA ACATCATGCC	180
CATGAATTGG TGCTCGATTT TATACTCAAT TGGATGCTGC TCAAATGAGA AATGATGTCA	240
TAGAGGAAGA CCTTGCAANG AGGTTCAAAA TGGAAGACTG TTTAGGCTNC TAGCAAAATT	300
GGGAACATNC AATGAGAGGC CGGGTTTCAG AAGGATCCCA CTTGGTCCAG AGACNNGGAGA	360
CCNTTATCTG TTGNAACTCT TTAGGGGTCC NNNTTTTCCT CAGGTGACAG AAGCAGTGCN	420
TCCCTGGATT GACCCAGGC TATNATTCNT TGTCTTNACA GTTGGTGCTG GTNTGCCANA	480
AAATNAGCCC GNT	493

(2) INFORMATION FOR SEQ ID NO:495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

CTCCCACCTC GGCCTCCCAA ATTGTTGTTA TTACAAGTAT GAGCTACTGT GCCCAGTCCC	60
ATTGGGGTAT TTTTCTGTGG TTCTCAAGGG TTGCCACAG AGAGACAGAC CACTTTTGGG	120
ACTCAGGAAA TCTGGGATGT ACCAAGACTA AATCTATATT AACCTTCTGA TCTACTGTGC	180
AGGATGGCAA AGTGTTTTAT TTCCTGTGNA CAATTCTGGA TCTAAAAATG TAAGGGTTGA	240
AAAAAAAATG TAAGGGATGA GATCAACTAT TTGTGAANGT TGTCCGAGAG GNTGGGTTTG	300
CAGGTGTGTG GGTGCAANCA GTNCCCTNCA CACTCA	336

(2) INFORMATION FOR SEQ ID NO:496:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 331 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

GGCANAGGNC CCTGGAGGGN TGGAGCCCAG CCTTAAAGAC CCAGGGCAAG CTGAACACCA	60
GGCCTGGNAA AGGTGATCTT CTTCTCAGAG TCTGGCTGCC ANGGCAGTGG CAGGAAGGTC	120
TGGGGAGACA TCGTTGATGC CTCAGGCTGG GCCCCCGTAG CCTCCATAAG GGTAGTTCGA	180
GGCTGCTGGG TGCTGTACGA NGAGCCAGAG TTNCGGGGTC AGAAGCTGGT CCTGCCTGAA	240
GNGGTCATGG GACTCAGANC CCCAGGGTCA AAGTGGAGTC CCCAAGGTTT CGGNTCCCTA	300
AGGNGGGTTG TCTGGGGACT TACAAGCANC C	331

(2) INFORMATION FOR SEQ ID NO:497:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 484 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

GCCCAGCCCA ACTCGGGTCT GCTGCAGGCC TCGGTCATCA CCCTCTACAC CATGTTTNTA	60
ACCTGGTCAG CCCTATCCAG TATCCCTGAA CAGAAATGCA ACCCCCATT T GCCAACCCAG	120
CTGGGCAACG AGACAGTTGT GGCAGGCCCC GAGGGCTATG AAGACCCAGT GGTGGGATGC	180
CCCGAGCATT GTGGGCCTCA TCATCTTCCT CCTGTGNCAC CCTCTTGCAT NCAGTNTGCG	240
ATCCTNCANA CCACCGGTCA GNGAAGCAGC CTGNTGCAGA CCGAGGAGTG CCCACCTATG	300
GTAAGACGCC ACACAGCCAG CAGCAGCAGC AGGTGGNCAG CNTGTGAAGG GCCGGGGNNT	360
TGAACAAGAA GNCAGGACGG NGTTCACTGA CAGTTNATTC TNTNTTTCCTA TTNTTGNCNG	420
GTGNTGGGCT TNATTGCAAG TTNAGGATGA GGTTCACCAA TTGTTACAAG CCCGTGGAGA	480
CCGG	484

(2) INFORMATION FOR SEQ ID NO:498:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 72 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

ATGACAAGAG GCCCTCTATA TATCTCTTCC CACTCTAAAG CTNACCACAC CAACCTACGG	60
NATCTTAACC AC	72

(2) INFORMATION FOR SEQ ID NO:499:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 259 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

GGCAGAGCCC CCATCCAGAG CATGATGTGC CAGTACTGGC CAGAGTCCTG GTGGAGGACG	60
ATGAGATTCA TGCAGGGATT CATCAGGGCT TTCAGGCCCT GCCCAGGCAC CTATGGTACT	120
TTGCTGGACT TGAACAGAT GGAAGAGCGT GCCGTTTCTA GGTGAGCTCT GCCTGGTCCG	180
CCTCTGGCTC ACTCCGCCTT CAGAGACCAG ACTCCACCTT CACACTCANG CATGGGATTC	240
TCTGCCTTNA AGATAACAC	259

(2) INFORMATION FOR SEQ ID NO:500:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 99 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:

GGTTACCCTG GCTACCAGTG CAAACACTAC GCNTGCNTCC GGCGAAGGGC GGCTACTGCG	60
CTGGTACCNN GGNTGGGCCC CCCCCTATAA AGCATCATT	99

(2) INFORMATION FOR SEQ ID NO:501:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 334 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

GGCAGAGGTN AGCTCGCAA AGCGATCGGA GCACAGTGCT ACTTGGAAT GTTCAGCTCT	60
GA CTCAGAAA GGTCTCAAAG CGGTTTTTGA TGAAGCAATC CTCACCATT TCCACCCCAA	120
GAAAANGAAG AAACGCTGTT CTGAAGGGTC ACAGCTGCTG TTCAATTATC TGAGGTTGTC	180
TGGGACCTGC CTCCACCCCA TCCAGGGGAT GAGANTGGNC AGCCAATCTC TGTGGCCAAG	240
CTTCCAGCCA AAAAGGAGGG CACGACCAGA AAGGAACTCC CTTTGGCAC GGGGGNTTTG	300
CCCCATTNAC CTTTCTTNAG GCCCTTNCCC NAAA	334

(2) INFORMATION FOR SEQ ID NO:502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:

GGCAGAGGTG CTGCAGGGGG TCCTGCCGGC CCTGCCTCAG GTGGTGTGCA CTACCGCGAA	60
TGTGCGCTTC GAGTCCATCC GGCTCCCTGG GCTGCCCCGCG CGGCGTGNA CCCCCGTGGTG	120
CTCCTACGCC GTGGCTCTCA GCTGTNNAAT GTGGCACTCT GCCGCCGAG CACCACTGAA	180
CTGCGGGGGT CCAAGGNAC CACCCCTTGA ACCTGTGAAT GACCCNNGGT TCCAGGACTN	240
CCTNTTCCTC AAAGNCCCT CCCCCGAGC CTTTCCAAGT	280

(2) INFORMATION FOR SEQ ID NO:503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

GGCANAGAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	60
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAANAAAA CNCCNGGGGG GGGN	114

(2) INFORMATION FOR SEQ ID NO:504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:

GGCANAGGAC AGGATCAAGC ATGCTTTCCT TATCAAGGAG CAGAAAATCA TTGTGAAAGT	60
TTTGAAAGCA CAAGCAGGGA GTCAGAAAGC TAAATAAAAG ATGAAGCTTT TTTGNAGTAN	120
TAAAAATTAA AAGACTTTTT AAAAAATTA GAAGGCAGGG AACCCAGATG GGNAAGTGTC	180
TTCTGAATG CTCCTTGGCC TTGGGAGGGT CCTTCTGTG TGTTCATG ACAAATCTG	240
AAAAATGCCG CTAATTGGGC AAAGAGAAAT GTTTATAGGG TCTAGCTCTA GTATNCAGGN	300
AAGGGAAGC AGNGGAAGG GTGGGTTTGG GACNGNTTAG	340

(2) INFORMATION FOR SEQ ID NO:505:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 112 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

GGCACAGGTA GAACCCACCA TGGTGCTGTC TCCTGCCGAC AAGACCAACG TTAAGGTNTG	60
TTTGGGGTAA GGTGCGNGC GTACCTGGNG NAGTATGGTT TCGGTGGTAN CT	112

(2) INFORMATION FOR SEQ ID NO:506:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 403 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

AAACCAAGCT GTACTTGGCA ATGAACAGTG AGGGATACTT GTACACCTCG GAACTTTTCA	60
CACCTGAGTG CAAATTCAAA GAATCAGTGT TTGAAAATTA TTATGTGACA TATTCATCAA	120
TGATATACCG TNAGCAGCAG TCAGGCCGAG GGTGGTATCT GGGTCTGAAC AAAGAAGGAG	180
AGATTCATGA AAGGGCAACC ATGTGAAGAA GGAACAAGCC TGCAGCTTCA TTTTCTGCCT	240
AAACCACTGA AGNCCCCATG TTACAAGGNG CCATCACTGC ACGTTCTTCA CGGGGTTTCT	300
TCCCGTTCTT GGAAGCGGGG ACCCCCAACC AGGGGCAGAA GTGTTTCTG GCGTTGCTT	360
GAACGGGGGG CAAATNCCNT GGGGCCACAA TGGATCAACG TGG	403

(2) INFORMATION FOR SEQ ID NO:507:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

GGCCCCGAGCA CCAACTTTGG CAACACGACC ATTGTGGTGC CCAAGCCCTT CCGCCCCGATA	60
CTTGGCCTGC ATCTGGACTT GGAATCCTG TACTATGTCT ACATGGGGNT GCTGGCAGTG	120
TTCTGTACCA ATGCCATCAA TATCCTAGCA GGAATTAACG GCCTAGAGGC TGGCCAGTCA	180
CTAGTCATTT CTGCTTCCAT CATTGTCTTC AACCTGGTAG NGTTGGAAGG TGATTGTGGG	240
GATGATCATG TCTTTTCCCT CTACTTCATG ATACCCTTTT TTTTTCACCA CTTTGGGGAT	300
TGCTCTTACC ACAACTGGTA NCCCTCANGG GGTGTTTTTT GGGGAGAAAA CNTCTGNTAA	360
ATTTTGCTGG GNAAGA	376

(2) INFORMATION FOR SEQ ID NO:508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

GGCAGGAGGA AAAACAGTCC TGGGAAATGT ACGACACTCA TTCTGCTAAA GAAATAGGCA	60
AGTAACAATT TTTAACAAGT GAAATATATT ACTACTTAAT TTTATTCAAA ATTCACCAAC	120
TTAATGTGCT TTATAAATAT TTNCATACCT TTCAAGCTCT ACTGATAAAA CATAATTTAC	180
AGTTAATTAA AANGTGAAGT TAAAGTAAGT ACAAANCAT TTTCAAGGTG ACAAATTAG	240
GAAGGTGACA GTNCCGATTG AAACACAGAC ATATCACACC CAAGGGTCAA GTCAAGCCCT	300
TCTATTTACT TGGGGTATTT TCCCCACTC ACATCTGGTT CAGTGGAAGT GGGGTCCTGG	360
ACCATCCTAC CAGGNGCCGT TACCCTGTGG TTNCTCTGTG TTCCNTGGG GGTGGCTTTT	420
AACTTTGCAG GTTTTTGCAC TGCCTCANTA GGTGGGGT CTTTGNCTT TTGGNAATAT	480
TTTCCTTTNC CCTTAACCAT TTTT	504

(2) INFORMATION FOR SEQ ID NO:509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

GGCAGAGCAG CCCTGAGATC GAGGGAGATC TGCAGCCTGC CACACATGGC ATCCGCTTTN	60
ATTTCTGGAC CAAGTAAAGA TGGGTCCGTG GCCCACACTC GGTTCATGTGC TCAGACAACG	120
ACTGNTGAAA ACGCCCATGN CAGTTTGCAT CGNACTGATA GTGTGTTCTT TCCGGGNNTC	180
ACAAACATTA ACAAAAAAGT TTAACCTATG TGAACCTGGG CAGTTNATTC TATGACCATT	240
TCCTGTGCCA TNTAAAATTT TTAAGGGATG AAAAATTNTG NAAAAAANA AAAAAAGTCTN	300
GNGGGGGGGG CCCCAGTG	318

(2) INFORMATION FOR SEQ ID NO:510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:

GGCAGAGGTG AAACCCTACA CTTGTTGTNA ATGTGGGAAG GGTTTCAAAT ATGGCTCAGG	60
TCTCCTTAGT CATAAGAGAG TGNACACTGG CGAGAAGCCA TACAGATGCC ACGTGTGTGN	120
GAAAGGGCTA TAGTCAGAGC TCACATCTTC AAGGTCATCA GAGGGTCCAC ACTGGTGAGG	180
AAACCCTATA AATGTGANTA GTGTGGGAAG GGCTTTGGCC GCAACTCCTG TCTTCATGTT	240
CATCAGTGAG TCCACACTGG AGAGAAGCCC TATTACGTNT GGTGTGTGTN GGNAAGGCTT	300
NCAGTTAATT ACCTCAGGTN TTGCGGGAAC CACCAAAGAG TGCCATTTTA GGCGNAGTNA	360
CCCTTATTAA GTAGTTGTTA CCATAGGGNT TTTCCCATCT TGGGANTTCN AAGGNTTTTT	420
TATTCN	427

(2) INFORMATION FOR SEQ ID NO:511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:

GGCAGACCTC GGCCTNNATT CNTNCAAAGG CACATGGACA CAGCCCTTTA ACCTGGCAAG	60
CACCAGGGAA GGAGAACTTC TATGTGGACG AGACAACTNT GGTGAAGGTG CCCCATGANN	120



GTTGCAGTCG AGCACCATCA GTTAACCTTC ATGAACTCGG AAGCTCCCCT GCCNAGCTGG	180
TGCAGATGAA ACTACGTGGG NCAATGGGAA CTNTTTTCTT NATCCTTCCG GACAAGGGGA	240
AGATGAACAC AGTTCATCGC TGCACTGAGC CGGGGACACG ATTNAACAGG TGGTCCGNAG	300
CNTTGACCCA GNAGCCAGGT GGGACCTGTT ACATTTCCAA AGGTN	345

(2) INFORMATION FOR SEQ ID NO:512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:

GGCANAGGAC CACTTGAGCT TCCTCAACTC CTTCAAGATG AAGATGTCCG TNATCCTGGG	60
CGTCGTGCAC ATGGCCTTTG GGGTGGTCCT CGGAGTCTTC AACCACGTGT CACTTTGGCC	120
AGAGGCACCG GNTGCTGCTG GNAGACGCTG CCGGTAGCTN CACCTTCCTG GCTGGGAACT	180
CTTCGGTTAC CTCGTGTTTC CTNAGTGCAT CTGACAAGTG GGCTGTGTGT CTGGGNTTGN	240
CAGGGGNCGA CT	252

(2) INFORMATION FOR SEQ ID NO:513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

GGCAGAGTAG AAGTCGGGCG GACCCGGAAC CCAGAGGACG CGACACCATG ACTTATGCTT	60
ATCTCTTCAA GTATATCATC ATCGGAGACA CAGGTGTGGG GAAGTNATGT CTCCTCCTGC	120
AGTTTACAGA TAAGCGGTTC CAGCCTGTCC ACGACCTCAC AATAGGTGTG GAGTTTGGNG	180
CTCGTATGGT CAACATTGAT GGAAAACAAA TCAAAGTCA AATCTGGGAT ACGGCTGGGC	240
AAGAATCCTT CCGTTCTATC ACCCGTTCCT ACTACAGGGG AGCAGTTGGA GCACTGCTGG	300
TGTACGACAT TACAAGGCGT GAACCTTTCA ACCACTTGNC CTCNTGGTTA GAGGATGCCC	360
GGCNACANTN T	371

(2) INFORMATION FOR SEQ ID NO:514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

GGNACGAGCA AGCACTGCTC AAACAAGGAG GTGGTGTCTT TNGCCAAAGT CCTTATNAAA	60
AACTGGAAGC GGCTGCNAGA CTCCCCTGGC CCCCCAAAAG GAGAAAAAGG AGAGGAAAGA	120
GAAAAGGCAA AGAAGAAGGA AAAAGGGCTT NANTGTTTCA ACTGGAAGCC AGAAGCAGGC	180
NTTTNTCCAC CAAGGAA	197

(2) INFORMATION FOR SEQ ID NO:515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:

GGCAGAGNAA CATTCTAGCA GGGGTAAGTG ACCATAGCTG AATTCTTTTC TTATCAATCA	60
GGAAAATGAA AATCCTTCCT TAATCAATTT CTCCAAAGTC TCTGACACAT AACAACAAC	120
CCAAAAATGC ACCTCTCTTT CCATCAAACT CCACTGATAT GAAAAATGGG CAACCTGTTT	180
TTCCTTGCCC TGTTAGTGAA CTTGTGGGTG TACCCAGTGG CCACTCTAAG GATCTCTATA	240
ATCAACAAGA CACAGTTAAC AAGTGTGGC AAGCAAGTGG AGAAATCAGA AACTCACAC	300
ATTGCCAGTG GGGATGTAAA GTGGGAAAAC AGTTTTGGAA GTTNCCTCGA AAAGTTTAAA	360
CCNGGGATTT AACCTTACAA CTCCGTAATT NCCATTACT TCNAGGGTGA TTNTCCCAA	420
GGANNTGAAA ACGTNTGTTT AACNCCAAA NCNGTTACAC AATGTTTCAC AGGGGCNTTT	480
TTCCTTATTN GCCCAGGGTN	500

(2) INFORMATION FOR SEQ ID NO:516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

TATATGCGTC TAACAAAAGA GTTACAAAAT ACATGAAATA AAAAGATACA GACATTAAAG	60
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GAGAAATAGA CAAATCTACA ACTATAGTTG GAGACTTCAA AGTACCTTTT TCAGTAATCA	120
ATAGACCAGT TAGAACACCT CAGCCAAAAA TAGCAGAATA TAAATTATTT TTGAGCTCTC	180
ACAGAACTTT GCTGAGATAC ATTATAACCT GGGCCATAAA ACAAACCTCA ACCAATTAAT	240
ACAGTTGAAA CCAGAGTGTG CTCTCTGGAC CACAGTAGGA TTCAANCTAT TAATTAGTAN	300
TNTTANTANT GG	312

(2) INFORMATION FOR SEQ ID NO:517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 457 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

GGCAGAGTGC AAGATTGGAG AGGGAATGCT GGCAGACTTT GTGTCCCAGA CTTCTCCAAT	60
GATCCCCTCC ATTGTTGTGC ATTGTGTAAA TGAGATTGAG CAAAGAGGTC TGACTGAGAC	120
AGGCCTGTAT AGGATCTCTG GCTGTGAACC GCACAGTAAA AGAGCTGAAG AGAAATTCCT	180
CAGAGTGAAA ACTGTACCCC TCCTCAGCAA AGTGGATGAT ATCCATGCTA TCTGTAGCCT	240
TCTAAAAAGA CTTTCTTCGA AACCTCAAAG AACCTCTTCT GACCTTTCGC CTTAACAGAG	300
CCTTTTTTGA GGCAGCAGAA ATCACAGATG AAGACAACAG CATAGCGCCC ATGTTACCAA	360
GCTGTTGGTG GAANTGCCCC AGGCCAACAG GGACACTTGG TTTTTCCTCA TGTTTCATTG	420
CAGNGAGTGG TTCAGAGTNC NCNTATTAAA TGGGTGT	457

(2) INFORMATION FOR SEQ ID NO:518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

GGCAGAGCTT TTTTGTATTT TTAATTTTGT ATTATTGAAA GCCTTGGAGA TCTCACAGAT	60
AGATATGCCA AATTCTATAT TTTGTAAATN CTCTATATTA GAAAACAGCT GTGCACACAG	120
GGCGGGTGTG CTCATTTGTA CTGTGTGTAT GTCGGTGTAT GTA CTGTTGTGT ATATGTGTGT	180
GTGTTTCATGC TGTGGACTGG TCTCACACAG GATGTTTTCC CTGATTTTCAG ATTTGGCAGT	240
TTTGGGTTTT CCAAGGTACC ACCAGAGCAG TGGGTGTGTG CTTTTGGGGT ACNTATGCTC	300

CAGATTAAGT AGGAGGATGC ATGGGNCCAC ANTGCCCCAT NTTTCNGGAC ACAGG

355

(2) INFORMATION FOR SEQ ID NO:519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

GGCANAGACG GAATTACTCC TTGTNTGTNT ACCTGGTGAG GCAGTTGACT GCAGGGAANN	60
CTTGACANA AACTCAGAGC AAAGGGTATC CGNANCNCAG ACCACTCGGG GGNCACTGAT	120
CAAGGAGNAA TTGAACTGCT GACCCTGAAC AGTGAAGGTG GCCACTACAA GTCTCCGGGT	180
GTCACATG TGCCCCGCTAG NAAGNNTGCG CCTGAACTGT CCCTTGTTNGT GCCCTCACCT	240
GCGNCCACCT GCAGAGCTTN GGATGCTGCC CTTTATCTAC AGATGAATGA GAAGAAGCCT	300
ACATGGACAT GTCCTGTGTG TGACAAGAAG GTTCCCTATG GAATNTTTAN TCATGANGGG	360
TTNATTATGG NGAT	374

(2) INFORMATION FOR SEQ ID NO:520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

CCANAACGCC AACGCCTCGA CAACTATAAC CATTNACCTA ACACGCGCGA AAAAAACGCC	60
TGGATGCCTC CCACCCCGCC GGCTGGCCGG CCGGCCTCCT ACGAACCTAC GCTGCGACTC	120
CNCCCCNGCG GCCTCGCCAC GCGAACTCTC CGACTACTNC ACACGCNCTC NACTCCCGC	179

(2) INFORMATION FOR SEQ ID NO:521:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

GGCAGAGGGN GACCGAGGCG ATGCTATACG ANAAGTTCAG CCCGGCCGGG CCTTATCCTC	60
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TCCATCCGGG TCTGCAGGGA ACATGATCAC CCGCCGCTCC TTGGGTACG CGTAGTTAAA	120
CTTCCAGCAG CCGGCGGTAC GCGGAGNGGC TNNTGGAACA CCATGAATTT TGAATGTTAT	180
TAAAGGGCAA GCCAGTTACG CATCATGTGN GTCTTCAGCG TGNATCCATT CACTTTCGGC	240
AAAAGTGGGA GTAGGGCANC ATATTTTCATT TAAAAATCTG GGACAANTCC ATTGNTAATA	300
AAAGCACTGT ATGATACATN TTCCTGNNTT TTTGGTNACA TCCTTTCCAT GTAAGTTGGT	360
TTNTAATTGN AATGGGTTCN CAAGGGGNTT TGGGNTTGTA CATTTTTAGA NGTGGTGNNT	420
NTCCTTACGA TGGTNGTTNN NAAAAANTGA TTGGAATGTT CCNNAATGGA TCNCAAAGTT	480
TTTTTNGGGN	490

(2) INFORMATION FOR SEQ ID NO:522:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 365 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:

GGCAGAGTNA AAGGAGGAAT TGCAGATGCC GATGGAAGAC TGATGCAGGG TGACCAGATA	60
TTAATGGTGA ATGGGGAAGA CGTTCGTAAT GCCACCCAAG AAGCGGTTGC CGTTTGCTAA	120
AGTGTTCCTT AGGCACAGTA ACCTTGGGAA GTTGAAGAA TCAAAGCTGG TCCATTCCAT	180
TCAGAGAGGA GGCCATCTTC AAAGCAGCCA GGTGAGTGAA GGCAGCCTGT CCATCTTTCA	240
CTTTTNCAC TCTCTGNTC CAGTACATCT GAGTCACTGG NAAATTAGCT TCAAAGAAGA	300
ATGCATTGGC ATCTGAAATA CAGGGGTAA GNACATCGAN ATGANAAAGG GCCCTATTGA	360
TTCAN	365

(2) INFORMATION FOR SEQ ID NO:523:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 127 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:

NGGGNCAGTG AATCCTCCGN CCTCTTGGA CACCAGGGAC CGCTCGTGGG ACTCCACATC	60
CTCCAGCCCC CACAATCCTN TTCAGGGCTC CCTGACATNC CTGGGGNTGG NAGAGNCCAT	120
CCCGGGG	127

(2) INFORMATION FOR SEQ ID NO:524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

TCCNTCCATA GGCACACTGG NTCATNTNAG AGCCCCTGGG ATCGTTTACA GGGAAGTTCC	60
CACATGAGGG CCCATGTGTG ACNTGTTATG GTCCGATCCC GNTGNTCTGN GTGGATGGGT	120
TTTTNACC	128

(2) INFORMATION FOR SEQ ID NO:525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

GGCAGAGTG GCAGTGGGCA TGGCGACCCC CTCCATTTAA AACTCTAACC ACCTCCCCCT	60
GGCTCCAGCT CTTNATCAAT GCCCGAACT GGACCCTGGG AAGAGAGNCT GNCTGACTGG	120
CCANNGGAGC TCACCTGGGA CCCCATGGCN TTTNAACCTA AGTGGGTCCT GCCCCCTCCC	180
CCATGAACCT TNAGGAGCAC CCCATATTAT TTCCAAAAT ATCTTGGACA GGCAAGGNCC	240
AAAATGCCAA AATCTCAGNG GACTTGATGA TCTGCCTGCT GATGTTTCCT TCTGTGGGNT	300
GTGGTCTATT TTTNAGTTNC TGCTCTT	327

(2) INFORMATION FOR SEQ ID NO:526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:

GGCAGAGTGG AGATGTTTNA TTACCTGGAG TGTGAACTCN NCCTCTTNCA AACAGTATTC	60
AACTCCTGG ACATGTCCCG CTCTGTGTCC GTAAGGCAGC AGGGNAGTGC CGCCTCGCCC	120
CGCTGATCCA GGTCATCTTG GNACTGCAGC CACCTTTATG AACTACACTG TCAAGCTTCT	180

TTTCAAACCTC CACTCCTGCC TCCCAGCTGA CACCCTGCAG GCCCACC GGG GACCGNTTTC	240
ATGGGNGCAG TTTTACAAAG TAAAGTGGGT TCAAGTAAAC AGGAATGGAG GTGAATTTCA	300
AGGGCGTTNT AAAATNCATT TAAGGCCTGG GAGTGCAATG GGGGAATTTG GGGTTCANTG	360
GNAACTGNCT TACCGGTTCA AGGG	384

(2) INFORMATION FOR SEQ ID NO:527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

GGCAGAGCTC TGGAGAGGCA GGCACAGGGG CACCNGNCNC GTNATGCAGC TTCGCCCTGG	60
GTTACCTCTA TGGCTCGGAC CAGCTGGTGG TGAGGATCCT GCAGGCCCTG GAACCTCCCT	120
GCCAAGAACT CCAACGGCTT CTAAACCCC TACGTCAAGT ATCTACCTGC TGCCTGACCG	180
GAAGAAAAAG TTTCAGAACC AAGGTGCACA GGAAGACCCT GGAACCCCGT TCTTCAATGT	240
GAACGTTTGC AATTCTGCGG TGCCCCTGGC CGGAGCTTGG CCCAACGNC AAAATTGCAC	300
TTTCAGCGTG TTATGAANTT TGAACNNTT TTGGTGGTCA GGACCTCATC GGNNCAGGTG	360
GTG	363

(2) INFORMATION FOR SEQ ID NO:528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:

GGCAGAGTNT GACTTCAAAA TCAAACTGT AGAGCTAAGA GGAAAGAAAA TTAGATTACA	60
GATCTGGGAC ACAGCAGGTC AGGAGAGATT CAACAGCATT ACCTCAGCTT ATTACAGAAG	120
TGCCAAGGGG ATCATATTAG TATATGATNA TCACTGAGGA AGGAGACATT TGAATGATTT	180
GCCGAAATGG ATGAAGATGA TTGATAAGTA TGCTTCAGAA AGATGCAGAG CTTCTCTTAG	240
TTGGGAANTA AGTTGGA CTG TGAACGGGAC AGNGGAATCC ACCAGGCAGC AGGGGAAAGT	300
TTTGCACAGC AGTTCACTTG GGTGCGGTCT TTTGAGCAAG TTCCCAGGGT AACTTCCATG	360
TGGGNCGGGN TTTTTTNGAA ACTTGTCGGT GNCCTTCCN	399

(2) INFORMATION FOR SEQ ID NO:529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:

```
NTGATTGTTT CAAGAGGTTT CGTTTTTTGG GGCCTTGGGT NAACCTTTGG GGGGGGTAAA    60
CATTTTTTNC CCCTGGTNGG CTTAAAGGNG CCCCCTTTAG    100
```

(2) INFORMATION FOR SEQ ID NO:530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

```
GGCAGAGCCC ACGCACAGCA CTTCCACAAG CACCAGCTGT GGCCCAGCCC CTTCCGGGCG    60
CTGAAACCCC GGCCAGGNCG NCAAGACCG CAGAAAGNAA GGGCCAGGNG GTGTTTCATGG    120
CCGCCTCGCA GTGCTGGTAC TTTGACGAGA AGACGATGCA GAAAGCCCGG AGTAAGCAGT    180
GGGATGAGCC GAGGGTGTGC TCCCGGAGTT ACCTGAAGGT GGACTTCGCA GACATCGGCT    240
GGNATGAAAT GGTATAATNT CACCGAAATC TTTTGATGCC TACTACTGCG CGGGAGCATG    300
TNAATTCCCC ATGTCTNAAA TCGTTTCGTT CCATCCAACC ATGCCACCAT NCAGAGCATT    360
GTTCAAGGNT TTGNGGCATC ATCCCTGGG    389
```

(2) INFORMATION FOR SEQ ID NO:531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

```
ATGGTGCAGA GCAACCNAGT GCTCTATACG CCCGGCAAAG AGCCTGAACC ACTGNTAGNA    60
TNCGAAGTAT GTGCCCCTAC GTGGGTNAAC AGCAAGCCCG CGCTGGAATG NGTATACCTC    120
GGAGNCTGAA TGCTGGGAGG NAACCAACAC ACTGGTGCTG CACAACACGT GTAAGGGTCT    180
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CGCTGCTGGC CGCACCCATC ATGCTGGAAC CTAGCGCTGC TGAACCGAGC TGTGCAAGNG 240  
AGTGAGTTTT CTGNCNCTGA NCATGGGACC CCGAAGNCG 279

(2) INFORMATION FOR SEQ ID NO:532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

GGCANAGAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 60  
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAANGNCCN GGGGGGGGNC CCCN 114

(2) INFORMATION FOR SEQ ID NO:533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

GGCANAGGNC TGCTCAAGGC CACGGAGCCC GGGTTATTCG GCGTGTGGGC GCACAATGGC 60  
GAGGTGCGTA CCGCCAGTCT GCTGAGCGAG CGCAACGCAG CCAAGCAGAG GCTGGTGGTG 120  
CTGGTCAAGG ACAATGGCGA GCCTCCGCNC TTNGCCACCG CCACGNTGCA CGTGCTCCTG 180  
GTGGACGGTT TCTCCCAGCC CTACCTGGGG CTCCCGGAAG GCGGCCCCGG GACCAGGCCA 240  
ACTNCGCTCA CCGTTTTACC TGGTGGTGGC GTTNGCCTTC GGTGTCTTCG GTTCTTCCTN 300  
CTTTNTNGTG CTTCTGTTTT CGTGGGCGGT GNGGNTTNC ANGNAGNAGC ANGGGGGNCC 360  
CCGTTGGGGT TCGTTGNTTC GGTGCCTNAA GGGCCCTTTT CCAAGAAAAT TGTGATTT 420  
TAGGGGNAAC GGAACCTATT CCANAGTTAC CATT 454

(2) INFORMATION FOR SEQ ID NO:534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:

AATGCCGTTT TCTGTTTCGT GGGGCATCCT CCTGCTGGNA GCCTGTNCTG CCTGGTCCCT	60
NNTTCCNTGG NTGAGGATCC CCAGGGAAGA TGCTGCCCAG AAGACAGATA CATCCCACCA	120
TGNATCAGGA TCACCCAACC TTTCAACAAG ATCACCCCCA ACCTGGCTGA ANTTCGCNTT	180
CAGCCTATAC CGNCANTGGN ACACCAGTTC CAACAGGACC AATAT	225

(2) INFORMATION FOR SEQ ID NO:535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:

CATCTNGAAA ATNCATGNGA AAATTAGTGN AATGAAGTTA ACTGANATTT GTCAAAAACA	60
TGTGTTGCTG ATGAGTCAGC TGAAAATTGT GAACAAATCA CTTTCATACC CTTTTTGGGA	120
GACAAATTAT GTCACAGTTG CAACTCTTGG TGAACCTATG GTGAAATGGC TGA CTGCTGT	180
GCAAAACANG GAACCTGNGN GAAATGNANT GGT TTTTGGC AACCACAAAG	230

(2) INFORMATION FOR SEQ ID NO:536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:

AAGAAAAGAC CCAGCCTCCC TTCCAGCCCG TCTCCTGGCC TCCCAAAGGC TTCTGCCACC	60
TCAGCCACTC TGGAGCTGGA TAGACTGATG GCCTCACTCT CTGACTTCCG CGTTCAAAAC	120
CATCTTCCAG CCTCTGGGCC AACTCAGCCA CCGGTGGTGA GCTCNACAAA TNAGGGCTCC	180
CCATCCCCAC CAGAGCCGAC TGGCAAGGGC AGCCTAGACA CCATGCTGGG GCTGCTGCAG	240
TCCGACCTCA GCCGCCGGG TGTTCCCACC CAGGCCAAAG GCTTCTNTTG GCTCCTGCAA	300
TAAACCTATT GCTGGGCAAG TTGGTGACGG CTCTGGGCCG CGNCTGGCAC CCCGAGCACT	360
TCGTTTGCGG AGGCTGTTTC CACCGCCCTG GGAGGCAGCA GTTCTTCGAG AAGGATGGAG	420
CCCCCTTTTG CCCCGAGTGC TACTTTGAGC GGT TTTTGCC AAGATGTGGG TTCTGNAACC	480
AGCCCA	486

(2) INFORMATION FOR SEQ ID NO:537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:

TNAAATTTTA ACCATGTGGG AAATCNTGCA CATCCAGGTC TGGNCAGTTT GGCAACCANA	60
TCGGTGCCAA GTTCTGGGAA GGTGGATCAG TGATGNAACA TGGCATCGAC CCCACCGGNN	120
ACCTGACCAC GGGGACAGCG GACCTNGCAG CTNGGACCGG TATCTTTGNG GTACTGACAA	180
TTGAAAGCCA CAGGNGGCAA AATATGTTNC TGCCTGCCAT CCTGGGTGGA TT	232

(2) INFORMATION FOR SEQ ID NO:538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:

GGCAGAGCTC GNCNTNCGNC CTCCAGCCTG CAGCTCACGG TGACCCAGGT AAAGACTTGG	60
TTCCAGAACC GCCGCAACAA GTGGAAGCGG NCANTCTCGG CTGAGCTGNT AGGCGNCCAA	120
NATGGCGCAC GNNTCGGCGN AGACTNCTGG TGGAGCATGC CGCTGGTGTT CCGGGAACAG	180
TTCGCTGCTG NCCGTGCCGG TNCCGCNTTC GCTCGCCTTT CCCGCGCCGN TCTACTACCC	240
GGGGAAGCAA CCTCTNGGGC TNACCNTTCT ACAACCTATT ACAACAAGCT TCGACTAATG	300
GACCGGGCC	309

(2) INFORMATION FOR SEQ ID NO:539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:

GGCAGAGAAG ACATTTCCCA GCAACCACTG GTGCAGGTGG CAGCCTGGGT GCATTGGGGA	60
GTATGGGGAC CTCCTGCTGG CAGGAAGTGG AAGTTGATTG AGCCCCTTCA GGTGGACGAG	120
TAGGAAGTGC TGGCATTGCT GGGAAAAGGT GCTGCAGTCC CACATGTCCC TGNCAGTTA	180

CTCGAGGGAT ATGCCCTCAN AGCCCTTCAT GTAAGCTTCA GCACTTCGCC TCTTTGGGGG	240
ACAACAACCG GCATCCGCCA GTGGNTGTTT CATCTACGGG AAGCTGNTTT GGGACGTGGA	300
GCTGTCANCA NCGGTGCTTT GGGAGTTNGG ACACAATTTT TCCGGAA	347

(2) INFORMATION FOR SEQ ID NO:540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:

GCTTAATAAA ACACATCCGG TAATTTATAA CGTCTGCAAT TATCAGAAAC CCGTGCCCGG	60
TGAGCCTGCG TTGTTACTCT GGGATGATGT CATAACCTTA TTCCATGAAT TTGGTGATAC	120
GCTGCACGGC CTTTTTGGCC GTNCAGNNTT ATGCCACGCT TTCCGGCACC AACACGCCGC	180
NGTTTTTTTT CGAATTTCCG TCGCAAATGC AACGAACACT GGGGCAACGC ATCCGCAGTA	240
TTTCGCTCGC TACGCCCCGC ATTATCAGAG CGGGGCAGCA NTGNCTGACG AACTGCAACA	300
GAAAATGCGT NATGNCAGCC TGTTCACAA GGGTATN	337

(2) INFORMATION FOR SEQ ID NO:541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:

GGCANAGGGN ACCATGGAGG GTGTAGAAGA GAAGAAGAAG GAGGNTCCTG CCTGTNCCAG	60
AAACCCTTAA GNAAAAGCGA NGATTTTCGC AGAGCTGNAA GATCAAGCGC CTGAGAAAAG	120
AAGTTT	126

(2) INFORMATION FOR SEQ ID NO:542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:

TTAAATCCAN NTCCATACAA CGCTCCGCCG CCGNTCCTGC CGNGAACCCG GAACTGCCCCG	60
CCACNCGCCC CCTGCCCCGAC AGCTCCGTNA CTATGGAGGA TATGNANCGA ANTACAGCAA	120
TATAGAAGGG AATTCGCCAG AGGGGATCCA AGATCAACGC GAGCAAAGAT TCAGCAGGAT	180
GGACGGTGAA AATNTTTTATT GGAGGCTTGA GCTGGGNTAC AAGCAAANAA GATCTGGACA	240
GAGTACTTTG TATCGTTTTG GGGGAGTTNT AGACTTGCAC ATTTA	285

(2) INFORMATION FOR SEQ ID NO:543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:

CTGGGGCCGA CGCTCTGNCC GGNTGCTGCC CTGAAGGAAA GCCGGGACGC GGNGCCCCGC	60
CGAGAAGCTT CTTTGCTCCG GAACGCCCCT GGACGTGGCG GGCAGCCGGA AGGNNTAACC	120
ACCATGAATC CCCTGGGTGC TCCTGGCCTG TGNCCCTCCC CTGTGNCTGC TGACCCACTG	180
CTTGGCGCCT TTGATTGCA GGGACTTCCG GAAAGGGTCC CCTCAACTGG TCTGCAGCCT	240
GCNTGGCCCC CAGGGCCCAC CCGGNCCCCN AGGAGCCCCA GGGNCCTTAA GAATGATGGG	300
ACGAATGGGG TTTTCTCTGG GAAAAAGGG TCCAAATTGG ACNAAGAANG GGGAACCGGG	360
GGGGACAAAC GNGNAGGAAG AAATTTTTTT TTTCNAA	397

(2) INFORMATION FOR SEQ ID NO:544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:

AGCACGAGCT GGCATGTNAC AACCCAGGGC TGCCTGAAAA TGGATACCAA ATCCTGTACA	60
AGCNACTCTA CCTGCCAGGA GAGTCCCTCA CCTTCATGTG CTACGAAGGC TTTGAGCTCA	120
TGGGTGAAGT GACCATTNNT TGCATCCTGG GAACAGCCAT CCNACTGGAA CGGGNCCNNT	180
GCCGTNTTGT ANAAGTAGGC AGAAGCGGCA CAGAGACGTC GCTGGAAGGG GGGGGAACAT	240
GGCCCTGGNT ATCTTTCATC CCGGTCCTNA TCATNTNCTT TANTGTTGGG AGGAGG	296

(2) INFORMATION FOR SEQ ID NO:545:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 234 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:

ATGNTTTGTG CCGCTGAGCA GTACACACCC AAGGCCAAGT ACCATGGCAA CGTGATGCTA	60
NTGCNCGCCA AGACGGGTGG NGCCTACGGC AGGTNCCTGG GCGCGGACTA CAACCTNTCC	120
CAGGTATGCA ACGGGAAAGT ATCCGTCCAC GTGCATCGNG AGGTGACCAC CGCACGCTGC	180
TGGTAGGGCA GGGNCCTNGT AGTTCCATCA TCAGCATCAT CCACAGNTCC CTNG	234

(2) INFORMATION FOR SEQ ID NO:546:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 493 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:

GGCAGAGGTT TTAANATCTT CTTCAAGAGA CGTCTGATGA ACCTCATGCG GGATGTGGAG	60
CGGGAGGGCC TGGACTGGGA ACCTCATCTA TGTGGGGCCGG AAGCGGATGC AGGTGGAGCA	120
CNCCGAGAAG GCTGTGCCTC GCGTGAAGGT AACCTGGTGG AGGCCGACTA TTCCTACTGG	180
ACCCTGGCCT ACGTGAATCT CCCTGCAAGC GGCCCGCAA CTGCTGGCTG CTGAGCCGCT	240
CTCCAAGATG CTGCCTGTGG ACGAGTTCCT GCCCGTTAAT GTTCGACAAA CACCCAGTGT	300
CCGAGTTACA AGGCCCCACTT CTCCCTCCGC AACCTGCATG TTTCTCTGTG GAGCCGTTGT	360
TCATTTTACC CCACACATTA CACAGGAGAC GATGGGTATN TGAAGTTAAC ANCGAGACTT	420
CATCGTATGG AACAATGAGC AAGTTAAGAC CGATTGGAAC NGGCCANTTC CAAAGTTTNG	480
GGGNAGCAGG ATT	493

(2) INFORMATION FOR SEQ ID NO:547:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 115 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:

CCTCAAAAAG TCCGGGAAGC TGAAATCCCC GAATGGNTGG TATACCGTCA NGCTGGNCAA 60  
GCACAAAGAG CTTGACTNCC TNACGATGAA GGAAGTGGTT TCTACACGCG AATCT 115

(2) INFORMATION FOR SEQ ID NO:548:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 65 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:

GGCANAGGNC ATTTTNCCTG GCTATAAAGC GGGGTCTCCG GAACCAAAGG NNGCACACAG 60  
CTCTT 65

(2) INFORMATION FOR SEQ ID NO:549:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 272 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:

GGCACAGCTC GGCGAGANAN AGCTTACTCA AATTGGCCAA CATACCCTCA GCTGTATGTG 60  
AAAGGGGAGC TNGTGGGAGG ATTGGATATT GTGAAGGAAC TAGAAGNAAA TGGTGAATTN 120  
CTGCCTATAC TGGAGAGGNG AAAATTNAAT AAATCTTAAA CTTGGTGCCC AACTATTGTA 180  
AGAAATATTT GAATTNACAT TGGGAAGCAG TTTCATGATT TTAGTCCTCA GAAATGGGTT 240  
CTAGGGNNTT AGGAAAATTT CCTGNCTTTN CT 272

(2) INFORMATION FOR SEQ ID NO:550:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 377 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:

TACAACTGAA ACCTCCAGTA CCTTAGAGGT AAGANCTCAG GGCCCTATCC TCACAGCAAG 60  
TGGCAAAAAC CCTGTAATGG AGCTCATTTGA AAAAAGAAGA GGTCTCAAGT TATGANCTCA 120  
TCTCAGAGAC TGGTGGNAAG CCATGNACAA GCGCCTTTGT GAATGGAGGT AGCAAGTAGA 180

TGGACAGAAA TTCAGAGGCG CAGGTCCAAA TNAAGAAAGT GGCAAAGGCG AGTGCCAGCT	240
TTTGGCTCCT TGNGNAGTAA ACTTTTTTTT GGGACCCAAT GCGGGCAAAT TAATTAAGGA	300
AAAAGNAAGA TTTATTCCCT TCAGGGCAAA GGGGNCGTTT GTGGAATTAC AGCTNGTTTT	360
CTNNCAGCAG TCCCAAG	377

(2) INFORMATION FOR SEQ ID NO:551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:

GGCAGAGCCC TGATCGACCC CAACATCTTG TNTCTNAACA TCCTCTCTTC CGGATACATC	60
CACCCAGCCC AAGATGACCG GACCTTTTAC CAATTTAAGG CTGCGTGGGA CAGCTCCATG	120
CACAACTTTN TCCTGCTGAA CCGGGTCACC CCTTATCGAG AGAAAATCTA CATGACACTC	180
TCCGCTTATA TCGAGATGGA GAACTGCACC CAGCCGGCTG TTGTNACCAA GGAACCTCTG	240
CATGGTCTTC TATTCCCGTG AATGCCAAGC TTGCCAGCCT CGGGGTNCCA TCCGCAACCT	300
CTTTGGGCAG TGGGAGCCTT CGGGCCTNCA NAGGAGTNAA CCGTGTGAAC TGGTGTNTTA	360
	360

(2) INFORMATION FOR SEQ ID NO:552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:

GGCANAGNAT TTTTNACTTT AGCAACGTGA TCTTCCTTTA AGGGGAAGTA TGTCCCCTCC	60
TAGAAACACT CCCGCCTTGG AGAAGGGGTT GAGTTCGCAA CTCCACTTAC AGACTACGGA	120
GGGAACCCCA GGGTCAAACC AAACCAAACC AATTCTGGCC AGTTGCTTAG CGCATTCAAG	180
TTACTTAGTG CGCTGGAAGG GCATTTTCAG GCAATCCAAC TTCTGGCTCG AACCTTCTCG	240
GAGTATTCCA AGGGATGGGA ATACTCTNCA CTTGAGGCGC TTGCCGAGGG TGGCCGCTTT	300
GAGGNAAAAC GTGANTTTNT TGAAAGAAAT GTTTTGTGTTNG CCAGATTACA GTTTCCACCA	360
TTCTNACATN AAGTATGTGG GAAAACAGGA NGTTATCCCT TTTGGGTTCC NGGGGTCTTC	420



CAGAACCATT AGGGGGCAAA CATCCCAATT TGNTTNTGGG CACTTCCAAG AGNC

474

(2) INFORMATION FOR SEQ ID NO:553:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:

ATGAAGATGG GTGGNCTGCC GCGTACAACA CCTCCAATC AAAAGCCCCC TAGTCCCCCT	60
ATGTNAGGGA AAAGGGACAC TTGGGCGGCA CTCCCCCTAT CGCACACTGG AGCCAGTNCG	120
TGCCTCCAGT GGTACCAAAT GAATTACNTA CCTAGCCCCA CCNGTAAATA TGGCTCCCTC	180
GCAGCAAAGC CCTGTGAAGG ACAGTTTCTT TGAAATCAAA GAAATCGAAC TTACAGCAGC	240
ANTGGGNGTA NTGGAGGGAA GCCACCCAAN TAGTCGGAGC ANCAATCGAG AGAACATTGG	300
AATGGGTTAT TTGGGGG	317

(2) INFORMATION FOR SEQ ID NO:554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:

ACTNGGCCCC TTCCGCGCCA GCAGTTCCCC TATGAACCGC AAGCTNNTTT CCACTGCNTT	60
TTTGGCAAAC AGCGAANGGG ACTTCTATTA TGAGTGGGGC AGTTTTTCGGG GGGCAAAGTG	120
GCCAGGGTAT ATGATTTTAC TAGGGGCTGC CACATGGCCA TCCTGGNGGA CAAGGCCATG	180
GGCATCATGG NTGCNTGGNG GGGNGG	206

(2) INFORMATION FOR SEQ ID NO:555:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:

ANATGGCCCC CGGGAAACAC AGCAAGANTG CCAGCTTCCT GTTTGGNATG CGGAACAGTG	60
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NCAGCCAGTN AATGAGGACT CAAGCTGGGC TACCTTTATC CNAGGGNCAG CCCCTGCCTA	120
ATGGNTCCCC AAAGGACACA GAATTCCTTC TGGAAACCCC AACGCCTTCA AGAACGGATT	180
CCAACCTGCC GGTGGATGG TTGAGGGTCC AGGACACCTC AGGGACCTAT TNACTGGCAC	240
ATTCCCAACA GGGGACCACC CAGTGGGGAA CCCCCGGGC CGGGNTNTCC NNTTTAAAGG	300
GG	302

(2) INFORMATION FOR SEQ ID NO:556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:556:

NAAGCCCATA GCTCAGCAGG CGGCACGGCG GCCTGACCTT NAGGGCAGCN AGCTCCCTCC	60
CGGTTTCGCN TTCCCTCGCG GTCAGCATGA AAGCTTTCAN TCCCGTGANG TNCCGTTAAG	120
AAAAANAGCC TGTGGGAACC ACAGCCTGGG NATCTTCCCG GTGGCAAANN NCCTNTGGGA	180
CGACCCGNTG AGCCTGCTAT TACAACATGA ACGANTGTTA NTCCAAGTTC AGGAGTTGGT	240
GCCCAGCATC CCCCAGAACA GGAGGTGAGC AAGNTGGGAA TTNCTGCAGC ACGTCATCGA	300
TTACATTTNG GACNTGCAGT TCGCCTGGGA TTGGNTTCCA TTTTGTT	347

(2) INFORMATION FOR SEQ ID NO:557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:

GGCAGAGGGN CGGGCCTAG TAATGGAAGG GGTGANATGT GGGCGGGCG AGCTGTGGGT	60
GGGGCCTAGC CATGGGAAGA GGTGAGCTGT GAATGGGGCT AGCTATGGGT GGGGTAAGCT	120
GTGGACAGGG CCTAGCCATG GGAAAAGGTG AGCTNTGGGC GGGGCCTAGT CACGGGAAGA	180
GGTGAGCTGT GGGCGNGGCC TAGTCATGGG AAGGGGTGAG CTGTGGATGG GGCCTAGCCA	240
TGGGAAGGGG TGAGCTGTGA GTNGGGCTGA GCCATGGGAA GCAGCAAGCT NGTGGAGTNG	300
GCTNGGCCGG ACTGTGGN	318

(2) INFORMATION FOR SEQ ID NO:558:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 454 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:

TGAACCAGCA GTATATGTAA TATNNTNATG CCCAGGACAC AGAGACTTTA TCAAAAACAT	60
GATTACAGGA CATCTCAGGT GACTGTTCTG TCCTGATTGT NGTGTGGTGT TGGTGANTTA	120
AGTGGTATCT CCAGANGGGC AGACCCGAGG CAGCCNTCTG GTTACACACN GGGNAACAAC	180
TATTGTCGTG TTACAAANGG TTCCATGNCC ACNACANCAA NGATNNGGAA TTGTTAGGAG	240
TCACATTACA TAGNATTGGT ACACCCGACA CATAGCATTT NCCANTNCTG GTGGATGTGC	300
ACNGTGGNCC AGTGNTACAG CTTGNTCAGG GTGGAAGTCA CNTAGGTGGC ATGCCATGGA	360
CCNGTTGTTG GGCNTGGATG CNTCTACCAC CACTGTCCAC TGACAGCCTT GGGCTGCNTT	420
CCAGGTGTTT CAAATTGGTG GTTTGGTANG TTCC	454

(2) INFORMATION FOR SEQ ID NO:559:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:

GGCANAAAAG ACGCAANCCC ATGAAGCTNA GGTCTTGAAG CAGCTGGCTG AGAAAACGAG	60
AGCACGAGAA AGAAGTGCTT CAAAAGGCAA TAGAAAGAGA AACAACAAC TCAAGTAAAA	120
TGGCAGANGA GAAAAC TGAA CCCACAAANT GGGAGGCTAA TTAAGNNGAA CCGAGAGGCA	180
CAANTGGCTG CC	192

(2) INFORMATION FOR SEQ ID NO:560:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 52 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:

TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTCCCCCT NNAGGGNCCC CC	52
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(2) INFORMATION FOR SEQ ID NO:561:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:

TGAAGGGCCA TGGCTATGCT TCCCTGGCTC CAAGGGCCCA TTTCCCTCCTA GATGCCCTTT	60
TGGCCTTTNT GAGGGAGCGA GGAACAGGCT CGAAGGCTCC GGGGTATCTG CCTTCTGCTG	120
GGCTCCTGTG AACAGGCCTT CTGTGCCAG CGTTTGTACT TGCCTCCCC AACAGTGGGC	180
CTGTTCTTNN CCGTGCCAGG CCCCAGGAGA GCCGCAGGGG CCTGNACAC ACTCCCAGCT	240
CACCCTCACC CCAGCCTTTT TCCCCACATT NAGGGGTTTT TTGGGAAGCT GGGTTCTCAA	300
TCCCTTCCAA CTCAGNTAG AGGTTAGGT TNTCCCTGAT TTCCTGGGGG TTNCCAGCCT	360
TAAAAANTNA ATTGGCTTTC CCAAGGGGC CCCTTTAAGG GAGGGTTTTG GGGG	414

(2) INFORMATION FOR SEQ ID NO:562:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:

TTTCCAAACA TTCTATAGAA ACTCACAGTG TATATAAATA TAATACATTC TGCTTTTACC	60
TTTTTNACCA GATTCTTCAT TTTCCTGATG GAGAAAGGTA TAAAAATGTC AATATCATGA	120
TTCTTGATGA TGACATTCCA GAAGGAGATG AAAAATTTCA NCTGATTTTA ACAAATCCTT	180
CTCCTGGACT AGAGCTAGGG AAAAATACAA TAGGTAATTA ATAATTNCTT ATAAACAGCT	240
TCCTCTCCTT CATGCTGGGT TCCTTAATAT GGGGGAAGAT GTAAAAGGGN TGAGGAAAGT	300
CTTGGTGGTT TTNCTGTGGN TTAAATGGG GAATGATTTT TAAGTTCNNG GCATTTCCAG	360
AATTTCCCGT GNTCNGGTGT AACATGGNCC CTTTCCACGG GTGTAATGTT GGGNGGTATA	420
TATGCCAGTT ATGTNAAAAG GCCAAGGTAG GGTGGTTACC CCCGG	465

(2) INFORMATION FOR SEQ ID NO:563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:

GGCACGAGGT CCTGCAAAAG NGTTGTGGGA AAAGCTTCTA TGTCCTGCAG AGGCTNAAGG	60
TGCACATAAG GNNCCACAAT GGAGAGAAGC CCTTNATGTG CCATGAGTCT GGCTGTGGTA	120
AGCAGTTTAC TACAGNTGGA AACCTGGAAG AACCACCGGC GCATNCACAC AGGAGNGGAA	180
ACCTTTCCTT TNT	193

(2) INFORMATION FOR SEQ ID NO:564:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 193 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:

GGCANAGGGA AAGGTGCGTN TGGGGCTGGG TCTCGGAGTG GGAGACGTGG AGTNCAGGGT	60
GGAATGTAGC AAAGCCCATC CACCAGCCAT GTACTACCCC CCAACCCGGN CAGGCTGGAG	120
CAACCGTTTN TGGGGAGCCG AGCCCCGTTT CTNGCTGCGG TGAGCCCGGA CTGGGGCACG	180
NACTGGCCAN ACT	193

(2) INFORMATION FOR SEQ ID NO:565:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 469 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:565:

AGCCAGANTT CGTCTCTTGT CCTGCACTAT AGATTTTACA CTGGAGAGAA ACCCTACAAA	60
TGTAATGAAT GTGGACGAGC CTTTGGTCAC ACTTCATCCC TTATTAAGCA TCAGAGGACT	120
CATACTGGAG AAAAGCCCTA TGAAATGCCG GGTAATGTGG GAGAACCTTG AGCCAGAGCT	180
NCATTCACTG CATTGTGCAT TACAGATTTT ATACTGGNAG AGNAAACCTT CACAAATGTA	240
ATAAATGTGG GAGAGCCTTC AGCCAGAGTT CCATCTCTTC ATTCAACATT TACAGNTTTT	300
CACACTGGGA GAGAAACCCT ACAAATGTAA TGAGTGTGGG AAGGGCCTTT GCNTCCTAAT	360
GTATNCCTTN GTTAAACATC CGGTGAAGTC NTGTTGGGGA AAAAAACCC TATAAATTCC	420

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AGTGGATTTT AGNAGGGGNT TTCAAGTGGG NGTGCCAGAC CTTCATTGG

(2) INFORMATION FOR SEQ ID NO:566:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 487 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:

GGCACGAGTG CCACCTGACT GGANGAGAGC ATCCTTCCAA CAGGGCAGTC AGGCCAGCCC	60
TGATTTAAAG CCAAGTCCAC AAAATGGAGC CACGTTCCTG TCCTCTGGAG GATATGGCCA	120
GGGAATCACT GATAGCCGAT GAGGAGTCCC AGGAGTTTGA ATGATTTAAT ATTTGCATTA	180
AAAACCTGGTG CTGGTCTCAG TGTCAGTGAA TANTGAAATC TGGTCAAGGC AGCCAGGAGG	240
GGGGCACCTT GGAAGTACTC CCAGATCGTG GAGCTCCAGG AGGATACCCA TCGCCGACAC	300
TCACCTGTAG CACCTTCACT TAACCATTTC GACTGAGGCA CATTTTCCAT ATTTGTATTC	360
AGCTTTTTGT GGTAAAAAT CTCTAAGTNA CATCCACCTG TGTAATTAGG AACCNGTGGA	420
ATTGTTACTG GGTGGTTTAA TACCAAACGT GGTGTGTTGN TATTTGGNGT ATAAATTACT	480
GGNTTGT	487

(2) INFORMATION FOR SEQ ID NO:567:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 380 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:

GGCAGAGTGC CACTGNCCAC CCGGTTTCCA AGGCTCCAAC TGTNAGAAGA GGGTGGACCG	60
GTGCAGCCTG CAGCCATGCC GCAATGGTGA GGCCTGGAGG CTGNANCGGC GAGGGNTGGG	120
GTGGGGGTCC TGGATGGCTC ANACAGTNCA GGGTTGGGAA TCCTGGCTTT GAACTCTTCT	180
GAACCCTAGG GCCTGGGGAC CTGACCTTCT ACCTGCAAGC CTGTAAAATG GGCAAGGAGA	240
CATTCCCTAT CTNATACTA TTAATATTTA CTGAGGAATT ACTGTGTGNC CAGGCCCTAT	300
TTTATAGGCAC TGNGGTTACA GCAGGGAATG AAACCGACAA AGTCCCTGGG CCTGCCTGTT	360
AGAGNTNAGG TGCCCGGTNT	380

(2) INFORMATION FOR SEQ ID NO:568:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 65 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:

TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTNTNGGGG 60  
GCCCN 65

(2) INFORMATION FOR SEQ ID NO:569:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 271 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:

CTAGATGAAA TGGCCAAACA AGCTCGAAAT CTCATCACTG ATATTTNCAC AGANCAGTGT 60  
ACCCTTAGTG ACCAGTTGCT ACCCAAGCNT TGTCCCAAAN CTATCAGTCA AGCAGTGNA 120  
TAAGAAATCA AAAAAGCAGA CTGGTAAGAA AGGGGAACCT GNAAAGGNAG NAAACCAGGT 180  
GTTGAGAGCA TGAGGAAAAA CAGGCTGGTT GTGNACCAAC CTTGNATAAA TTGCACACTG 240  
CACTTTNTGN AGTTATGCTT CTNTATGATT T 271

(2) INFORMATION FOR SEQ ID NO:570:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 329 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:570:

GGCAGGAGCN ACAATCCGGC CAGTGCCCAG GCTGCCATCC AGGCCATGAA TGGNTTCCAG 60  
ATCGGCATGA AGCGCCTCAA AGTCCAGCTA AAGCGGCCTA AGGATGCCAA CCGGCCCTAC 120  
TGAGGGCCCC CAGGTCTGGA GATCCCANAG GAAGGGGCGC CTCANACCCT CTTCCCACGA 180  
CTGGCCNCGG CCATCTCCGC ACACCTGCCC TGGGCCTTGA CTGGGTCTTG GGGCAAACGA 240  
TGCTTACGTG GCCCCGGGGG CGCAAGANNA CCGGCCNTTC CCACNCCCCT GNCTGTTTGA 300  
AAGGGCCATG GGTGATGATT TCCCTGGGT 329

(2) INFORMATION FOR SEQ ID NO:571:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 221 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:

```
GGCACGAGGN ACACCAAAGG CTTGGTGAGA NCGCTCGGGG AGGAAGCCCT GCTGAGAATA      60
CGTTCTCTCC ATAAATNAAG AAGGGCTAAG GCGATGCGAN GAGAATACAA AAGTNTTTGG      120
TCGGCCTATC AGCTCATGGA CCTGCCTGGT GGA CTGGA GGGCTGAACA TCGCCCACTT      180
NTGGAGNCCT TGTGTNAAAA GCGCTNCTGC GGTATNCATC G                          221
```

(2) INFORMATION FOR SEQ ID NO:572:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 143 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:

```
CTCCTACCTG CNGGCTNCCC TAGNGGTNAA CTCCTCCCTT AGTGGCCAAN GACATCAAGA      60
AGATCTTGA CAGCGTGGGT ATCGAGGCGG ACGGACGACC GGTNCAACAA GGTATNCAG      120
TGAGCTNGAA TGTGGGNAAA ACA                                              143
```

(2) INFORMATION FOR SEQ ID NO:573:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 323 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:

```
GGCAGAGGTG CTCACTGGAG CTGTGCAAAA TGGGCTTGCC CTGGTGAGGC CTCCCGGGCA      60
CCATGGTCAG AGGGCGGCTG CCAACGGGTT CTGTGTGTTC ANCAGCGTGT CCATAGCAGC      120
TGCACATGCC AAGCAGTAAC ACGGGCTACA CAGGATCCTC GTCGTGGANT GGGATGTGGA      180
CCATGNNCAG GGGATCCAGT ATCTCTTTGA GGATGACNN AGCGTCCTTT ACTTCTCCTG      240
GGCACCGTTA TGAGCATGGG CGCTTNTGGC NTTCTGCGA GAGTCAGNTG CAGCGCATNG      300
```



323

GGCGGGGACA GGGCTCGGCT TNA

(2) INFORMATION FOR SEQ ID NO:574:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 230 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:

AGTAGAGCCA CTTTCATCTCT GGNATGGTNT TACAAAGTCA GNCAGNAAAG CAGAGCAGGA	60
CANGGAGGGC CTTTTGTCCC TGGTAATGTG TTTGGGATCT ANTTCCCGAT GCTGCGATGC	120
TGCGGGAAGC CTTGGGAGGG CTTTAAAGCA GGGGCGTGGC TTGCCTGTAT TTATTNCAGC	180
TGTGTNGGAG AATGATTTGT AATACAGCAA ANGNTTNAAA GGAAGGGCAG	230

(2) INFORMATION FOR SEQ ID NO:575:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 355 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:

GGCCATAAAA CAAGGCTTCC AGTTTCGCCG AGTTTGGNAG GGTGTTTTTCC GGCAACGNCA	60
GTANCCAGAT TGGTCACATC ATCGTAAATA CCAACCGTAA AGCGCGCTTT CGGTTTAGCC	120
GCGTTGAGCT CGGCAAATAC CGCCAGTACA CAGTCTGGGC CAAATTCTTT GGATGAANGA	180
CCATAGCGCC CACCAATGAA CACGGGGCAG AGTTTCGCGC TCGCNATTAT TGAAAGGCTT	240
CTGCCCAGTG AGGGTACATT TACATCCAGA TAGAGCGGTT TTGCNTGGGG GCACCGGGGT	300
TNCTTTGGGT TCTGTCCAGT TACCGTCANG GTTGGGTACG GGNTNCCGGG CAGAA	355

(2) INFORMATION FOR SEQ ID NO:576:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 437 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:

TCGCCAGACG GCAGCAAACCT GGCATTTCGCN TTGTGCAAAA CCGGTAGTNT GAACCTNTAC	60
---	----

GTAATGGATT TGGCTTCTGG TCAGATCCGC CAGTGAAGTG ATGGTCGCAG TAACAATACC	120
GAACCGACCT GGTTCCTCGA TAGCCAGAAC CTGGCATTTA CTTCTAACCA GGCCGACCGC	180
GTGNGCANTN TAAAGCCGGG CGTGGCTTGC GCCANTGCGG GCTGACGGTG GAGCAACTGG	240
CCAGACAGGT GGAGCCGGAA TACACACCGG CGCGAAAAGT TCATTTTAC CATTGCGAAC	300
CACCGGGGCC TGNCGTGGG GGTTCATCAG CNAAGACGGG CATTACGGCG TGGCGCGGGG	360
GTATTTTAT TGANTGGGGC AACCAGTTA ATGAGGNGAA CCCGTTTCAC TTGCAACAGC	420
GTACCTTTNN CCAAGG	437

(2) INFORMATION FOR SEQ ID NO:577:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 298 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:

ATCAGCAGGC GGTACGGTT AACTGCTGA ACCTGGAACN NCGGGNANAC CGGTTGNNGT	60
CGCGGCTTGT GTGCAGCGTT ANNGCACGGA GATGATGAAC GTNATTTNGG CCGGTNTGGA	120
TNGATCTGCC ACTGACGNCG CGANCAGTCG ACCGATCATT CGAGTTCAC CTTCTTATTC	180
AGCAANCGAG AAGCGCGCCA TAAAGGGGCA ACATCAGGCC CATNACGNTA NCAGCGTAAT	240
GCTTGTTAGC TGCANCCAA CGGGCAGTCA CGNTTTTAA GGGACTGGG CCTTGGTG	298

(2) INFORMATION FOR SEQ ID NO:578:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 194 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:

NNTANAAGGN GGCCAAGTG GCACAAATGC AGNAACTCC CTCTGGTGAT GATTTCAGCC	60
TCTCCTTGGC AGATACTAAA TCTACCATCC GGAAGTGGAG CCAGAGCTNC GCATTTGCAT	120
TGCTAAAGCG TCTTTCAAGA GGTGCAGTCT TTGAAGGGCT GGGTANNGTN GCATCTGTGG	180
GANCTGAAAA TTCC	194

(2) INFORMATION FOR SEQ ID NO:579:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:

GCTGGCTGAT GAAACGCCGG AAGCCGNCAG TATTGTAATC CTCGCCAAGC AGCGTTTTAN 60  
CCTNCGCGAC CCAATGTGCA GTCGCTCCAT GCCACCTTT 99

(2) INFORMATION FOR SEQ ID NO:580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:

GAGGAAGCCA ACACCTTTAA ATTACCCGT TCGGGGCCAG CTGCGGTGCC CAGCATATAG 60  
TGC GCGGTTT CGTAACTACC GGACCAGTCG CGCNGCCTCG TTACAGGCAT CTTTNAGCGT 120  
CGCGAAACCG TATGCACCGG GATCACTTCC GCACCCATTA AGCGCATACG AAAAACGTTA 180  
GGCGACTGGC GTTCAACGTC TTTGGCACCC ATATGAAATA CGGCATTTNA GGCCGAGCAG 240  
GGCGCTGGCA AGGGCCGACG CCACGCCATG CTGACCGGCA CCGGTTTCGG CGATGATTTT 300  
GGTTTTACCC ATCCGTTTCG CCAGNAAAGG CTGNCCCCAG CACTTGTTAA TTTTATGNNG 360  
GNCGNCGTGC AGCAAATTTT CAGGTTT 387

(2) INFORMATION FOR SEQ ID NO:581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:581:

AACATCAACG AAACACGCC GCGTTTTNAA GATGCNTTTA TTGATTTCCCT GGGCGGTGCC 60  
GGAACCTCGG AATCGCCGNT GGGNGCAATA TTACATACGG TAGAAGGCAC ACCCGGCGAG 120  
ACGGTGATCG AAGCGAAAGA NCTGACCAAG AAATTTGGGG ATTTTNCCGC CACCGATCAC 180  
GTCAACTTTN CCGTTAAACG TGGGGAGATT TNTGGTTTGC TGGGGCCAAA CGGCGCGGGT 240  
AAATCGACCA CCTTTAAAGA TGATGTNCGG TTTGCTGGTG CCGACTTCCG GCCAGGCGCT 300

GGTGCTGGGG ATGGATCTGA AAGAGAAGTT NCCGGTTAAA GCGCGCCAGC ATCTTCGGGC 360  
TATTATGGCG GCAAAAATTT TTCGCTTTTA CGGTNAACCT GGACGGTCGA ACAGAATTTA 420  
CGGTTTTTCC TCTGGTGTGT ATTGGCTTAC N 451

(2) INFORMATION FOR SEQ ID NO:582:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 397 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:

GGCACGAGTA AGGCTGGGGT ATCCTGGTGA NAACTGGAGA GGATCTACTC GGNTCCCTGC 60  
CTGGCCAGTG GGGAAACACC GGTCCCCCAG GCACCTTCAC CTAACCAAAG CGATAGATTT 120  
CCACCGCCCC TNATGCCGCC CTTTGGAGGN AAAGTGAAAA GTGAAAAGGA AGGAAGAGGA 180  
GGCTTCATGG CTGAGGAGGT CGCAGCGCCA TGAAAGTCCC TGTTTCTGCC TCCTCGCTGT 240  
GGCTTTGGGT GAGCNAACCC CGCGAACTCA TCGCCCAAGA AACTAGAGGG AAGCGGAGGG 300  
GAGGTGGCCC CACTGGGAGC CGATGCCANG NTTGGGGAGT GGGGCAGGTT CACCAGACAT 360  
ACAAACCGTT TCTTNATTNG TTTCCCTATN AGGCAAG 397

(2) INFORMATION FOR SEQ ID NO:583:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 502 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:

GGCACGAGAA CGGAGACTGC ATTGACATAG ACGAGTGCNC CAACGACACC ATGTTTGGTA 60  
GCCNCGGCTT CTNTAACAAC ACTNATGGCT CCTTCCGCTG CCTCTTTAAC CAGGGCTTCG 120  
AGATCTCTCC CTCAGGCTGG GACTGTTTGG ATGTAAACNA NTGTAAGCTT ATNCTGGCGG 180  
TATGTGGGGC CGCGCTCTGT NAGAACGTGG AGGNCTNCTT CCTGTGCCTC TTTGCCAGTA 240  
ACCTGGAGGN GTACGATGCC CAGGAGGGGC ACTGCCGCCC ACGGGGGGCT TGAGGTCAGA 300  
GTATGTTTGA GGGCCNCAAC GGGGGGACCA TGCCCCGGCC CCCACCCGGT TGGACTGCNA 360  
TTCCGGGNAG AAGGGNCATG CGCCCTGCTC CAGTNTCCTG GGCCGGAACA NCACANAGGC 420  
TGAATNNNTG TTGCACCCAG GGCCTTAGTT GGGGAGTGCT NTAAACCTGT GCCCGTTTTA 480

GGAATTAGTT GAATTCAGGG AG

(2) INFORMATION FOR SEQ ID NO:584:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 491 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:

CCAGCCATTT CCTGCTCTAC GTACGTAATT CCNCCGCCGG ATGGCAGGGT GACATGGATT	60
TACCGCCGCA GCCGCTGATA CCTTACGCCG ACTGGTAAGT TTTCAGANAG CGCCTCTCTT	120
AATGCCGCTG CGATCGGGTA TACTCGGGCG GCAATCTGGG ATTTCCGGGG GGAGACAATT	180
TGCGCGTAAG TCGCTCGTTA ACAATCAAGC AGATGCCAGC NCTTGCCAGA ATNAGCGCGT	240
CGGTGAAAAA AACAGCCGCA TNAATTGAGC ATCGAACAGG GTGCCGCCAG CATTGCGCCA	300
AACAGAGGTT TCAGGACTTC TCTACGNTGT GAAAAGAAAG CTGGCGACTG CTTCCAGGAA	360
GAATGAAAAA TAGCAAGCCG ATTTCAGGAT GCCCGGCAGC CCGNAAAGCG NCTTTNATGT	420
GCGTCGCCAG AAAAAGGCAC ACCACATTGA AGGGGGACAA AAANCAGCAG GTTTGCCCCC	480
GGCCCAACGT T	491

(2) INFORMATION FOR SEQ ID NO:585:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 337 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:585:

GGCAGGAGCN AGNCCCGACG CCGCCGACGC CCCTACGACC CCAACAGCGT CCGCATCANC	60
TTNGCCAAGG GCTGGGGGCC CTGCTACTCC CGGCAGTTCA TCACCTCCTG CCCCTGCTNN	120
ACTGGAGATC CTCCTGCAAC AACCCAGAT AGTGGCGGCC CCGCGGGAA GGGGCGGGTG	180
GGAAGGCCGN GGCCACCGNC ACCTGCCGGC CTCGAGAAGG GGCCGATGCC CAGAGNACAC	240
AGCCCCCAGG GACAAAACCC CCCNGATTAT CATNTTACCT AGATTNAAT NTAAAATTTT	300
ATATATTATA TGGGAAATTA TNTGATTATA ATTTGTT	337

(2) INFORMATION FOR SEQ ID NO:586:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:

GTTTTTTTAC TGGCAACCCC NACGCTGTGG CNGTTTTNCG CNTGGGGCGG TAATGCAGTC	60
AGCGTAACGG TACTGGTGGC GCTGCTGGTC TGTNTNATCC CAACCACTAT TGGCGGCCTG	120
TNGTCAGCGA TCGGNGTCGC CGGGATGAGC CGGATGCTAG GCGCGAATGT AATTGNCACC	180
AGCGGACGTG CAGTTNAAGC GGCAGGTGAC GTTNACGTTC TGCTACTGGA TAAAACCGGC	240
ACCATCACAC TCGGTAACCG TCAGGCGTCG GAGTTTATCC CCGCGCAGGG CGTGGNTGAA	300
AAAACGCTGG CTTGACGCCG CACAACCTGGG CTTGCTGGC TGATGAAACG CCGGAAGGCC	360
GCAGTTATTG TGAATCCTCG CCAAGCAGCG TTTTAACTT GCGGCGGACG CGATTNTGCA	420
GTCGTTCCAT GCCACTTTTT ACCGTTTANT GCGNAAGCCG GTTNAGCGGG GTCAACATCG	480
GCAACCGNAT GNTCCGTA	498

(2) INFORMATION FOR SEQ ID NO:587:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 431 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:

GGCAGAGCNA ACGGCGNGGC AGCGCACNGC AGGCGGNATT CATTCCACTT AAAACCTGAA	60
AACATTGGAC CACACAAAGT CTTACTGATT TCAGGTAAAA ACAATAATTG AAGATGTCCA	120
GCAAAACAGC AAGCACCAAC AATATAGCCC AGGCAAGGAG AACTGTGCAG CTTTTAAGAA	180
TTAGAAGCCT CCATTGAAAG AATAAAGGTT TCGAAGGCAT CAGCGGACCT CATGTCCTAC	240
TGTGAAGGAA CATGCCAGGA GTGACCCTTT GCTGATAGGA ATACCAACTT CAGAAAACCC	300
TTTTCAAGGA TAAAAAATT GCATCATCTT ATAGTGGATA GAGAAACAGT TCTTGGCTCT	360
TCCAACAAG GCAATTTTGA GCNGTCCTTG NAGNGTTTAC CTCAGTTATT TGTAACCNN	420
GTTATAATTA A	431

(2) INFORMATION FOR SEQ ID NO:588:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 339 base pairs
  - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

GGCTGCGGTC AGGGCTTCAA ACATGAGTCC TTTGCCCTGC CATTTTTGCC CAATCGAATA	60
ACCGAGATAG CAGGCATGAA AAGAGCCACG AACAACTTG GAAAAATTGG CAACGCATGA	120
AATCTCTTTT TCGTCCGGGT CGAATAAGCC AAAGTAGAAA GCTGNAACCT TGTTTATGAA	180
AATTGGTTAA ATCATCCCCA GCCTGGCCTG CCAACCTGAT GGATAAACAG TGGGCTTTGC	240
GTCGCGGCAC TGGCTTCCCA GGGCTTTGAG GGAAATGGGC GNTTCTNCT GCGTGAATAA	300
NTCCGCAAGN ACGGCCAGGC ATTCACGNTT CATGCACCA	339

(2) INFORMATION FOR SEQ ID NO:589:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 340 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:

AATTTGTCTC ANCCGATGCC GGCTACCAAG GGGCGCCACA GCCGNAGGNG CTGGTCCGAG	60
GTGGATGTGG ACTGGCTGAT CGCCGAGCGC GCCGGCAAGG TAAGAACCTT GAAACAGCAT	120
CCACGCAAGA NCAAAACGGC CATCAACATC GANTACATGA AAGCCAGCAT CCGGGCCAGG	180
GTGGAGCACC CATTTCGCAT CATCAAGCGA CAGTTCCGGG CTTCGTGAAA GCCAGATTAC	240
AAGGGGTTGC TGAAAAACGG TAAACCAACT GGTGCATGTT ATTTACGNT GGTCAACCTN	300
TTTTCGGGNG GNACCAAATG ATTACGTCAT GGGGGAGAGN	340

(2) INFORMATION FOR SEQ ID NO:590:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 247 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:

CGCCTTAATG GTCCGACGNG CCTAAAGTTA ATTNAGGATT TAAGTAAGCG GAAAACGCGT	60
NATCGAATGG GTACGCCATT TATGCGTGAN CTGGAAGAGA AACGCAATCN NTTAATGGTA	120
AATCGGGGGC GTTCTGCGC CCCCATGCTG CCAACATTTA CAAATNCTTT NCACTTCCCT	180

GCACTATCCG ACACTGTCAC CATCCATAAT TNAGGCTTAT NTGTTTGTTA NCAGTAACCT 240  
TATGTTT 247

(2) INFORMATION FOR SEQ ID NO:591:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 257 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:

AACAACACCG GTATTACGCA AAACCTTATCG TACATTGGCG GCTAAAACGN CAAAAGGAGA 60  
GATCAGATGA GTCAGGTAAG CACTGAATTT ATCCCGACCC GTATTGGCTA TTCTNACGGT 120  
TTCNAATCGN CGCGGTGAAG AAGACGATAC CTCCGGTCAC TATCTGCGCC GATTCGGCGN 180  
AAGGAAGCGG GCCATCACGT TGTCGATAAA GCCATTGTGA AAGAAAACCG NTGACGCTAT 240  
TNGGGCTCNA NGTATCT 257

(2) INFORMATION FOR SEQ ID NO:592:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 277 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:592:

AACCTGGTCA CAGTNAGCGA TCCACAAGAC CTGGCAGGCG ACGGAGTGTN CCTTGATCAT 60  
AGCGAGCCCT ACGAAGCCTC GCGGGAATTT ACCCAGGTNT GGCGGCGTTT ATTGCAGAGA 120  
AGAAACCGTC GNATTTCAAC GGTAACATA TTCATGTGCC GCGGAGCAAT AACTNCTCTT 180  
CCCGGCGAAT TTCAACAGCC GTATCCGCTC ACTTTANCTT TGGCGGATCG TNNAGATGTN 240  
GCCCAGNAGC TGGCGGCAGG AACAGGTTGA TCTCTAA 277

(2) INFORMATION FOR SEQ ID NO:593:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 250 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:



TGCCCAGAGN CGGGGGTTAA AGAGGAGGAA GATGGCAGAT AAGGTTCTAC CTCACCNAAT	60
CCGGGAGCTT GTTCCANAGT NTCAGGCGTA CATGGNTCTT TTGGCTTTTG AAGCGGAACT	120
GGTACCAGAC CATTGCTNCG CAAGCGGGAT GGAGATCCAN GTAGGCCATC AAAAAGCCTC	180
TGNNCACAAA AGCGAAGTTT CGGGATCTGA CATTTTCCAA TAAGTTCATT CCCAGCAAGG	240
AGGNAAGGNG	250

(2) INFORMATION FOR SEQ ID NO:594:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 269 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:

ACGTTTTNAG CGGAGGCCCA GCTAATGTTT NAGTATTTAC CCGAACTNAT GAAAGGGCTA	60
CACACNAGCC TGACGCTAAC CGTNGCCTCG CTGATTGTGG CACTNATTCT GGCATTNATT	120
TTAACCATCA TCCTGACGCT GAAAACGCCG GTNCTGGTGT GGCTGGTGCG GGGTTATATC	180
ACGCTGTTTA CCGGTACGCC GCTGCTGGTG CAGATCNTNC TNNTTTATTA CGGGGCCGGG	240
CCAGTTTCCG ACTTNCAGG AGTATCCGG	269

(2) INFORMATION FOR SEQ ID NO:595:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 352 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:

AAAGAAGCGA TTAGCATNAA ACAGGTTCTA TCGGTTTCTC NGGTTTNCAC AGCTTCACGC	60
CACGGAANGA TTACGCGGTG CATCAGGCAC AGNTTTTNCG GCGGTGTAGA AGTATCANCC	120
TGCGGTTNAT TCAGCAAGCT GCTGGCTTTC ACCAGCNTAA TGTCTGGCGG CAGGTTATAA	180
ACCATCTTTT GCAACACGCG TACCGTTGCC AGGGTGAGGA TGCCCAATGG NAATGGTTCCG	240
ANCCGTTGCG AACGCGGCCA GGTTCAATTG NGCCGATTGA AATTGTCACA CGGNTGTCCC	300
GTTTCATTTT GCGGAANCGT TCGAGGGATG ACCTTCCCGT TTNGGTCCNA CC	352

(2) INFORMATION FOR SEQ ID NO:596:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596:

AATAACGCGG GTAAACGGAA TCATCCATAC AAGCANGATA ATGANCGGGA ATGGAACGGA	60
AAATNTTCAC AATCGCAGAA ACGGTANNAT ACAGCTTCGC NTTNACAATG AATTTGCCCC	120
GGAACGCGTG AACATAAAGC AGAACGCCAA CCGGCAGNAC CAATGCACAA AGCCAAAAAA	180
ACCGGATACG AAAGGTGCAT TGCCAGCTTT TCCCATTACG GCCACGGAAC CAGCAGCCAC	240
ATGCTNCGGC TTCAGAACAT TAACCCAGTT ACCTCTGATT TTTAACATGG TGTTTCCTGG	300
CAGCCCAGGC AATGGGGGGN TTGCGNTNAT NCT	333

(2) INFORMATION FOR SEQ ID NO:597:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 274 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:

CAGCAATGGC GTCAAGTTGG GCAAAAANTAA CATNTNCCTG ATCGGNCCGA CCGGTTCCGG	60
TAAAACCCCTG CTGGCTGAAA CCCTGGCCGC CCTCCNGGAT GTCCCGTTNA CCATGGACCG	120
ACGNGAACTN AACTGAACC GAAGCCGGTT ATGTGGGTGA AAGACGTTGA AAAACATGCA	180
TTNNAGAAAG CTGTTGCAGN TAATGCGAAC TGNGAATGTC CCAGAAAGCN CAGGTGGTTA	240
TTGTCTTACA TGGGTGAATG GACCAAGATT TCTC	274

(2) INFORMATION FOR SEQ ID NO:598:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 78 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:

ACAGACCCTC CTTNNTCCGT TTNTGGGGAA TACTTCCCTC GGGTGAAGT AAAGTAAATT	60
TTTTTTTTTTT CCCAAACA	78

(2) INFORMATION FOR SEQ ID NO:599:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 320 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:

GTNAAAAAAG GGCTCGGTGT ATTCNAAAAT AGCGGCGCGA ATTACCTGAA NCGCAATTGG	60
TGGTGGTTCT CCACAGGNTA CTTGTAAAAG CNAATTGGGA ATTATCAGCA ACAACCCGGA	120
AGTTTGCCGA TGTGCCGTAC CTGGGAAGGG CTTTCCCCGA CCAATAAACC CAGTGTACCG	180
ATTCTGGCAA TTCCTAACCA CAGCAGGTTA CTGGNCCAAA GGTGAACCAT TAACTTACG	240
TGAATNCACT GNACGGAGAA GGAAACGGGC GCCAATTTTT GTTTTGCTTN ATGGATNCCG	300
CATGATATTC CCCGNCGGTG	320

(2) INFORMATION FOR SEQ ID NO:600:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 333 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:

GGCAGAGGTA AAATGGACAT TTTAGGGGAA ANTCCTGTGG AAAGATAGCC CTCCTCCTG	60
TTGTGTCTTC AGGGCCATTT CTTTTTATCA AATTTGTCTC TGAACACGA AAACACATGG	120
TGCAGGGTTT NCCATACGTT AATGAAATTT TCAAGANAGG TCCTGAATGT NCCCAGTAAC	180
TACACAACAC CTNAGTGGGA GTGAATGAAA GTCCCCGGG ATTNCCCTGA ANAAAATAAT	240
GCCCAACAGC CTTGGAATGT CACTTNATNA TTGGTNCTTT TNCGCNCAAA GAATGTCCAG	300
AGAATTTATT CCTGGGAATT TGAAAAGGTT TTG	333

(2) INFORMATION FOR SEQ ID NO:601:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 123 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:

TGTAACCTC CCAAAGGNGC AGCTGGCCAN AAAACCATCG NTGCCCTTCT CNGTTGCCTT	60
--	----

CTGGTGAAAG GANTGATGAG CCACCGTGAA CGGAAGTTCC GTGCCCTCAG CATTANCACC 120  
CTT 123

(2) INFORMATION FOR SEQ ID NO:602:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 306 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:

GGCTACGTAA AGAATAAAAT CAATCTCCCT NCNCAACGGT GGTAATTACN TTAAATGAT 60  
GGCCTCAAGT CGGTAAGCCG CTATGGNTGA TCCNGTTTTG AAACATTATG GCATGAAGGC 120  
GAACGGCNTT TATTGTTACC TCANGCATCA AACGTCACCC GCAGAAGTGG AACCCAAAAT 180  
CGCNGCAATT TATGAANCGT TTNTAAGCTT AACGGAAATT CGCGAATGTA TTTGATTTCC 240  
CAGTCACCAT ACCCCTTTTT TNGCCATCGG GGTTAGGTGG GTTATGCGGN NGACCCNTAN 300  
TTACTG 306

(2) INFORMATION FOR SEQ ID NO:603:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 388 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:

CTGCACTGGG NNCATGAACT AGGCCTGGCC TTCACCAAGA ACCGANTGAN CTATACCAAC 60  
AAATTCCTGC TGATCCCAGA NTCGGGAGAC TACTTCATTT ACTCCCAGGT CACATTCCTG 120  
GGGAATGAAC CTCTGAANTG CCAGTGAAAA TCAGNCAAGC AGGCCGACCA AACAAGCCAG 180  
ANTCCATNCA CTGTGGTCAT CACCAAGGTA ACAGACAGCT ACCCTGAGCC AACCCAGCTC 240  
CTTCATGGGG ACCAAGTTTG TTTGCGAANT AGGTTAGCAA CTGGTTCCAG CCCATTTTAC 300  
CTTGGGGGCC AGTTCTNCTT GNCAAGAAGG GGACAAGCTT ATGGTGGAAC GTTCATANCA 360  
TCNTTTTTTG GTGGNTTTAC ACAAAGG 388

(2) INFORMATION FOR SEQ ID NO:604:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 365 base pairs  
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:

AAGCTTTACT GGTGCGCGAA AAAGTTGAAG CCGCGCGCAG AGCANTGCTG CTGTATCCGC	60
AAGGTTTAAG CTGGGAATTG GTGGGATGAC GTCACCGTAG AGATCCGTTT CTGGCTTCCG	120
GCGGGTAGTT TTGCAACCAG CGTTGTCAGG GNAACTTATC AACACAACAG GTGATTATGC	180
CGCATATTGC TGAGTAATGA TGACGGGGTA CATGCACCCG GTATTNGAAA CGCTGGCGAA	240
GCTTGCGTGA GTTTTNTCTGA CGTTCCAAGT GGTCGCCCCC GTTCGNTAAC CGCAGGGCGN	300
TTCAAATTCT TCTGNCATGG GATTCTCTCC TGCGNACGTT TTACCTTTGG AAATGGGGGN	360
TTATT	365

(2) INFORMATION FOR SEQ ID NO:605:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 234 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:

TTACAGANNT AAGCCGCCGT GCCCAGNCAC AAAGTTCTTT AATNACAACC ACGNAAGGGG	60
CACACATGGG TCCTGTCTCT GGTATGGATT CACACACACG TGCACAAATT GAAGTCCAAT	120
AAAAAGCATN TGCCACAGA CCCACCATGT GCCATTAAAG ANCTTCTCTN CCAGCACAGA	180
CTNGTTGGTG TTGTTCTTNG TGCTTGNAGC TCTTCAACAA AGAGCTTTTG CCGT	234

(2) INFORMATION FOR SEQ ID NO:606:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 108 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:

TCTCTNCGAC TCATTGAGCC AGATGCTGAG GAAAAATGTA GAAAAGCGAG CACANCCAAG	60
NACAGCGGCA CTACCGGNCA CGNGACTCGC TTGTATAAAA GGTTTTTN	108

(2) INFORMATION FOR SEQ ID NO:607:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:

```
TGGTGGAGCT CNGCATCCAC GAACAACCGC ATCCGCAAGT GCCCAAGGAA GTTTTCAGCG      60
GGCTCCGGAA CATGAAGTGC ATCGAAATGG GCGGGAAACC CACTGGAGAA CAGTGGCTTT      120
NAAACCNNGA GCCTTCNAAT GGCCTGAAGC TCNGCTACCT GCGCCATCTC AAAGGNCAAG      180
CTGGACTGGC ATCCCCAAAN ACCTCNCTNA GAACCCTGAT TGAAACTCCA CCTAGACCAC      240
AACAAAATNC AGG                                                              253
```

(2) INFORMATION FOR SEQ ID NO:608:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 143 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:

```
GGCAGGAGGN CCCTCAAAG NAGNAATCAG CTNCANTGAC AATAAAGATG GGACATGCAC      60
AGTGACCTAC CTGCCGAGTC TGCCAGGCGA CTACAGCATG CTNGTCAAGT ACAATGACAN      120
NNACATCCCT NGCAGCCCCT TTA                                                              143
```

(2) INFORMATION FOR SEQ ID NO:609:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 242 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:

```
CCCNTNCTCA TGGGGNTGTT TCCTACTAAC CCCAAAGNGA AGACCCAGGA GGAACCCCTT      60
GGNCCAGAGC AGGGCCCCCTG TTTTGACCGT GGTGTCCAAG TTCAAGGCCT CACTNGAGCA      120
GNTTGTGCAG GTCCTNNACA GNACCACGCC CCACTNCATT CGCNGCATCA ACCCAACAGC      180
CAAGGNCAGG CGCAGACCTT TTTCCAANAG GAGGTCCTAA GCCAGCTCGA GGGCTGTGGN      240
TT                                                              242
```

(2) INFORMATION FOR SEQ ID NO:610:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 71 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:

CCCCTCCATG TACAGCCGCT CCATCCAGGG NCACCATGTC TGNCTCCTGG TGAAAAAGGG 60  
TGAGANCTCT N 71

(2) INFORMATION FOR SEQ ID NO:611:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 120 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:

AGTACACTGG TNCCCGTACC GGGCAATGTA CCANTACAGG CCCCAANCGA AGACGAGCTG 60  
GAGCTGCGCN AGGGGGACAG GGTGGATGTA ATGCNGCAGT GTNACGATGG CTGGTTTGTG 120  
120

(2) INFORMATION FOR SEQ ID NO:612:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 455 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:

CGTGNGCCCC NCAGAAATG GNCCCGGGTG CAGAATCGGC AGAGCGGGTC TGCTACTGGT 60  
CCCNTAAGCC AGAGTAGCCA AGACTGAAGT CACTGCTCAT CCGGAATGGA AATCCCGCCG 120  
ACCAACTACC CAGCCTCCAG GCGGCCTTG GTGGCACAGA ACTACATCAA CTACCAGCAG 180  
GGGACCCGCA CAGGTGTTTN AGGTGCAGAA GGTCAACAAG CCAGCATGGA GGATATTCCA 240  
GGAAGAGGAC ATAAGTATCA CCTTTAAATT TGCTGTTGAA GAATTATACA AAAACAANTA 300  
AGGTGAACTG CACAGNTGAA GTACTTTACC CTCAACGGG ACAGAACTGA CCAGAGTCAC 360  
TTCACATTTG AAGGGGAACT GGAAGATNCA GATGAGAGAC AACTTTNTC AAGCTTAGTC 420  
CTGAGGACGT AGAGACAATT TCNGCATTTG GATNN 455

(2) INFORMATION FOR SEQ ID NO:613:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 366 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:

GGCACGAGCT ATGCCAGCA GTGCCAGTNA CTTTGGGGAC CTGGAGCCCA GCCCGCTGCG	60
CCACTTTGCC TCCAGACAGC TAATACTCGG GGAAATGCTT TTGGGAGCTG TGGGCGCAAC	120
CCCAGTGGCA GTTATGTGTC CTGCACCCCT AGAGATGGCA TTTGTGGGCA GCTCCAGTGC	180
CAGACAGGTA GGACCCAGCC TCTGCTGGNC TNCCATCCGG GGATCTACTC TGGGAGACAA	240
TAGATGTGAA TGGGACTGNG CTGAACTGCA GCTGGGTGCA CCTGGGACCT GGGCAGTGAT	300
GTGGCCCAGN CCCTCCTGAC TTTGGCCTGG CACAANCTGT GGCCCTGGNC TGGNNGTGTA	360
TAGACC	366

(2) INFORMATION FOR SEQ ID NO:614:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 495 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:

TTAAGGTTTC GCTGACCGGG ACATAATGGC TTACACCTTC TCCAGTTTGA CCGCGCACTT	60
CTTGAAGTCC GTCTCTTTCG AGAGCGGATC GGTTCGCATCC AGCGTCAGTT TGTTAACCAA	120
CTGTGCCGGC GTCGAAGAAC GGCATGTACA CCAGGCCCTG TGGCGGACGG TTANNACCGG	180
CCGTTTCAAC AATCGAGATC ACTTCGCCAC GGCGAGAAAC CACTTTNACT TTGTCGCCAC	240
GGCGCAGATC GCGCGCTTTC GNATCCAGCG GGTGGAATAA AACAGGACCG CTTCCGGGGA	300
AGGCGCGGTG CANTTCTGGT NACACGGCGA GTTCATAATT GCCGGTTNTG NCCAGTGGTT	360
CCAGAACGTG TTCCGGTTAG AGAGCCACAA GTTCGTAATT CTTTCATCCGG TGGTTTCCGC	420
CGNCGGTTTC NATGGGNATT CGGAAGATCA NCGTTTTGCC ATTCCGTTTT ACCTTAGAAT	480
TTTTAGCTTT GGGCC	495

(2) INFORMATION FOR SEQ ID NO:615:

- (i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

GGACTGCACC GGCACAGAGG CCCACATCTC CAGCTGCAAN NGTTNCCCCA GGTGTCACTG	60
GACCCCATGA AGAATGTCAC CTGCNAGAAT GGGCTACCGG CCGTGGTGAG TTGTGTGCCT	120
GGGCAGGTCT TCAGCCCTNA CGGACCCTCG ANATTCCGGA AAGCGTACAA GCCAGAGCAA	180
CCCCTGGTGC GACTNAAAGG CCGTGCCTAC ATCGGGGAGG GCCGCGTGGA GGTGCTCAAA	240
AATGGAGAGT GGGGGACCGT CTGCNACGAC AAAGTGGGTA CCTGGTNTCG GNCAGTNATG	300
GTCTTGACAG GAGCTTGGGG CTTTGGGAA GTNCCAAAAA GGCAGTTNAC TNGNTTTCGG	360
ACTTAGGGTA AAGGGTTTCG GACCNATTCC AACTGGAACG GAGTTTCCA	409

(2) INFORMATION FOR SEQ ID NO:616:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 289 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:

GGCAGAGCNC GANTTNAAAA AAGGAAGGCA ATCATTGGAT TATACAACTA TGCCCATGAA	60
ATAACTCATG GAGCAAGTGN ACAGAGAAAT ACCCAGCCT TGGCCAGATG ATTGTGGATT	120
ATGAAAAACC CTTTAAAGAA GATGATGGNA AGATTTNNTN NCCCCATNAG CAAGTNTCTT	180
TNAGATGCAC TAATTTCCCT TCCAAATGGT ATATCCTCGA AAGGAATCT TTTCACCTGG	240
ACCAGTGGAG AAATGNCCAG TTATTGAGNC TCATCAGTGN NACCTTNGT	289

(2) INFORMATION FOR SEQ ID NO:617:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 303 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617:

GCCCCAGGAA AACCGTGTNC NATNAGCCAT GAGTCAACNC CACCGTGTTC TNCNANATTC	60
CCGTCAACGG GAAGNCCCTT GGGCCGCGAT NTNCCTTTAA CCTGTTTGCA GACAAGGTCC	120

CAAAGACAGC AGAAAATTTTC CGTGCCTCTG AAGCACTGGN NGAGAANGGA ATTTGGTTAT	180
AAGGGTTCCT GCCTTTNCAC AGGATTCATT CCAGGGTTTA TGTGTCAGTG TGGTGGANTT	240
CACACGCCAT AATGGCACTG GTGGGCAAGT CCTTTNTGGG GGGGAATTTG AAGGTGNGNN	300
TTT	303

(2) INFORMATION FOR SEQ ID NO:618:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 111 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:618:

CCCATTANN TCGGATANTT GCCGNGAAAT CGGCCGGATT AATGGCGAGT ATTTGGCACA	60
TCCNTTGGCA ATGCTGAAGG TGGTCAGGAA GCCACGGGTC ATCAGGTTTN N	111

(2) INFORMATION FOR SEQ ID NO:619:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 355 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:

GGCAGAGNCA GAAAACTGCC CCAGGGGATG CAGCTGGATT NTTGGAAGAA ACGAGAGTTT	60
TGGGAAACCG TCCTGGCATC CTGGAAGGGG CCTGAAAGCA GCCCCTTATT CAGAAGCAGA	120
GCCGGCNCCA CAAAAGGAA GCCCCAAGA AACTAGGNGA GCTTGAAATT AAAACATGA	180
GTAAAAATNT CATAAANCA GGGAAGCTTC AAAGACACAG GGNACATTGC CAGAAGCCAG	240
AGAAGGTGTA AGNAGAAAGC CGTGAACCTC CCGGGGCTGT NTGTGGAGTC TNGCAGGGGC	300
TGCCTGGTTT GCCGAGTCCC ACGTTTTCGN CAGTGTGGTG GTNCCGNTGG GGAGG	355

(2) INFORMATION FOR SEQ ID NO:620:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 510 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:620:

GGCAGAGGGA AGACACAAGA TAAAATTAAC ACCAAAAATA AAGAAATACT TAGGTATAAN	60
TCCAAGAAAG CATGCATAAG ANCTGTATGA AGAAAGCTAC AAAACTCTTA TAAAAGACAT	120
AACATTTTCA CGATAATAAG TACAAAGTTG GAGGGATGAC TTCGAGACTT ATTAGAAAGG	180
TACTGTGAAT GAAGACAGTN TTGTATTGGT CCAAAAANTC GGCCAATAGA ACACATTGGA	240
AAGCCCAGAA AATAGACTCA GTGCCAGGCC GGGCGTGATG GTTCAAGCGT GTAAATCCTA	300
GCACTTTGGG GAGGTCCGAG GCGGGCGGGT TCACAAGGTT CAGGAGNTCG AGACCNTCCT	360
GGGCCCAACN GGTAAACC CCCTGTTNTA NTAAAATTAC CAAANNATTT AGCTGGGCGT	420
GGTGGCAGTG CCCGTAGTNC CCGCAANTTG GNGGTTTGG GCAGGCGATT GGGGTGACCC	480
GGGGTTGGA GTTTTCATTN NGGGGTTTG	510

(2) INFORMATION FOR SEQ ID NO:621:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 502 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:621:

CAGCGGATCG GTCTGCCCCT GTANNCAGTT AGCTCTTCAT GCACCCGCAG CATAAACGG	60
TGNAAGTGCA GGCNCTGTTT CCGGTCTCCC GGCAGGCTTT GATAGAAAAG GTCCATCAGC	120
CAGGTTTTCC CGCGTCTTAC ACCGCCCCAN ATATATAAGC CACGCACTGG CGTNATGCTT	180
TGTGTCTTCG CGTTTACCCC ACAGCTTACC GACCCGGGCC ATTAGCCAC TCGTCCTGGG	240
GGCTGGTGGC GTGCTATTGA TGAGTTCCTG ATAAATAAAT TTCCAGGCGG CTGACGGCCT	300
CTTTTTTGAA CGTNGTCGGG TTGATGGCTG NCNTTCATTA AAGCGNCTTC AGGTATTGCG	360
ATGTTGGGGT AACGGTTTGC ANGATCNTAA TGTTANTCCN TGGATAAATC GGTGNGCCTT	420
TGTTCAAGGT NNAGGAAAAA AAGGCCGTTT ACATTACGGG TATNCATCGG GGTTCATTT	480
TTGGNTTAAC GGTAAAGGGG GA	502

(2) INFORMATION FOR SEQ ID NO:622:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 413 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:622:

ATTGAACGTN GCCCAGGAAT CAAAAGTCGC CGTTTTTCCA GACAAGCCGG GNACGGTTTT	60
TTTGGTGGTG GATTTGTACA CCAGAACTC ACGCCACATT CGCCAATTCT CACGGAGAAC	120
AGGCCTTCCT GCTGCNTNGA GTCTATCGGA CAGTCAGAAA TGAATCATAT CCAGTTTATG	180
CTGACTTAAT TGCTCCAGCA GNATTTCTGT GGTGGNTTCG AAGCAGNGGA AGATGAATGG	240
GCTCGTCTTC TACCACTGCG GCGTTAAGTA CGCTACTGAC CAGGCGTTTG GTAAAGTGCA	300
TCAGCCACGN CAACGTCAAN CAATGAATTG GATTCTTTGC GATAGTTCAC AATATCCCAG	360
CCATTTCGGG GNTNAGGTGA ACATTTTTTT CGGCTTAGNG TTAGNCCATT TTT	413

(2) INFORMATION FOR SEQ ID NO:623:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 334 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:623:

GNCACGAGTG GGTNATNATA CCCCTGNCAT TGACAGACAT CTAGNGAAC CACATAAATT	60
TAAAANAGAG TGGTCCAGTG TAATGCGGTG TGTAGCAGTG CTTTGTGGT ATAAATCATG	120
NCAGTNCTAA AGTGGATTTC NATAACAACA TACAGTTGTC TCTNACACTG GCTGCACTAT	180
CCATTGGACT GTGGTGGNCT TTTGNTAAGA TCTAGANGTG GTTTTGGCCT TGGAGTAGGA	240
ATTGGCCNTC TTGGCAACTG TGGTCACTGC AACTGCTAAG TNTATAATGG TGTTTTACCA	300
ATATGACCTN CTCCAAGATN TCCNGTGAT GGT	334

(2) INFORMATION FOR SEQ ID NO:624:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 266 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:

GGCAGAGNCC GANCCACCAT CTNCTNGAAC GTCAACGGCA NACAAAGTAA ACAGGACCAA	60
GATCCACAGC GNAGTCCTGA GCACCCTGGA NTNTCCTCGT AAACCCCGGC NGCTGTTNGA	120
GANANGTNGT TGAATNCACG GCCCTCCNAN CGACCTGGGT CAAAACACC AGCATCCTCT	180
TCCTGGAGCT GGTCAATTTT AACCACCNTC ACACNAGACT CTCACATAAC CACTGGACTC	240
AGCACTTCCA NTGNCAGTCC CGNATA	266

(2) INFORMATION FOR SEQ ID NO:625:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 343 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:625:

```
GGCAGAGCTC ATAGCTTGTT GGTACCTCC ATGGGGCACA TAAAGCTGAC AGATTTTGGA      60
TTATCTAAGG TGGGACTAAT GAGCATGACT ACCAACCTTT ACGAGGGTCA TATTGAGAAG      120
GATGCTAGAN AGTTCCTGGA TAAACAGGTC TGTGGCACNC TGGAATACAT TGCACCAGAA      180
GTGAATTCTG AAGGCAGGGT TATGGAAAGC CGGTGGGACT GGTGGGGCCA TGGGGATTTA      240
TCCTTNTATG ANATTCCTG GTTGGGATGC GTGCCATTCT TTTGGGGATA ANTCCANGGG      300
NCTATTTTGG GACAAGTTCA TCATGATGAG ATCAATGGGC CTA                        343
```

(2) INFORMATION FOR SEQ ID NO:626:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 363 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:626:

```
CTGCGGNGCA AAAGCGGTTT GCCAGATCTT GCCCAGTCTG CGANGATAGT TGGTCAGCAA      60
CACCAGCGGC AGGCCTTTAT CCATAATCCC GTGCAAAAAT TCCGCTGCAC CCGGTAGNCG      120
NACGTTATCG TGCATCAGCG NCGCGTNCGC ATATCGCAAA TTACATTTTT GAATGGTCAT      180
GGACTACCCA GAATATTGAC AACAATTAAG CGCCACTTAT TAAAAGCACA TTAAATTTTC      240
CAGCAAATGC TGGAGCAAAA TACCGTTGAG CATGGCGCGT TTTTACCAGC GGCAAAAGCN      300
CCGTTTGCCG AGCGGTTGAT TCCAGCTTCA GAACGTNACC ACCGGNCAGN TTAGTGCGN      360
AAA                                                                363
```

(2) INFORMATION FOR SEQ ID NO:627:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 354 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:627:

GGCAGAGGGC ACCCTNTCGC CGCGAANCGG TGC GCGCGCA CTCGTCCCGG CCCTGGCCCCG	60
CCGCAAACAA GGATCCGCTG CGCTCGGGGA ACGCAACNNN CGNCTCGTGG CCCC GGACCT	120
GAAAGACCCT TCCAGCATGC NAAAGGAAAG TTCCCCCAGG CGGACCCCGC AGAGCATTC	180
CTACCAGGAC CTCCCTGCAC CTGGTNAATG CAGACGGACA GTAACCTNTT CTGGCAGGTA	240
CTGGGAAACC CACAGGCACA CCCAAGGCC TCATCTTTTT TTTCCCATGG AGCCGGAGAG	300
CACATGGGCC GTTATGAAGA GNTGGNTTCG GATGNNTGAT GGGGCTTGGA NCTG	354

(2) INFORMATION FOR SEQ ID NO:628:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:628:

TANNCGTAGT GGTGGTTAAC CACTATAACT GGGAAAGATG ATGCCCCGCC GNGCAGCCG	60
TGGGGCAGCA CCATCATRNA TAAAGCCCAT GTNAAAGGAT TAATGTACTT GCCNCCCGGA	120
GATCCCGGTC AAAATCCGTG GCACTTATNA AAGCCCTCGG GCATCCGGTG AATGNTCGCT	180
ATTTGAAACA TTTGGGCCAT TACCGNGCTG GGAAGTCTG CCATGGCGCA TTTTGCCAGT	240
NAAACCAGTT TGNAAAGCNT GGGGGGTNAG TAACTTATTG GGGTTTACAA CCCG	294

(2) INFORMATION FOR SEQ ID NO:629:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:629:

AAAATCGTTA CCACGTTAGG CCCAGCAACA GATCGCGATA ATAATCTTGN AAAAAGTTAT	60
CGCGGCGGGT GCCAACGTTG TACGTATGAN CTTTTCTCAC GGCTCGCCTG TAAGATCACA	120
AAATGCGCGC GGTATGAAAG TTCGTGNAGA TTGNCCGCAA AACTGGGGCG TCATGTGGCT	180
ATTCTGGGTG ACCTCCAGGG GCCCAAATC CGTGTATCCA CCTTTGAAAG AAGGCAAAGT	240
TTTCCTCAAT ATTGGGGATA AATTCCTGGC TTCGACGGCA NCCTGGGGTG AAAGGTTGTA	300
AGGCGNCAAA GTAAAAGTTG GTGTCGTTN ACAAAGGNC TGNCGGCTGA ACGT	354

(2) INFORMATION FOR SEQ ID NO:630:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 352 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:630:

CTGGCTTTGT GTTTTGGTCA TTAATGGGGT GAGTGTGCGG NTCACCGCTG CCATGTATTC	60
CTGAGCTTTC GCTTTCGCGG CTTTTTGCTN TGGCCCCTGG ATGGGTAGCC AGGTCATTTG	120
AATGCTTTTG AATTTTNAAG GTACCGCGCT CCAGCTGTTA GNAAGCATAC AAGTNCTCAT	180
TAATTTTACT TGCAGCACGA GTGAAGATTG GCTTTGTCGG GACTGCTGTC GATGGCACGA	240
AATTCGTTCC AGTGGCAGGC TGGGATTCTG GCTGTAAAG TCTTCTCGAA ACTGGCTGAT	300
GGAGAGATCG AANTNNGGGC TTAGCCAGC AGATAAGGCG CGGTNNTTTG CC	352

(2) INFORMATION FOR SEQ ID NO:631:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 330 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:

GGCAGAGCGC ATGTGTGNAG GCGCTCAACA TGAAATTCAA GGCCGAAGTG CAGAGCAACC	60
GGGGCCTGAC CAAGGAGAAC CTCGTGTTCC TGGCGCAGAA ACTGTTCAAC AACAGCAGCA	120
GCCACCTGGA GGNACTACAC TGGCCTGTCC GTGTCCTGGT CCCANTTCAA CAGGGAGNAC	180
TTTNCCGGGG CTGGNAACTA CACCTTCTGG CANTTGGTTT TTACGGGGTG ATGGGAGGTT	240
GTTGAAGAAG CACCACAAGC CCCACTTGGA ATNNATGGGG GCCATCCTAG GGTTTTGTG	300
AATTAAGCAA CCAGTCCCCA NGNNCTGGTT	330

(2) INFORMATION FOR SEQ ID NO:632:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 428 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:632:

GGCAGAGAGC ATACCATCTT TGGACGGGTT GTTGGGGGCT TTGACGTACT GACAGCCATG	60
GAGAATGTGG AGAGTGACCC CAAAACTGAC CGCCCTAAGG AGGAGATCCG CATTGATGCC	120
ACTACAGTNT TCGTGGAACC CTATGAAGGA GGCCGATGCC CAGATTGCGC AGTAGCGGNA	180
AGNACACAGC TCAAGGTAGC CCCGGAGACC AAAGTGTAAG AGCAGCCAGC CCCAGGCAGG	240
GAGCCAGGGC CCCAGACCT TTCCGCCAGG GTGTGGGCAA GTTACATCAA CCCAGCAGCC	300
ACGANNCGAG CAGCAGAGGT AAGGAGNCCT TTAACCATTG GCCATTTTTC CCCNNTTNCA	360
AGAAGAAGNC CATTCCGGGT TTTTGGGGAT TTCAGTTCTG GTTAGCAGCA NAATTTTtag	420
GTTTTACT	428

(2) INFORMATION FOR SEQ ID NO:633:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 442 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:633:

TTTGCAGCTC ACGGGNAAAT TTNTGCGCCA CTACCGCATC ACCAAGCATG ACCGGAATAA	60
TGGCGTGATC GGNTCCCGCC AGGNTAAAGC CCGNCGNCGA CATTGCTCA CGGAAGTAC	120
GCGCGTTCGC CCACAGACGG TNACGNAGTT CGCTGCCCCG TTCGACCATC TCCAGTACTT	180
TNATGGACGC GGCAACAATG GCCGGTGCCA GCNAAGTTGG AGAACAGGTA CGGACGAGAA	240
CGCTGGCGCA CACTNCAACC ACTTCTTTGC GCGCCGCGGT ATTAACCACC AGAAGCCCCG	300
CCCAGCGCTT TTACCAAGCG TACCGGTGGN TAATATTCGA CCCGGCCCAT CACATTCGCA	360
GTATTTTCATG GGGGAACCAC GGACCATTTT TNAACGGACA AAACCGACCG GNTGGGGAGT	420
TCGTNTTACC TTCANCAGGG NA	442

(2) INFORMATION FOR SEQ ID NO:634:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 470 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:

TGCCGCTCTT TATGTGGGCC GCGCGTCACT GTCAGCCCCC AGGTAATCAG CGGCGCGGCC	60
ATCTTCCGGC CAGCAGGTCA TAATGGGAAT GCNATTGANA TCGNCGTCAT CGCCAGANAC	120



GATTTTTTGT TGGCAGGGCG CACCACGCAG CCGCTTTGTC GGCATGTTCA ATACTTGCTT	180
AAACTGCGGC AGTTTATCAA ACAGGTCGCG GAAACCTTTT GCGGCTCCG GCTCTTTCAG	240
AAACGCCAAT AATTACCAA CTTCACGCAG CGCCGNAAAC ATCTTCCTGC CCCATGCCCCA	300
TCGCCACGCG CTTTGGCGTT ACCGAACAGG TTGCACAGCA CCGGCATTGN GTAGCNTTNA	360
GGGTTTTTCG GAACANCAGC GGCAGGCCCA CCGGGAAGGC AAATGCGGTT CAGCAATTTT	420
CATGGTTTTN CAGATGGGGG ATNCCACCGG GAGNGTNGTA AGTTTTTAGG	470

(2) INFORMATION FOR SEQ ID NO:635:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 270 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:635:

GGCAGGAGCG CTCCTGGGG GACCGAATCC GGGATCTTGC TCAGCTCAA AATCTCTATC	60
CCAAGAAGCC CAAGGATGAG GCTTTCGGA GCCACTACAA GCCTGAACAG ATGGGTAAGG	120
ATGGCAGGGG TTATGTCCCA GCTACCATCA AGATGACCGT GGAAAGGGAC CAACCACTTC	180
CTACCCCA GCTCCAGATG CCTACCATGG TGCCTTCTTA TGACCTTGA ATGGCCCCTG	240
NATTCCTCCA TGAAGCCCCC TTTNNNTNT	270

(2) INFORMATION FOR SEQ ID NO:636:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 327 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:636:

GGCANGAGCT GGACCCCCCA ATGCGGGCAA GAGCAGCCTA GTGAACCTGC TCAGTCGGAA	60
GCCTGTGTCC ATCGTGTCCC CGGAGCCAGG GACCACCCGT GAACGTGCTG GAGACCCAG	120
TCGACCTGGN CCGGATTTCC TGTGNCTGCT GAGCGACACG GCTGGGTTGC GGGNAGGGCG	180
TGGGGCCCN GGAGCAGGAG GCGGTGCGN GCGCCCGTGA AGTAGGCTTA GAGCAGGCTG	240
ACCTCATTCT GGCCATGNTG GGATGCTTTC TGAACCTGGC CTCTCCCTCC ANTTGGCAAN	300
TTCTTGGGTC CACCGTNGTT AGNCTCT	327

(2) INFORMATION FOR SEQ ID NO:637:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 392 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:637:

```
GGCAGAGCTG AGCCTTGGAG ATTATCATCA AGCCAGACCC CTCAGCAGCA AGTGGAGCTG      60
TTTGACTTGG AGAATAACNN AGAGTACGTN TCCAGCGGAG GGGGCTTTGG ACCGGTTGCT      120
GATGACGGCT ATGGTGTGTC GTACATCCTT GTGGGAGGAG AACCTCATCA ATTTCCACAT      180
TTCTTCCAAG TTCTTCTTGC CCTGAGACGG ATTCTCATCG CTTTGGGAAG GCACCTGAAA      240
NNAAGCAATG ACTGACATCA TCACTTTGTT TGGNTCTTCA GTTCTNAATT TCCAAAAGTA      300
ATTCCACTGG AGCTGCTGGG GAAGGTAAAA CGAGCTCTTT NTGATGCAAA CCAATGNAAA      360
ATTAGGCATT AATCCNGGNC CTNAGTTCGG GA                                     392
```

(2) INFORMATION FOR SEQ ID NO:638:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 167 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:638:

```
ACTTTGCCGG AACATCCTGC TGGGGCTTGA TCCACGTCGC AGTTGCTTCT CGCATGACTG      60
CNTCGGTGGG CAGTTTGCAA AACTTTGCCA GCTTCATCTG CGCCTCTTTT GCGCCGATCA      120
TTACTGGTTT TATTGTTGAT ACCACCCACT CATTCCGTCT GGCAC TA                                     167
```

(2) INFORMATION FOR SEQ ID NO:639:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 113 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:639:

```
AGAGCNGAGC AGTCAAGATG TGTGAACTCC ACCGAAGACC AGACCGNAGA GTTCAAGGAG      60
GCCTTCCAGC TNTNNTAACC GAACAGGTGT ATGGCAAGAC CCTGTTACAG NCA                                     113
```

(2) INFORMATION FOR SEQ ID NO:640:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 374 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:640:

```
AGATAGCAGC CTTGTAAC TTATGACTACA TTNTCGGCCT GAGCAGGACA AGTTCTCTCA      60
AGCTGCCAAA GTCCGAGAAC TTGAAAAGCG CCTGANAGAG CTGGAGACAC TGTNACGTTG      120
TGAATCAGGA ATGCTCAGAA ATCCCCTTTT TGNCAGGTNT ACAGGGAAGC CTGTNCTCAT      180
GGAGACTGTA GGAGCTGTTG CAAAGCAAAA GGTGGAGCGC CCTAGAACCT TGCAGTTTTG      240
GGATCAAGTG GGAGGCTCGG CTTACAGAGT GTNCCTGGGG AAAGGTTGAA CGAGATTGTC      300
CCAAGCTTAA AAGCCTCTNT TAGGAAGTTG CAGTTTCCNC AAAGCAAAGT TGCNCCNGTT      360
TTTTGGNAAC TTTT                                                              374
```

(2) INFORMATION FOR SEQ ID NO:641:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 196 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641:

```
GGCAGAGGAT GACATTNGNN TNANCTACAA GATTGGAGAG ANGTGGGACC ATCAGGTGCN      60
AANTGGNCAT ATGATANGNT GNACATGTTT TGGGAACGGA AAAGGCGAAT TCAAGTNTGA      120
ACCCTTCATG GAGGTCAACG TGTTATGNAT GTTGGGTAAG ACATACCACN TAGGCNGTAA      180
CAGTGGNCAG AAGGGA                                                              196
```

(2) INFORMATION FOR SEQ ID NO:642:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 357 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:642:

```
GGCAGAGCTG AGATCAAGGG CCACAGGGGA CCTACGTGGG CGCNATGCCG GGAAAGATCA      60
TCCAGTGTTT AAAGAAGACC AAGACGGAGA ACCCCCTGAA TCCTNATCGA CGAGGTGGAA      120
```

CAANATCGGC CGAGGCTACC AGGGGGACCG TCGCTCGGNC ACTGCTGGAG CTGCTGGTAC	180
CCAGAGCAGA ATGCCAACTT TCCTGGNACC ACTACCTGGN ACGTGNCCCCG TGGGANTTGT	240
TCCAAGGTAG CTGTTTNATC TGGCACGGGC CAANGTTCAC GGGACACTTA TTCGCCNAGC	300
CGTTGGAAGG ACCGTTATGG NGGTTGATTC AACGTGTCGG GGTANTTTGG NCCCAGG	357

(2) INFORMATION FOR SEQ ID NO:643:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 359 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:643:

GGCACGAGGT GGCAGGGNNT GTGTGTGCTG AGGCGGCTGA GCGGCGGACA TGCACACTAC	60
AGTGCGTGGC GATGGAACAG TAACCGGGT TGTNAGAGGG CTCTGCAGTA TAAACTAGGA	120
GACAAGATCC ATGGATTAC CGTAAACCAG GTGACATCTG TTCCCGAGCT GTTCCTGACT	180
GCAGTGGAGC TCACCCATGA TGACACAGGA GCNAGGTTTT TACACCTGGC CAGNGAAGAC	240
ACGAATAATC TGTTACGCGT GCAGTTTCGT ACCACTTCCA TNGACAGTNG TGGTTGTTC	300
TCAAAATTCT TGAGGCATAC CGTNCTTTNT GGGTTTTTCTG AAATATTCGT GNAGAGACC	359

(2) INFORMATION FOR SEQ ID NO:644:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 299 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:644:

GGGGCAAAAA TGCCGAAGAT GCGGTGCATA ACGCATCGT GCTGGAAGAG GTCGCTTATA	60
TGGGGATATT CTGCCGTCAG TTAGCGCCGC AGTTACCGGC ATATGCAGCA AACGCTGCTG	120
GATAAACACT ATCTGCGTAA NATGGNCGCG TNGGCATATT ACGGGCAGTA ATGNCTGTAT	180
AAAACCACAG CCAATNCAAA CGNAACCAGG CTATACTTCA AGCCTGGTTT TTTGNTGGNT	240
TTTCCAGCGN GGCGCAGGTC AGGTTTTATC TTAACCCGNA CACTGGCGGG GACACCCCG	299

(2) INFORMATION FOR SEQ ID NO:645:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 483 base pairs
  - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:645:

CGGCCGCGCT GCTGGACAAG CTGTATGCTC TCGGCTTGGT GCCCACGCGC GGTTGCTGG	60
AGCTCTGCAC TTTCGTCACG GCCTCGTCCT TCTGCCGCCG CCGCCTCCCC ACCGTGCTCC	120
TCAAGCTGCG CATGGCGCAA GCCTTNCAGG CTGCCGTGGC CTTTGTGGAG CAAGGGCAGC	180
TACGCNTGGG CCCTGACGTG GTTACCGACC CCGNCTTCCT TGTNACGCGC ACATGGNAGG	240
ACTTTGTNAC TTGGGTGGAC TCGTCCAAGA TCAAGCGGCA GTGCTTAGAG TNACAATGAA	300
GGAGCGCGAT GATTGNTCT GGAAGCCTAG CGGATTTCCT ATTTGCAATG TTGTNTTTTN	360
ACAGTGGGAA AATTGAGGCC TGATGTTGGA GATTTTANGA GGGTGTTTTT CTCAAGGGTT	420
NTNAAACGGT TGTAGTTTTT TAAGAATTG ATTCATCATT GGCANGCCAG NATAGAGCCA	480
GGG	483

(2) INFORMATION FOR SEQ ID NO:646:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 172 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:646:

TCAGCTGCCC TGGGGGCTGC TTTCNTGGG CACGGGCTCC AGGGATCATN TNTGGGCACT	60
CCCTTCCTGC CCCAGGNCCT GGNTCTGCCC TTCCTTGGGG GGTGGAGCAG GGTCCAGGTT	120
TNAACTTGC NACCTCCTGG AGGTCAAGAA GAGCAGAGTC CCCGTCCCTG NT	172

(2) INFORMATION FOR SEQ ID NO:647:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 518 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:647:

GGCACGAGGG GATTACAGGC GTNAGCACCA CACCCGGCTT CATTTAAACC ATTTTAAAGT	60
GGCATGAAGT ACATTCAAAT TGTNGTGCCA CCATCCATCA CCCAAACCGA AATCCATAAC	120
CATTAAACCA TAACTCCTCA TTCCTACAGT NTGTTTCTTT TCATTACGGG ATAATATTC	180

ATTGTNTGGA TGGGCCACAG TTTGTTTATC CACTCACCTA TTGANGGACA NCTTGTTTCT	240
TCCCACATCT TGCCAATNAT AAATNANGCT GCTATAAATA TTTGTNTGCA GGTTTTTGTC	300
TGCACATAAG TTTTCANGTC ATTTGGGTAA ACACAAGGGG TGTGATTGCC GGGCCTCTGT	360
CTGACTTTAT TTCCATCAAC CGCNTCAAGC ACCTGGNGTG NGGGCAGGAG CCANGCCCCAA	420
CANTTATGTT TGTAAACCTA TTTAATTAAC AGNCCACAAT ACAGNCCAGG CACATGGGTT	480
CNGCNGNAAA AACTTGGGAC TTTTGGGAGG CCCAGGCG	518

(2) INFORMATION FOR SEQ ID NO:648:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 322 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:648:

GGCAGAGCAA ACTGTGACTC AGTGGATATT TGTATGCCCC CCAAAAACAT TTAAAGCTG	60
AGCAATTTTT AATAAGATG TATAATAAT TTTGNATTAT TCTCATTGTA GTTAAGTTAC	120
TGTTAGTTTG GTGCAATACA TTCTTTCCTT CCTCATCCTT TTAAAATTAA ATATATAAGA	180
NGTATGTTTT GTTTTATTAC ATTAAGTGCT ATTTTTAAAA AATTCATTGT GTGTATATGN	240
AGNCTAATAC TTGATTTGTT TCTGTATAGC ATGATTAAAG GTAATTGGAA ATTTTGCCAC	300
CNATTTAGGN CCNTGGGAAA TT	322

(2) INFORMATION FOR SEQ ID NO:649:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 453 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:649:

AACCGCTTCA CCGCGCGANT GGTACCAGTC AATCAGGCGG TTAGCGACAT CCACCGTACT	60
GTCACCTTCC GGCACGGCGN AGCGCGCCAC CAGCACAGAA ATCATTTTGT AAATCGACCA	120
GTAACAGGGC GCGAGGGGGC ATTACAGTNT CCTTAATCAT CCGGCGTAAG TTCGCCGCGC	180
AGGTTTTGGC TCATGGCCTT GCGAATGGTT TCAGTATCCA GTTCCTGGGC TAAAGCAGGT	240
AAATGCAGTT TGGTTAGCTT GGGCTTTCTT ACAGTCATAT CTGCACCGGN GAATNACGCT	300
GGTATGGGGC GAGGGGGTTN ACCGGTTGGG GATAACCANC CATGTTTCAN TTTAACGGGA	360

CATACATTGT GTTCAGGTTN ACCACCACAA TAACCGGGGN TCGCTGGGTT TTTTGTTAAT 420  
TTNCTGNCAG GAAAGGTTTT TTTTTTTTGG GNG 453

(2) INFORMATION FOR SEQ ID NO:650:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 405 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:650:

GGCAGAGGGA GAGGCGCTGA GGTGTGCTGG GTGCACTGGA GCCACCGGGA CCCCTTGAGG 60  
ACATCGCCAG GNTCNGTGGC TTNTTCCCGA GCGGGAGAGG TGGAGATGCT TATAGCAGTT 120  
ACGCNTTAGG AAGGGGACAA CCAGGNCCCG CCACACGCTT CACACACAAA CCTGCTCACG 180  
CAACTGTGAA TGCTTGGCAC GGGGTGGCCA GTNCAGATGG AGCCCAAGGC CCCNTCGGNC 240  
TCCTGGGGCA ACTTGGGGTA CACAGGATAC TNGGGGTGCC CGTTCCTTAC TTAAACCCCA 300  
GCTAAGGGTT ACAACTGACC CAGTTGGNCT TGGGCCCGGG GCACTTTGGG TTGGTTCNTT 360  
TGGGGCCCTT GNACGTTGGG CCCATTGTTG GNAAGGTTN TTCTT 405

(2) INFORMATION FOR SEQ ID NO:651:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 268 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:651:

GTTGGGCATG TNCAGGTGGC ACAGGTNCCA GGNCGAGGGG AGCCCAGCAG CCCCAGAGAG 60  
CTGAATTTCC CCTATCTGTT TCAACTGCTG GNAAGNTGAA GGCTACAAAG GTTTCGTGGG 120  
NTGTGAAGTA TCAGNCTCGA GGAGACACAG TAGAGGGCTT GATTGGGCTA CGTTCATACT 180  
GGGNATAGGC GGGGCCACCC AGAGGCTGGC CAGTGAAGGG CCCGCACACC ACCCACGTGC 240  
CTNCAGNCAG NGAAGTGAAC ATNGCCAT 268

(2) INFORMATION FOR SEQ ID NO:652:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 354 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:652:

TCTTTCCTTT NACCTACAAG GGATCTGTTT ACTTCACTTG CACCCATATT CATAGCTTAT	60
CCCCTTGGTG TGCCACCAGA GCCGTGTACA ACGGCCAGTG GGAAGTACTG CCAGAGTGAA	120
AGATTACCCA CGCTGTATCT TCCCTTTGNA TCTATCGAGG AAAGGCTTAT NAACAGCTGC	180
ATCTCCCAGG GNAGCTTCTT AGGCAGTCTG TGGTGCTCAG TCACCTCTGT TTTCGATGGG	240
GAAACAGCAG TGGGAAATTC TTGTGAAACG GAATGAAGTA TGGGGGGAAA TTCTTCTTCA	300
GGNAAGGCCC TGGCATCTTN CCCCTCCATN TTACAGGAAA TAATGTGGGT CTNN	354

(2) INFORMATION FOR SEQ ID NO:653:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 253 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:653:

AATGGAAATC GGTCCAGTAA GGCTGTNATC TGGANGGTGC TGCGCAAGTN GGGGCTGCCC	60
CTGGGAATAC ATCATTNACT NTTTGGGGAC GTGAAGAAGC TCATCACTGA ATGGTTTGTG	120
AAAGCAGAAA GTNCCTGGGN CTATGNCCNG NNTCCCCANT AGCAATCCCC CTGATTATGA	180
NGTTCTTCTG GGGCCTGCGC TTCTTACTAT GAGANCCNGC CAAGNTGAAA GTCCTACAAG	240
TTTTGCCTGC AAG	253

(2) INFORMATION FOR SEQ ID NO:654:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 102 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:654:

CCATAGTCCT GGACAAGCTG GAACGNAGGG NCTTCCTTTT CCTGAGCATG ANGGGGGTGG	60
GCCAAACGCT GGTNTGGTGT NTGCACAAGG AGTGAACCTT TT	102

(2) INFORMATION FOR SEQ ID NO:655:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 258 base pairs
  - (B) TYPE: nucleic acid



(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:655:

CCACTGGTGC TGTGCTGTAC GGTGCAAGGA ATGCAGAANT ACTNTGGACG TCCATACTTG	60
CAAGCCCCCA AGANGGCAGA NTGGCTGGNC CAAACCTGAA NCACNCAGAT ACCTCATTTTC	120
TTCCTTCCAA TTCANGNNTC TNAACTCNAA AGCACNAGGT CCTTTGTTTG NACANTTTTT	180
TNCACCCTTC ACCCTGGGGT TGTACNTTT TTTTTTAAG GGTNTTGGG GGGTTATTC	240
TTGGGGGCCC TGGGGTTC	258

(2) INFORMATION FOR SEQ ID NO:656:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 121 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:656:

TTCAAACCTTG CNTCCNATCC TGCCTGCAGA AAACCCAGAC TGCATTCAGT GTCCTCAGTG	60
TAGCCACCAC TTTGNNTCCC AAGGTGGCTG AGCAACANAT TCCCAAGTNT AAGANCCATC	120
A	121

(2) INFORMATION FOR SEQ ID NO:657:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 327 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:657:

GGNTTTTTTCG CTCGGTTTAG CTAAATCNTC CAGCCCTTTC CGGCNTCGC GGTAATCTTC	60
CAGCGCTTTA TCCAGAACT TGCATCGGT TTTTCNTTCC ACCAATGGNA AGCAATGCAC	120
GCAGAGTCGG ACTTGATATC GCCGACAGT GCCATATCCA CCTTGCCTGT GAAGCGCCCG	180
ATGCTGGCTG GNTTGAATAT CCAATCTGNA ATGAATTTTG GGCATCGGTC GGGTAGNAAG	240
GCGCGGTAGG GGAAATTGCC GTTGCCGNAG TTAGCCACTA AACGTNTTCG GCGGGTTTCA	300
TCATGGGTAT GGGAAACCTG NACGGNG	327

(2) INFORMATION FOR SEQ ID NO:658:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 143 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:658:

```
CTCCTCCTCC TCCCTCCTAC AAGTCCAGTG GCCTTGGNCT TGGAAACTAA AGGANGAAGG      60
TCTGGCCCCC AGGGTGGGGC TCTCCTTTCC CTCCCANCAN CCCC GCGGTN AGCACTGCCC      120
CCTCTGTGAG GTTCGCTAAC TTN                                              143
```

(2) INFORMATION FOR SEQ ID NO:659:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 187 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:659:

```
ANCGGCCCTT TGAAGGTGC NTCCCGCAAG ANGAACGGAC GCCACTTAAT CCTCCGTGAA      60
AATTCCAAGA CCAGNAANAA CATCCAGAAA TCCCTGGTTG GNAGCTCCAG GCCCCGGGGC      120
TTCNAGCGGC ACCANCGGTG AACCACGGTN AAGCTCGTGG AACCGGTTTG CAAGTTTGGA      180
AGTGGNG                                              187
```

(2) INFORMATION FOR SEQ ID NO:660:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 135 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:660:

```
GGCACGAGAA AAAGTAGAGC ACAAATAGTA CAATGGCGAA TATAGACCCA AGCACATCAG      60
TAGTTACATG GAGGANGACT GTNTACTNAA AGANTTAAAT GTAGGCTAGA TTAAAAAAA      120
AAAAAAAAA CCNCG                                              135
```

(2) INFORMATION FOR SEQ ID NO:661:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 492 base pairs
  - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:661:

AGGCGAAAAG TTTCCACGGC AACTAAAACA CTTAGACGCT GTAGTACAGC TCAAACCTCTA	60
CCGGATGCGG AGTCATACGC ACGCGGTCAT CTTCTTCGCG ACGCAGAGNA TGTACGCATC	120
ANTTGCTTCG TCAGTGAAAC ACGCCACCGG CTTTNNAGGA ACTCGCGGTC CAGATCCAGT	180
TCGTTCACTG CTTCTTCCAG AGAGCCTGCA ACCTGTGGGA TCTCTTTNGC TTCTTCTGGC	240
GGCAGGTCAT ACAGGTTTTT NTCCATGGTT TCGCCCGGTA TGGGATCTTG TTCTTGAATA	300
ACCNNCAGGA CCGGGCCNTC AGCCAGGGCA GNCAAAGCAC AGGTTACGGG TTAAGATTGC	360
CGGGTTCCGG GAAAACGTNA CTTTGNTTAN GACGTGNTTT TCGGNGGAAG NAAACCACCG	420
GNATTACGGN TTAGANGCGG AACGGTTTAA GNGNCNNNT NAGGCCAGCT TTACCGTGTT	480
TCTAGCCGGG AC	492

(2) INFORMATION FOR SEQ ID NO:662:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 117 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:662:

ACCACCCCCC GCCCCATACA CACACACACA CATGCATACA CAAAGAAAAG CTAATAAAAA	60
TTGCATATAG AAATTTTTTT TTTTTTTNGG GGGGGGGTNT CGTTNTNTNA CCCAGGT	117

(2) INFORMATION FOR SEQ ID NO:663:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 304 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:663:

GGCAGAGAAT TAGGTTTAGC ATAGCCTATC TTTCTCCATC CNTTTACTTT NAATCTGTCT	60
TCATCTTTAT ATTTAGAGTG GGATTTTGT AGACATCATA TAGTAGGGTC TTGTCGTTTG	120
ATTTGCTCTC GGACAGCATG TGTCTTTTAA ACTGGTGTAT TTAGACCACA GATGTTTAAA	180
GTAATTATTG ATATAGTTGG ATTAATGTCT ACTGTATTTA TAACTGTTTT CTACTCCATT	240

GTCCCTTGTT CCTTNCCTTT TTCGGNCTTT GNACTTTGTG CTCTGCCTTC TCCATTNGNA 300  
ATTG 304

(2) INFORMATION FOR SEQ ID NO:664:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 226 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:664:

NTTCCATTCC ATTNAGATTCC ATTCCATTCA AATNAATTCC ATTCCATTCA TCTCCATTCC 60  
ATTCCATTCC ATTCCATTCC ATTCCATTCC ATCCAATTAC ACTNGCTTTG AATCCATTCA 120  
ATTCCATTCC ATTCCATTCC TTTCTGTTCC TTTGCATTCC ATTCCATTCA ATTCCATTCC 180  
ACTGGGGTNG TTTCAATTCC ATTCTATTCC ATNCCATTCA ATTGNA 226

(2) INFORMATION FOR SEQ ID NO:665:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 210 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:665:

GGCAGAGTTT TCCAGACGCA GGTAAGGCC CATGAAAGGC TGCCCTCTTC TCCCCTGCCA 60  
GGAGGGCACC TGGGCAGGCT AGGAGCAGCC TGGGCCAAGG GCACCCCAGG GACCAGCCCC 120  
AAGAGGCACT GCTGCTGACT CCCTGTTCTT GTTTTTTTTT TGTTTTGTTT TTTGAGANAG 180  
GGTNTCGNAN TGTNCCCCCA GGTTAGAGTG 210

(2) INFORMATION FOR SEQ ID NO:666:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 391 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:666:

GGCANAGCAA ACTTTTTCCT GTTGAGTGCC CTAAGACAGT GGAAACTTC TGTTTTTACA 60  
NCAGAAATGG TTATTATAAT GGGCATACTAT NTCACCGTAT AATTAAGGC TTTATGATTC 120

AAACTGGAGA TCCAACAGGT ACTGTNATGG GAAGGAGAAA GCATATGGGG AGGAGAATTT	180
GAAAGATGAA TTTCCATTNC AACATTACGN ACATGACAGG CCGTACACAC TTCAGNCATG	240
GGCTNAACGC GGGGTTCAAA TACTAATGGG ATCCCAGTTT TTCCATNAAC GGTNGTTACC	300
CAACGGCCTT TGGGCTTTGG ATTAATTNAG GCCTTTACCA GTTATTTTTG GGGACCGGAG	360
TTGGACTTAA AAGGGGAATT TGGGGGGNNN N	391

(2) INFORMATION FOR SEQ ID NO:667:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 276 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:667:

GGCANAGTGG CCATTTTCGT TGGTGGTGTT CANTTGCNGC GGTNCTGGT CAGTAACAGC	60
CAAGANGCTG CGGGAANCTG CTGGNTCTTC GTCAGATTGG GCAGAGGACG ATAAGGACTT	120
GCTTCCCGCA GCATTTTAAA AATAAAGTTC CGGTAGGAAG CAAAACTGT TCCAGGAGGA	180
TGATGAAATC CACTGTTATC TAAAGGGTGG GGTAGCTAA TGNCCCTCTG TTATAGNGCC	240
ACCANGNTTT TTACAAGTTG GGTGTGAACA TCNTTA	276

(2) INFORMATION FOR SEQ ID NO:668:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 336 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:668:

GGCANAGTCA TATTTCTACA GTATGCCAGT ACTGAGGTTG ATGGAGAGCG TTACATGACC	60
CCAGAAGACT TTNTTCAGCG CTATCTTGGA CTGTATAATG ATCCAAATAG TAACCCAAAG	120
ATCGTGNCAG CTCTTGGCAG GGAGTAGCTG ATCAAACCAA GGATGGGTGA AGTATCTTCA	180
TGTCATTTNC TGNAAACTN AATGTTCTCTG GGAATATATT GTTGAAAAAT TTNAAAAACC	240
AGCTGGGNCA CAGTGGGCTG CATGCCTGTN AATCCCAGCG CTTTGGGAAG GCTTGAGGCG	300
GGCGGTNTCA CCTGGTGGGT CGGGGNGTTT TTNAGA	336

(2) INFORMATION FOR SEQ ID NO:669:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:669:

```
GGCACGAGAG AAACCTCTATC TAGTTAAAAA GGCGANGAAG AAAGATAATC ATGCTCCTGT      60
TCCCATAAAG AAAGGGCAAG GAGTTGGGAA GGAGNAAGGG ACCCTCCTGG NTCCTGCAGC      120
CTGAATCTCC ACTTGTGCCC TCTGTCTTCC CCACTAGACT CT                          162
```

(2) INFORMATION FOR SEQ ID NO:670:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:670:

```
GGCAGAGNCT CTGAAAAAAC TCGCCAAGAA AAAAGTAAGA AATTGACTTT ACAGAAGTAA      60
AACCACACCG GGCTAAGTAC AAATACCTTC TAGTACTAGT AGACACCTTC TCCAGATGGA      120
CTAAGGCATT TGCTACTGAA AACGAAACTA CCAACACAGT AGTTAAGTTT TTACGCAATG      180
AAATCAACCC CCAATATACG CTGCCTGCTG CTATTAAAGT CTGATNAATA GAGGCAGCCT      240
TTACCTCGNC TATGAGCTCC AGTTCAGTCC AGTTAAGGCG TTNAAACATT TCAATAGGAG      300
GCTCCATTGT GGCCTATNCA ACCCCAGAGG TTCCAGGTCA AGTTGGAACG CATGGAACCA      360
CACCTNAAA AAAAATTCGN GGGGGGNCC GNTACCCATT T                          401
```

(2) INFORMATION FOR SEQ ID NO:671:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 488 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:671:

```
GGACAGTGCC ATTATCCACA CCAGCATGGG AGACATTCAC ACCAAACTTT TTCCTGTTGA      60
GTGCCCTAAG ACAGTGGAAG ACTTCTGTNT TCACAGCAGA AATGGTTATT ATAATGGGCA      120
TACATTTTAC CGTATAATTA AGGGCTTTAT GATTGAGACT GGAGATCCAA CAGGTACTGG      180
TNATGGGAGG AGAAAGCATA TGGGGAGGAG AATTTGNAGA TGAATTCAT TCAACATTAC      240
```

GACATGACAG GCCGTACACA CTCAGCATGG CTAACGCGGG NTCAANTACT AATGGATCCC	300
ATTTTTCATA ACGGTAGTAC CAACGCCTTG GCTTGNTAAT NAGGCTNACA GTNTTTGGAC	360
GAGTGANTAA AGGATGGTAG TTGTTACANG GTTNTCCAAG TCAAGTTCAT TCCCCAAAACN	420
GTTAGCCNTT TGAGGGTGTT CAGCTNCTTA AATTTTACTG TTCAGTTAAA TTAGGTTTNT	480
TTTNATGT	488

(2) INFORMATION FOR SEQ ID NO:672:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 398 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:672:

GGCACGAGAA AATATCAACT CCCAAGTTG ATCTGTAGAT TTAACAGAGT TTCAGACAAA	60
ATCACAGCAT AATTGTTTAT AGATATAAAC AGGCTGATTC TAAGATGGAT AAGGAAATGC	120
AAAGGAACTA GAATAGGCAA AACAATTTTA AAAAATAAAG TTGAAGGAAT CACTATCAAA	180
TTTTATGACA GTATAAACT ACAGTAATAA AGNTAGTATG TTAATAGGAA CTGTGTAAAC	240
ACCAAAAGCA GTGGTACAGA ATAGGCAAGT CTAGTAATAG ACCCATATAC ATNTGGCCTT	300
TTGACAAGGT GCACNGGGAA TTTTATGGGG AAGAACCTTT AATAATNAGT NTCGGACCAT	360
TGACCTNCCT TTAAANACCA AAAACTCGGG GGGGGCCC	398

(2) INFORMATION FOR SEQ ID NO:673:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 349 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:673:

GGCAGAGNCA GAGGCCAGGC ACGGTGGCTT ATGCCTGTGA ATCCCAGCAC TTTGGGAGGC	60
TGAGGCAGGC GGATCATGAG GTCAGGAGAT CGAGACCATC CTGGCTAACA CAGTGAAACC	120
CCATCTCTAC TAAAAATACA AAAAATTAGC CGGGTGTGGT GGCGGGTGCC TGTAAGTCCCA	180
GCTACTCGGG AGCCTGAGGC AGGAGAATGG TGTGAACCTG GGAGGCGGAG TTGCAGTNAG	240
CCGAGATCAG GCCCCTGCAC TCCAGCCTNG GAGACAGAGG GAGATTCCAT CTCAAAAAAA	300
AAAAAAAAAA AAAAAAAAAAN AAAAAAATT TNTNGGGGGG GCCCCCNTA	349

(2) INFORMATION FOR SEQ ID NO:674:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 199 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:674:

GGCAGAGCTT TCCATTCCAT TCCATTTTCAT TCCAGTTGAT TCCATTGGAT TCCATTCCGA	60
TCCATTCCAT TTCGTTCCAT TCCATTCCAT TCTATTCCAT TCCATTCCAT TCCACTGGGG	120
TTGATTCCAC TTCATCCCAT TGCATTACAT TCCATTTTCAT TCCACTNNNG GTTAATTANN	180
ATTCCGTTCC ATTCCATTG	199

(2) INFORMATION FOR SEQ ID NO:675:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 500 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:675:

GGGAGATCGT TGCCGGAATA TCCTCCAACG ACGCTCGACG GCGGGGTTTG TTAAACAGGC	60
CTTGTGCGGC AAGGTGAAGA TTACGCGCAT CAGCAAGGGN GAGGTGCGGC ACGACATTCA	120
TGACTCCATC AATCGAACGC TGCCGCGGCG TAACTAGTTG CCAGAAGCCA GCAAGGTTAG	180
TTGCGTAAGA GTTTCGCTGG TTCATCACCT GAAAGCTGTG CGTCTACAGG CAAATACCAC	240
CAATTTTNTT CTGCAAAGNC CCGGCATTTN ACCGCATCTT TTTCAGTCCA TTACCAGCGT	300
TTGCCCCGGCG CTTTACCAAC GGCATTGAC ATCCGNATGG TTNCAAAGAT TGATGGTTTCG	360
GCCCAGGGGT TACACNTTTT TNNCGGTTGT ACGGCCACAC ATNTTTCAGC GTGGGCAAAA	420
AAGCGCGGCG GATGCCCCAT TNCCCCGCCN TGGCATTACA TGTTCAGTT GAGCAACGTC	480
ACAANGGTAC CGTACGTAAT	500

(2) INFORMATION FOR SEQ ID NO:676:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 371 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:676:

AANTAATGCG CCGTCAAACA TACTGCTCAT AATGCGGGAG GTGTTGTNAT CAAGCACGAN	60
ACGCTGGCGA ACAGGAAGGT AAACATGATT AATCAATTGA TCTACTGGGT ACTCTCGACC	120
CAGTGAAATA ATTCTCGCGC GTAGTTTGGC AGGATTAGCC ATGCGAAGAA TTGACATCAT	180
CTCTTCTTGC AGGCGGCTCC AGTCATCTTC CGTATCCTGG CTGGTGGTTT CCAGTAATGC	240
TTTAACTTTG CCTACAGGN CGCCATTACT TATCCAACGC TTGATCTCTT CGATGCGTTG	300
TATGTCTTCT TCATCAAAGA GTNGGTGTTT CGCCTTAATN GNGTNGGGGT TTAAACAAA	360
CCGTGGGNGG T	371

(2) INFORMATION FOR SEQ ID NO:677:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:677:

GGCAGAGCCA GTTTTAAAG TATCTTAAA ATTTTNAATA AGACTTTTTC CAAATATAT	60
TTAAGGATCA AAGTACTTCT TGATGAATCA CTTTTTATCG TATTGATGCC TTTGAATCA	120
TCTTAGTTTG TCTGCATGTN GTTATTACCA ATTCGTGAGG AATGGCCATT TCAAAGTTTA	180
CCATAAATGA NGTAAACGT CTTCAAGTCA CACTGCTTGG CTTTGAATTC CTTACTCTAC	240
TCTTTCTTAC TGTNGTGAAC ATATGGCAAG TTAACCTTAG CTTCTGCACT TCCTGTTTGT	300
GGTTTTCCCC TTTATTGGGT GGTNATAAAC AGTCTCTGTC NTCCTAGGGA TCTNCCNGG	360
TTGTTGTGGG NGTT	374

(2) INFORMATION FOR SEQ ID NO:678:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:678:

GGCANAGGNA CAGTGCCATT ATCCACACCA GCATGGGNGA CATTACACCC AAACCTTTTTC	60
CTGTTGAGTG CCCTANGACA GTGGAAACT TCTGTTTTCA CAGCAGAAAT GGTTATTATA	120
ATGGGNCATA CATTTACCG TATAATTGAA GGGCTTTATG GTTCAGACTG GGAGATCCAA	180

CAGGTACTGT TATGGGGAGG AGAAAGCATA TGGGGGAGGA GGATTTGNNG GATGAATTC	240
CATTCAACAT TACGGACATG ACAGGCCGTA CACACTCAGC ATGGGTTAAC GCGGGGATCA	300
AATACTNATT GGGTCCCCAN TTTTTCATA ACGGGTNGTA CCCACGGNCT TTGGGTTTGN	360
T	361

(2) INFORMATION FOR SEQ ID NO:679:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 365 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:679:

CTCAGTTTGG TATATTCTCC TGTNAATGCT TGCAATTNCA TTATCAAATT TTTGTAGTGT	60
GTTTTTAAGN TCTATCAGGT CAGTNACATT CTTTCCTATA CTGGCTATTT NGTGTGTAA	120
GTNCCTATAT CATTTTATTG TNAATTCTAA GCTTNCTTGG ATTGAGCCTT CAATGTTCTC	180
CTGCATCTNA ATGGTCTNNA TTCCCTACCC ATATTCTTAA TTCTGACTCC TGTGNATTC	240
CAGCTATCTG CAGCCTAGTT AAGGAACCTT TGGCCTGGTT NAGGAACCCT TGNTAGNGGA	300
ATTACTGTGA CAGTTTAGAG GAAGGAATNC ANTCGGGCTT TTGGAGTTGT CCAGGGTTCT	360
TGCGG	365

(2) INFORMATION FOR SEQ ID NO:680:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 376 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:680:

GGCACAGGGA ATAGCTCTGG CTAAGCGGTG GCCAAGGATG TGGGCAGAAG ACAACCCTCC	60
AGGGTNGCNA ATCAACCAGG CCCCCATACT CATAGAATTT AAGCCTGGGG CCCAGCCAGT	120
NCAGGCAAAA TCAGTACCCG GTCCCCAGNG AAAGTTNTTG AAGGTATCCA GGTCCATCTC	180
AAGTGCCCTG AGGGCCTTTG GAATTAATAG TTCCTTGTCN AGTTTCCATG GAACACTCCC	240
CTCCTGCCTG TTCCCCAAGC CTGGGNNCCA AGGACTACAG GCCGGTAACA GGTTTTGCGC	300
TTGTTTCCAT CCAGGCTACA GTGAACCTTA ACATCCAGGA GTGACCTAAC CGGTNANACA	360
TTGTNGGGGT TNGNTG	376

(2) INFORMATION FOR SEQ ID NO:681:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 355 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:681:

GGCANAGGGA TCTTTGGAAG TTTGATTAGA AAATGCCTTG AGGTAGTCTT CTTTGGGGTTA	60
AACCTGCTTG ATGTTCTATA AGCTTCTTGT ACTTGAAATA TTGATAACTT TCCCTAGGTT	120
TGGGANCACTT CTGTNATTAT CCCTTTGGGA TAAACTTTCT ACGGCTATCT TCTTCTCTAT	180
CTCCTCTGTA AGGCCAANAA CTCTNAGTTT TGCCCTTTTA AGGCTATTTT CTGTATCTTG	240
TAGGTATGTT TCATTCCCTT TTAAATCTTN TTNCCTTTNG TATCCCCTGG ACTATACATT	300
NNCAAGTAGC CGTCTTCAGA CTCACTAATT CTTTCCTCCG GTTTGGAACC AGTTC	355

(2) INFORMATION FOR SEQ ID NO:682:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 382 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:682:

GGCANAGTGT AAGCTCAGAG AGGAGTGAAG CTCGCCGGA ACTTCGGGAA TGTAATGGTT	60
TAGTTAATGC CCTCATTTTN ATTGTTTCAGG CTGAGAATTG GGCAGAAGGA TTCAAACAGC	120
AAGCTTGTAG AGAACTGTNT TTGCCTTCTN CGGAACCTAT CATATCAAGT TCACCGGGAG	180
ATCCCACAGG CAGAGCGTTA CCAAGAGGCA GCTCCCCAAT GTTGCCAACA ATACTGGGCC	240
ACATGCTGCC AGTTGCTTTG GGGCCAAGAA GGGCAAGGGA AAAAACCTAT AGAGGNTCCA	300
GCAAACGATT ACATGGGTTT TCCCTTAAAA GNACGGGTTC CCATTNGGGG GGGGGCCCCG	360
TTANCCCAT TGGNCCTTTA GT	382

(2) INFORMATION FOR SEQ ID NO:683:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 366 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:683:

GGCANANAAG TAGCTGTAAC TACACTCCCC ANATGTNAGT AATTACTGCA GTGGTTTTTAA	60
CACAGGGCCA CACATCCTTG GCTCTCCTCT CCCAGGAGG TGAAGCTTCC TTTTCTCTTT	120
GCCATGTGNG TCTNCAGCTA GTAAAGCAAA AGCTATACCT TGAACAGTGG GAGTCCAGGC	180
AGACACTTCC TGCCCCAGTG AACCAGGGTT GTCCCCGGGC AAGCCATGGG CCATCAGGNN	240
ACCCATGTNT TTCAGCATGG ACTCCGGGAT GACAGGATGA GNAACCTCAT TCTGTGGGGT	300
TTTTTTCCNA AAACCCATCA NCCCCAGTTT TTAANCTGNG GAAATTTTCG GGGCAAACCC	360
AACCTG	366

(2) INFORMATION FOR SEQ ID NO:684:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 355 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:684:

GGCAGAGCGG CANGAGTTCT CAGGAGCCAC TCATCTGCTG GCAGAGGTAG CAGAAGAATG	60
CCCTTAGTGT AAGTCCTCTA CAACCATAACA CCAAATGTGC TCCCTGCATT TCAAATTCCA	120
TTGTAGAAAG TCTCTGNATA ATCTCACTTA TACTATGAGC CATTCCTCAG TATCTGTGCC	180
TCTTCCTGTT AGTGTTCTAC AATTCCTTTC TCCTTAATTT TTCTCCGCTT TACAAAATGT	240
CACACAGAGA AGTGCATAAT ACTTAANGCA AGCTTTTGAA AAATAATGCT CCATNAAATA	300
GCTTTGGTTC TGGTNCATGA TNATTGCGTN TTTATGAAAC ATTTTAAGGT GCATT	355

(2) INFORMATION FOR SEQ ID NO:685:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 312 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:685:

GGCAGAAAGC AGAGGCAGGG NACGGNTCTN AAACCTCCAG TNTGGAGGGC CCTGGGAAAN	60
TGGCCTCAAA TGTTTCCTTG TNCTCANTGG ATAGGCCTGG TCCGCCATCT GCAGTCCTCC	120
TCCCAGCCCA AGCCTGGTCA TCTCCAAGCC TAAGGACACA CAGCACAAGG NGCACTTNTN	180
CCGGTTGGTC AGCTCAGGTT GCCTCATGCT NCAGAGACCT CGCAGGGGAA TGGCTTAAAG	240

GAGAGAGTNA ACAGGTTTGT TAGAATTGGT ACCAGGNCCA NGTTTTNTN TTCTTCCCCC 300  
AGCTATAAAA CA 312

(2) INFORMATION FOR SEQ ID NO:686:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 216 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:686:

GGCAGAGGTG CAGAAANTA ANTNTCCAAG NAAGTNTGCC AACGGAGTCT TTCTTACGGN 60  
CAAAGCTTTT TAGCCCATT CNTCACTGTG GTCTTGTCTT GGTACAAAG TAAAGGCACA 120  
ATGGGCCCCC TGGCCTTCCT GTTTGNAAAT CCCCTTCCCA GGCTGTCTAA TCATNGTAGA 180  
TCTTTTCCNN GAGGAAGCAT ATCCTNTTGG TCTTGT 216

(2) INFORMATION FOR SEQ ID NO:687:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 377 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:687:

CTGCAGTTAT CCCAGGGCTT AAAATTAAAT TAAATTAAAA ACAAAGACCC AAATCAAAAC 60  
AAAATTAAAA AAAAGCCAAC CAACCAAATA AACAAAGAAA AAGNACTGCA GTTAANCCAA 120  
TCAGGTTTCA CTAGTAGGGA AAAGGAAAN TTATTAAAGA TATTGGGTCT TTTTATTTCC 180  
TTGCGGGATT AAATTAACCT CCCCTAGGGC TGTGCCAAGT CCTGGANCTG AACATATTAG 240  
GNGGTTTTTN TTNAACTCC AGNGNGGTGT AATTATNTTT CCCCTTAGTG TGATTGGTGG 300  
ATTTTAAGGG TTTCCNTCTG NCCGGGTTTT AACCCACCAC CTGGGGGGAC NTGGNGGGGC 360  
CTTTTTTTGN GGGGGGT 377

(2) INFORMATION FOR SEQ ID NO:688:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 118 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:688:

GGCACGAGGA AAATNATGAT TCCTGTCCCA ATGCACAATC TCAGGAGTGG TTATTGCCTT	60
AAAGACTTAA TCAGTATCGT TCATGATATC CTTTTTTTTT TTTTTTTTTT TTNNNNNGN	118

(2) INFORMATION FOR SEQ ID NO:689:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:689:

GGCAGAGCNG AGAACCACAA GGCGAGATGT CTGCTCATGC CTTCCCTGTG CAGACGTGCG	60
GGGAGGAAGA TCAGAAGAAA ACCCCACAAG TTCCTATCAA TTTCACAGAA CTTTCCAAGT	120
GCTCTTAGAG TTGAAAGATA ATGTCTGGGG AAAGAGNAAG TCTAAATCTG NATGAAAGGA	180
CAAAGGTGGA TAAAGTAGGC TGTGGGGGGA AAATGAAAGG ATGATGGACC AGCTTAAGGG	240
AGGCAAGGAG AAGGCCCTA AATGCCCCC CAAAGACCAC TGCCTGTTCT GTTCANGATT	300
CCCCAGCATC NAATTCCCTT AGNCCNTNGG GG	332

(2) INFORMATION FOR SEQ ID NO:690:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:690:

GGCAGGAGNA TTACAGCGGC ATAGAGACAT ATTGCAGGAT TATACACATG ANTTCCATAA	60
AACCAAAGCA AACTTTATGG CAATACGGGA AAGGGAGAAT CTTATGGGAT CAGTACGAAA	120
AGATATTGAG TCATATAAAA GTGGGTCTGG AGTAAACAAC AGAAGANCTG AGCTATTTTTT	180
GAAAGANCAT GACCACCTNC GAAACTCAGA TCGTCTGATT AGAAGAGACA ATAAGCATTG	240
CTATGGCAAC AAAAGAAAAT ATGGACTTCA CAGAGAGGAA TGTTGAAGTC AATTTCACAG	300
CAAANTGGAA CACTTTGGGC CATTCGTTTT NCCTGCTGTA AAACCGTNCG GNTCCAGAGG	360
GTCAACCTGA GGAAGNGGCG GGA CTCTAGGGG GTGTTATTNG GGTCTGTTC	420
CTTCNGTTGC TGTTGTATG CGTTCCNTTG NTGGGGCTC TTCCGGGACT NTGACAGNCA	480
CCGTTTTTCA CACCTGGTTT G	501

(2) INFORMATION FOR SEQ ID NO:691:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 204 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:691:

```
GGCAGAGGTC ATATCCAATN AATGTCCCCT GGTAATTTT GAAAGTNATT TAATGTTTTTC      60
AGTTGATCCC TACATATGGT TACTTTCTGT GGCACAATGA TAGTGTTCATT TACTGAAGTC      120
TCCAAGTAGG AGTAAAGGAG TAGCAGTCTG AATTTTGTCA GGAGCTATNA ATTAAACCAG      180
CATGAGAAAT CAANTTTTGC AAGT                                             204
```

(2) INFORMATION FOR SEQ ID NO:692:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 387 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:692:

```
GGCAGAAAGT CATTCTATAG TAACATCATC CCAGACTGCC TTCTGTATTC CCCTGTGTAC      60
AGTCTCCTTC TGTTTCTAGG TTTAGAAGTT CAGAGGTGAC TGTTTTTTTC CATTTCACACA      120
GCCAAATGGG GGAAGAGGTG AGGCTAGGGG AGTGCTGTGC TGATTCTCCA GCCATGGTNA      180
GACAGGTCAC CCAGGNAGCC TCGAGGAAAG CCCTGGAGGG GAATCACATG TGTACTTTTT      240
NNATGGAAGC TTTTTCGAAA GCACATCTGT GATTACACTT AGTTTATTGG AACTAATGTC      300
CCAGGAGTAG ACATGGATTG GTGGGCCAAG TTATTTNGGG GACACCTAAA CNGNTCATGG      360
ACCCGANNGA CTTTTTCAAA CCTTTAT                                             387
```

(2) INFORMATION FOR SEQ ID NO:693:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 314 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:693:

```
GGCANAGGGA AAAGTGTGCC AGTTTCCAGG AGGAAGTCAA TTTTCATGGCC CTCAATGGTT      60
```

AAATATACTT GGGGCTCAGT GAAGGGTGAT GACATGAGTT GGTGCTTGCC CTGGGCACCC	120
TCAGTCCTGT TGTGAGTCA TCTGGTTGGG GGCTTCTGGC CCAGAGGAAC CTTTGTCTC	180
TGGGGCAGTG CACCTTCCAG TGATTGTCTC TGCATAGCGG TTAATGGGGT GAGGGGGCAA	240
TTTTTCTTT GTTTGGACAA NNCNTTTTTA AGGTGTTTNT TGNAACCAC ACTTGTTAAC	300
AAAGCTTACC CGGG	314

(2) INFORMATION FOR SEQ ID NO:694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:694:

AGTCGGTAAA GTAGAGCGGC GACACGAAC TCTNCANCCG CTCCANNGTG GTACGCCAGT	60
CCTTCAAGGC CGGCGCACNC ATACGTGCGG GNNTCTCGCT CCTCTTTCCG NNAAGGCCCC	120
TTGCGACTAC CGTTCCGCTC CACGGNCAGG AAACCAAAGG TTCCGGCGTC CAGAGGGCGT	180
CTNCCAGTCC CGGGNCANCT TTTCTTGGGA ACACCGNCGG CTGTTGGTAA GCC	233

(2) INFORMATION FOR SEQ ID NO:695:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:695:

TGAGNTGTTT ATGGAGTTTT TAATCAGTAT GTCTNAAACC ATTAAATNTA NTNNGCATGA	60
TCATANAAC GTGTTTCTAA AANCACTAAA TNAACAACGC CTGGGAGGGG NNATTTTGTG	120
ATGATNGCTA TTGTGGTTGA GGATGTGANA ATTCAGAGCA CNCAGNTGTG TTCTTGCCTG	180
CCTGCAGACC TACTTTGAAA AAGCTTTTGC ANGAAGCTTG TGGTTGNTAG TTCTTCGGGT	240
TCATAGTNAT TTAGGTTTCC TTCGTTCTGG GTGTGTTTGA TAGAGGGTCC TGGAACNNC	300
	300

(2) INFORMATION FOR SEQ ID NO:696:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid



(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:696:

CTNCTCTGGG NATGCAGCGT CTGTTGNCTC CAGTGAAAGN CNATTCTGCA ACTGACAAGA	60
GCGGTGCAGG AAACCTCCCT CACACCTGCT CGCCTGCTCC CAGTAGCCCA CCAAAGGTTT	120
TCTACAGCCT CTGCTGTGCC CCCTGGCCAA AACAGATACT TGGCCAAAGG ACGTGGGGCA	180
TCCTGGGCCC TGGGAGGTTT TACTTNCCAG CCAATNTGT GGGNCCAAAN TTGNCCTGGA	240
G	241

(2) INFORMATION FOR SEQ ID NO:697:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 339 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:697:

GGCAGAGTTG CAACATCTCG GAGGGGAATT GTCCGGAGAG AATCATCACC TGACCGGCCC	60
CACCAATGCC ATCTTTAAGG CTTTCGCTAT GAATCATCGA CAAGCTGGAG GAAGATATCA	120
ACAGCTCCAT GTACCAACAG TTACCGNGGG CCAGCAGGNC CCCGGTTCAC CCTGAAGGCT	180
GGTGGTGCCG GCCACCCAGT GCGGCTNCCC TGNATTGGGA AAAGGCGGGT GTTAAGATCC	240
AAAGAGATCC GCGNAGAGTN AGGGGGCGCA GGTTCAGGT GCGGGGGGA TATGCTGCCC	300
AAATTCCACC GAGCGGGGCC ATTCACCATC GNTNGNGT	339

(2) INFORMATION FOR SEQ ID NO:698:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 324 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:698:

GGGCANNGAG GTGAATTGAG GGNGGAGCAC GTAAGNGGTT TTCCCAGAAG AACAATGACC	60
TAACAAGTTG CTGCTTCTCA NATGCCAAGA CTATGTATGA GGTTTTCCAA AGAGGACTCG	120
CTGTGTCTGA ACAATTGGCC CTGCTTGGGA ATNATAGTAA AACCAAACCA GCCCTACAAA	180
TGGCTATCTT TACAAACAGG TGTTCGTNTA GAGNCAGAGT ACCTGGGGTT CCCGTCTCTT	240

GNCATAAAGG TGTGTNAAAN CATTACCCA GGACCCAGTT TTNTTCGGGG GATCTTTTGT 300  
GTTCCAGAAT AGGNGCCCAT AGGT 324

(2) INFORMATION FOR SEQ ID NO:699:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 177 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:699:

GGCAGAGNCA GAGATGGCCC TCCCCTCCGT GGATCCAACA TGGNATTTAA AAGANCCAC 60  
AGAAGNGGGT NGAGCACAGA GACCACGAAC TCCAGNTTAA ACCTCGAAAC ANTCGTGAAC 120  
GCCCTNCAT TGNAAGTAGC CAATCCNAAC TCTGCCTAAT GCTTCCGGGG GTGCCCCA 177

(2) INFORMATION FOR SEQ ID NO:700:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 216 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:700:

GGCAGANAAT GGGCCCTNCT TGGAATATAG TGAACCAAAT AANCTCTNCA NATGGCTATC 60  
TTACAAACAG GTGTCTAATA GGCAGAGNN CCTGGNTTCC TGTCTCTTGG CATAANGGTT 120  
ATGAAATCAT GCACCAGNCC AGTTTGTGCG GACATCTTNG CTTAGCAAT AGGCCAGAGT 180  
GGGATCCANC TCCNAAATTG GCCTTGTTAA NACGTG 216

(2) INFORMATION FOR SEQ ID NO:701:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 153 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:701:

GNAGGCAGGG TCTTNTGTGTT CCTAATGTNC ATAACCCTCC TTAAC TTAA CGCCAACTTC 60  
TTTCCTATNG TCCAGAACAT TGTGAGCACA GCTCTAATGA TTNAGAGTGG NCATTGGTTT 120  
TAAAAACCAA GCTGGGCTTC NTTGAAC TCT NGT 153

(2) INFORMATION FOR SEQ ID NO:702:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 112 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:702:

GGCACGAGGA GACTGCAGTG NGTGTCCGTG TCTATCAAAT ACCTAAGGAG TCCCCAGGAG 60  
CTNGCTGGCC ATCGTAATAG GATNTNTCTG TCCTGTAAAC TGTGCCAATT NA 112

(2) INFORMATION FOR SEQ ID NO:703:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 72 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:703:

GGCACAGGNT TTTNGGGATC ATGTCTGGTG GCTCCCCGGA TTATAACACC AGAAAACATG 60  
GCGGTCCAAA GG 72

(2) INFORMATION FOR SEQ ID NO:704:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 159 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:704:

AGCTCCACCA GCATCAAATG AAACAATAGT NCAGTTNTNC TGCTCANAGA TATTCTCCCT 60  
TATCCACTTC AGGNACACCT GGCTCTGCAT GACAGATAGT CCACTGGGTT ATCAAAAAAG 120  
CCCTGNNATT TNAGAAGNAT GTAGGTCCAT GGTGATAAT 159

(2) INFORMATION FOR SEQ ID NO:705:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 88 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:705:

GGCANAGCAG GAATACCAGA GCAAGAACT GATGTCTGAC AACGGANNNG NAGTTCAAAG 60  
ATTCTTTGTA GCAGACACTG CAAATGAA 88

(2) INFORMATION FOR SEQ ID NO:706:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:706:

CAAATCTCTN AACGAATCAT GTAATTAATA AATATTTTAA GCACTCATCA GTATTCTCCA 60  
ATGTAACCTT CTNATTGGAG TACACAGANG GAAAGCAAAG AAGAGCATCT AACTTCTAGC 120  
TCTGGCTTNN AGCCTCTCTA CCAGGCCGAN GCAAG 155

(2) INFORMATION FOR SEQ ID NO:707:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:707:

NCTNAGGCTA TCCCCTTGTA AGNGTTTTGT ATCGGCTCGG AACCCCAAGT AACATACCAA 60  
CAGACANCAC GNGGGCAGTG TGGGAGCAAC ATGCTGGTTT TAATNAGTGG CCTGGGANGC 120  
AGNTA 125

(2) INFORMATION FOR SEQ ID NO:708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:708:

GGCANAGGNA CGGTGGGCAC TCTGTCCCAG CGGATCACAA ACCAGGTCCA TGGTTTGAAG 60  
GGACTGAGAC TCCAAGCTTC TGGATATNAG GNGCTACCTG GNAAAAAGTC GCCACAGGCA 120  
AGCTGCCCAT CAACCACCAG ATCATCTACC AGCTGCAGGA ACGTCTTCAA CCTGCTGCCA 180

GATGTGCAGC CTGCAGGAGT TCGTCAAGGC CTTTTAACCT GGAAGACCAA TGAACCAGAT	240
GGTGGTAGTG TACTTGGCCT CGCTGAATCC GTTCCGTGGT CGCCCTGCAC AACCTTCATC	300
ANCAACAAGN TTGCCAACCG GATGCAGAGA GGAAGNANGG CAGGGAAAGN AGTGAGCAAA	360
AAG	363

(2) INFORMATION FOR SEQ ID NO:709:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 116 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:709:

GGNAGAGGTA AAAAATGGCG CCACCCAGTA CCCGGGAAGC CCAGGGTCCT GTCGGCAACC	60
AGCNCAACCA AATCCATCGG AGAAGAATGG TGNTGANAGC TTCCCGGACG CCNACN	116

(2) INFORMATION FOR SEQ ID NO:710:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 105 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:710:

TTTTCCGCGA AATTTCTGN NGGAAAGGTC CCAGCATTTA AGGGTGAATG ATGGATTCTT	60
TGTGNTTAAN AGNAACGCCA TTGCTCTACT ATGTGAGAAA TGAGG	105

(2) INFORMATION FOR SEQ ID NO:711:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 109 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:711:

ATTCGGGCAA GTCCACCACT ACTGGCCATC TAACCTATAA NTCGGGTGGC NTCGACAAA	60
GACCCNTTGA AAATTTTAGA AGGNGGTNC TGAGATGGGA AAGGCTTCT	109

(2) INFORMATION FOR SEQ ID NO:712:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:712:

CGCNAAAATC CCAAATTTTT GGGTAACANC ATTTGNAAAA CCATCCACAA GTGTCTGNCC	60
TGCTTGGGGA GGAAGATGAA GAGGCATGCN TTATTTGAAC CGAGTTGAAG TGAACGATT	120
TGANGTNTTG AATCCGGTTT CCGN	144

(2) INFORMATION FOR SEQ ID NO:713:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:713:

TAACTGGGGG AAAACCCAGA GGGCATTGGA NAACAGGNTT NCGTAGAAGA ATTCAAGGGC	60
CAGATTTTNA ATGCCCAANA TTGGTTTATG GGAAGCAACA AAAAAANAAA GCACATGTTG	120
CCCANTGGGT TTCCGGNAAG TTCCCT	146

(2) INFORMATION FOR SEQ ID NO:714:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:714:

GGNAGAGGCC CAGGTTCAAG AAATTCTCCT GCCTCACCCCT ACCANGNAGC TGAATTNCA	60
GGTGTGTGGN A	71

(2) INFORMATION FOR SEQ ID NO:715:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:715:

GGAANACCGG TNCCAAGTGC CTGCCCTCTT TCCCCGGGGC TGGNTCTCGT NTGCCCCGGT 60  
TCCTGGG 67

(2) INFORMATION FOR SEQ ID NO:716:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 178 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:716:

TGCTGCTGGG AAAGATCTGG AGGTCCAAGT CCTGCAAGGN CATCTCTGGA AAGAGCCAGA 60  
TCCTGTTTNC CCTCGTCTTC ACCACCAGGT ACCTGGACCT GTNCACCAAC TTAATCTCCA 120  
TCTACAACAC AGTAATGANG GTGGTTTTCN TCCTCTGTNC CTATGTNACA GTGTACAT 178

(2) INFORMATION FOR SEQ ID NO:717:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 196 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:717:

GAGCAATATG GGATCAAACA CAAATCACT AGATAACAAC TATTCCACAC CAAATGAAGA 60  
GNGGAGACCA CAATAGAACA CTGGATCGAT CGGGGGATCT AGGCGACATN GAAGCCATTN 120  
ANAGGGAAAC AACACCCTTG AATGCAGAAAG AATTTAGCCA CCACTATCTC CGTNCCATCT 180  
GGGCTTATAT GNGACT 196

(2) INFORMATION FOR SEQ ID NO:718:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 139 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:718:

ATTGTNATGG GNTGCCCAT T GAAATAAAAG TATTATCAGA ACTTGGTAGA GAAGCTCAGA 60  
ATCTTTNANC TNTGGAAATT AGAAAGAAAG CTAGATCATT TGCTAAAGCA GCCATTGNGT 120  
ANCAGTAATC AGCATTTAT 139

(2) INFORMATION FOR SEQ ID NO:719:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 84 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:719:

GNAAGACCTG TAATGGTGGC TATCCTCCTN AAGCTTGGNA ACTCCTGGNC AAGAAAAGGC 60  
CTGGTTNCTG GTGGCCTCTA TGAA 84

(2) INFORMATION FOR SEQ ID NO:720:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 182 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:720:

GGNAGAGGNA GCCCACTCCT AATGATGTGG CCATATCCNA CCTCCCTCTG GCTCAAATGT 60  
TTAANAGGAT TGTNCAGGCT GTTGTGTACA GCTGTGGAGC CAGAGTTGGA ATTCTTCCCA 120  
AGGGGATATT CGGTTGCTGG CTGTACGNNA TGGAAGNCTT TGAAAGCCCN NATTGTITCC 180  
CG 182

(2) INFORMATION FOR SEQ ID NO:721:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 115 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:721:

TTGGGGAGGA GATGAAGAGG CATGAAATTA TTNGACCCAA GTTGAAGTGA ACAAANTTTA 60  
ANGGTATTAA ATNCGGTAC GGATTGNTTT TAAATTTAAT GGAAATCCTT TATTT 115

(2) INFORMATION FOR SEQ ID NO:722:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 359 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:722:

GGCAGNGAAG CAGTTGATCC TAAGACACGT TTAATTATGN ATAAAATGGT CAACTCTGGA	60
ATGTTGGAGA CAATCACTGG CTGTATTAGT ACAGGAAAGG AGTCTGTTGT CTTTCATGCA	120
TATGGGAGGG AGCATGGNGG ATNAAAAGGA AAGATAGTAA AGTTATACCT ACAGAATGTG	180
CCCATCAAGG TATTTAAAAC AACCCCTGAA TGNAATTTTA AGGAATCGTG ACAAATATNT	240
TGAAAGGTGG ATTTTCAGGT TTAAGATCG CTTTCAGTTA AACTTANATC CACGTAAGGT	300
CCATCCGCAT GTGGGGGCAG NAAAAGGAAT TGGCACANTT TNGTCAAGTA TTGGCNGTG	359

(2) INFORMATION FOR SEQ ID NO:723:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:723:

GGCAGAGNAT TTAATGTAAG TATTATGGGA ACCTTCATAA GGAAATNAAG ATTCNGAGAA	60
ACAGGTAAAC TCTGGTCTTT CTAAAACAGA CCTGATGAAG AGTAGAGAGT CATGGAGAGT	120
TNTAATAGAG CAAAAGAGT GTGNATCTCA TGGTAATATA GTAGGGGAAC TTAGCAAGGC	180
CTGTTTATTC CAGATTCTTC CCTGGGGATC CTGTGTCTTC AGAGATAAGG ATACTCGTTT	240
TCCTCTGGGG TATGGGGGGT TGGGGGGGTA CCTCTNCACC TGAGGGCCTT TTNGACCGNC	300
TTNGGAGGAA GGTCCAGAAA ATCCTTNCCG GGGNGNTTAT GAACCCGCTT TCATGGGGGG	360
GAAGGTCAGA GGNAAGGTT AGAGAGGAAC TTTNTTGCAC ATGCNGTTCT CAAATTNCCT	420
TTCCGGTTTC ATGGCAATNT	440

(2) INFORMATION FOR SEQ ID NO:724:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:724:

GGCANAGGAA ATGGCCCTGA AAAAAGACAG GGAAAGCATG GGAACACCGG TACATTGAGG	60
TGTTCAAGTC CCACAGAACC GAGATGGGAT TGGGTGTTGA AGCACAGTGG TCCCAACAGT	120

GCCCCGACAGC	GCCAACAATG	GCTTCGTGCG	GCTTCGAGGA	CTCCCATTTG	GNATGCACAA	180
AGGGAAGAAA	TTGTTCCAGT	TCTTCTCAGG	GTTGGAAATT	NTGCCAAACG	GGGTTACAT	240
TGCCTGTGGG	ACCCCGAAGN	CAAGATTACA	GGGGAAGCGT	TTCGTGCCAT	TTGCCTCGCA	300
GGAGTTTAGC	TGGAGNAAGG	CTCTAGGGGA	AACACAAGGT	GAGGTTTGGG	GCACCAGGTT	360
ACATTTGAGN	TGTTTTTAAG	AGNCAGCCCA	GAGGGAGNTT	AAGNTCATAN	TCAGATTCCC	420
						420

(2) INFORMATION FOR SEQ ID NO:725:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 486 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:725:

GGCAGAGCTC	ACCCACAGTA	ACCACACCCA	CGGTGACCAC	GCCCTCACTA	CCCGCAGAGG	60
TGGGCTCNCC	GCACTCAACC	GAGGTGGACG	AGTCCCTGTC	GGTGTCTTTT	GAAGCAGGTG	120
AGNNCCGCCA	TCCGCCCCCA	CCAGTGAAGG	CTGGGNTGA	AGCCTCCCGC	TGCGTGGCCC	180
CCGGGCGACG	GCGCTCGGTT	TTCCCCACAC	GAATGTGGAA	CCTGTGNCCT	GGTGTNACCC	240
TGTAAATTTN	AAGCATCGCA	AGGNGGTGCC	AATGNGCACC	AANNCTGATN	TTCCCCCGGN	300
AGCTTCGNAA	TGAANAGCAN	TTGCCCCGTT	CACAGGGAAC	GGGCANGTTN	GGCTNNGGGC	360
CCNAGNGAC	GGNCANCCAC	ATNCGTTTCA	NGAAGTTCCT	TGNNCCAANC	TGTTTTNATT	420
TGGAATTCCG	TGNCCCTGGG	GCCCCGGTTN	CGGGCAAATT	CAAACGGNGA	CACAAAGGGT	480
TTTGGN						486

(2) INFORMATION FOR SEQ ID NO:726:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 428 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:726:

GGCANAGCGT	GNATGAGGAG	CTCNTCTACC	ACAAAGTGAC	GGCAGCCGAG	CTCAGNACCT	60
TGTGTACCCG	CCATGCAACT	GGTTGCTTTT	TNTCAACACC	ATCTTCTACC	CCGTGGAGAT	120
CAATGAAATC	CNAGCCTATT	GTGGTCTATG	AACAAGGGAA	TACCTTGAGC	AGATCTCCAC	180

TCTCATCAAC ACCACCGACA GATGCCTGCT CCAACAATA CATGATCTGG AACCTGGTGC	240
GGAAAACAAG CTCCTTCCTT GGACCAGCGC TTTCAGGACG CCGATGAGAA GTTCATNGAA	300
GTCATGTACG GGGACCAAGN NGACCTGTTT TTCCTGCGCT GGGAANTTTT GGGTTGATGA	360
ACACAGGAAA ACAACNTGGG TTTTGNNTTG GGGGCCCCAT GTTTTTTTCA AAGGAAACCT	420
TTGGNNCG	428

(2) INFORMATION FOR SEQ ID NO:727:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 154 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:727:

GGCANAGTCA AATGNGAAGT GGTCAGTAA TCTAAAGGGA AAAAGGNGAT GAATGTCTTT	60
AATGGAGTCA TGGTTTGCAC TGNCCATCA CACCAATNCT CATTTACCTC TGGGAAAGCT	120
TGCCTGGGAA TTNGGAAAGT NTCAAAGGGA CAGT	154

(2) INFORMATION FOR SEQ ID NO:728:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 314 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:728:

AACATTCCTC TTCTCTGCCA CCATGACCAA GAAGGTTCAA AAATTTCAGC GAGCAGCTCT	60
GNAAGAATCC TGTGAAAATG TGCCGTTTCC TCTGAAATAC CAGACAGTTG GAAAAATTAC	120
AGCAATATTG ATGATTTTTG ATCCCTCTG AAATTCAAGG NTACCTNACC TGGTTTATGA	180
TTCTGAAATG NAATTGGCTG GNAACTCCT TTATGGATAT TCTGCAGCAC CTGTGAATAA	240
TACCCAGTNG ANCAGCTTTG CTNACTGCGN AAATCTTGGG CTTGCACTGG CCATGCCCCC	300
TTCCATGGGN GCAA	314

(2) INFORMATION FOR SEQ ID NO:729:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 355 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:729:

GGCANAGCAA CTTGGTGACC TTTGTGGTAA TGGTGGTTCT CTATGCTCAC ATCTTTGGCT	60
ATGTNCGCCA TAGGNCTATG AGNATGTCTC GGCATAGTTC TGGACCCCGG CGGAATCNNA	120
NNTACCATGN ATGAGTCTTC TGAAGACTGT GGTCATTGTG CCTTGGGGCC TTTATCATCT	180
GCTGGACTCC TGGATTGGTT TTGTTACTTC TAGACGTGTG CTGTCCACAG TGNGACGTGC	240
TGGNCTNAT GAGAAAATTT CTTTCCTTGC TGCCTTGGNT GAANTTCANC TCTGGNCATG	300
AACCCCATCC GTTTTACTGC TAANCGTGA CAAAGTTAAT GGAGCGGCCA CTTTT	355

(2) INFORMATION FOR SEQ ID NO:730:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:730:

GGCAGAGCGG GAAAGGCGGG ATCGAGGTGG GCCTGAGCCC NNGGATTTGG AGCGAACATA	60
GATGAGAAAC ACTTCCCGAG GTCTCCAGGT NTTNTGGGGA GCCAGGAGGG AAGTAGGGGA	120
TGAGTCCATC TTCAAACGG AGGGGGAAGG TCTCCCCTTT TTTGGGCTGG GAACCCGGGG	180
GAAGGCAGTG GGCCGGNCTT CTGGAAAGGT CGGCCTGGGA AGGTCTGCCT GGGGTCTGGG	240
GGATGTTCCC GTGGGTTAGA CCCGGCGCGG CCCATGTTTC CTCCANTTAN CTAAGATTTT	300
CCCGGCCTTN AAACGTTGTG CTTTCNGTCA AAGANCCAGG GGGTTCCECA AGGTTAC	357

(2) INFORMATION FOR SEQ ID NO:731:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:731:

GGCACGAGCT GTACTCTGGG GCTCTTGGCG GCTGGGTCTT GCCCTGCTGT GCTCTGCCAT	60
TTAACAGCCC ANTTGACGAG GAGAATCTAA CCCAGGAGAA CNATGATCGA GGGACANACG	120
TNGACCTCGN ATTNAGTCCT GCGNCCAACG TGGNACTTCG CTTTCAGCCT GTACAAGCAG	180
TTAGTCCTGA AGGCCCTGA ATAAGAAATG TNNATCTTCT CCCCCTGAG CATCTCCACC	240

GTTCTTGGCC TTCCTGTCTC TGGGGGNCCA TNAN

274

(2) INFORMATION FOR SEQ ID NO:732:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:732:

GGCANAGGNT GGGTTTNTGA ACTNCTGNGT TTTTGCTTGC TNCTCTGGAN ATGCAGCGTC	60
TCTTGNCTCC AGTGAAAGCG CATTCTGCAA CTGNACAAGA GNGGTGCAGG GAAACCTCCC	120
TTCACANCTG CTCGCCTGNT CCCAGTCAGC CCACCAAAGG TTTTCTACAG NATCTGNTGT	180
GCCCCCTGGC CAAAACAGAT ACTTGGCCAA AGGACGTGGG CATCCTNGCC CTGGGAGGTC	240
TACTTNCCAG CCAATATGT GGACCAAAC TACCTGGAGA NGTATAACAA TGTGGGAAGC	300
AGGTAAAGTA TACAGTGGGG TTGGGNCCAA ACCCGTATTG GGCTTTCTTG TTCCAATCCC	360
AAGAGGNCCA TCAAATNNCC TGTGGNC	387

(2) INFORMATION FOR SEQ ID NO:733:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:733:

GGCAGANACT GGGTTGGTGA AGATTCCACA TACAAATTTT TTAAGGTTAT CCTCATTAAAT	60
CCATTCCATA AAGCTATCAG AAAGAAATCC TGACACCCAG TGGGATCACC AANCAGTGCC	120
ACANGCNCAG GGAGTTNCGT GGGCTGACAT CTGCANG	157

(2) INFORMATION FOR SEQ ID NO:734:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:734:

CTCTCNTNTT CACCACCAGG TACCTGGACC TNTTCACCAA CTTNATCTCC ATCTACAACA	60
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CAGTAATGGA AGGTGGTTTT CNTCCTCTGT GCCCTATGAG AACAGTGTAC ATGAATGTNA	120
TGGGAAAATT CCGTGAAAAN TTTTGAGCAG TGAGGAATGA GCACATTCCG CCTGGNGTTT	180
CTNCTGGTCC CAGTGNATTG GCCTTTGCCT TCCTTGGAAG CTACAGTTTC ACTCTGCTGG	240
GGATCCGTGG GAATTTNN	258

(2) INFORMATION FOR SEQ ID NO:735:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 501 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:735:

GGCAGAGCCC ATGCATCATG CCTCTGGTCA TGACACTCGT GGCCCTTCCT CACATGAAAT	60
GAGGGGAGGG CCATTAGGAG ATCCCAGACT GCTAATTGGA GAGCCCAGAG GCCCCATGNA	120
TAGATCAAAG GGGTCTACCT ATGGNTGGTA GAGGTGGTAG AGATTNTCGA GCGAATGGAG	180
ACTCGTGCCA TGGAAACTGA AGGTCTTAGA GACACGTGTA ATGGAGAGGA GAGGAATGGA	240
GACCTGTNCG ATGGAAACCA GAGGGATGGA AGCAAGGGGC ATGGTTGCAA GAGGATTGGA	300
GNTGAGGGGC CCTGTCCCCA GTTCAAGAGG CCCTATGATT GGTGGGAATT TCANGGTCCT	360
GGTCCCATTA TTTTAGGGGC AGTTGGCCCT CCTTCAGGGA NCCCGACAGT TCCCGGGCAT	420
TTTAAGGGTT GGGGNATCTT GGAGGTGGTA TGCAGGTAC AGGNTNACAG GNACCGGTTT	480
TTAGGGGGCA GTTTTACAAG N	501

(2) INFORMATION FOR SEQ ID NO:736:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 69 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:736:

AANCCAACAN TAAAATCCCT TCCCTCCAAC ATATGCAAAG ACGTTNTNAC CGNACCTGGT	60
GATATGCTG	69

(2) INFORMATION FOR SEQ ID NO:737:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 337 base pairs
  - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:737:

GGCAGAGACG GTNCTCACAT TCTCCCCANA GGCCGANATG CGGGTAATGG CGCCCCGAGC	60
CCTCCTCCTG CTGCTCTCGG GANGGCCTGG CCCTGAACCG AACCTGGGC CCTGGCTCCC	120
CACTNATNTG AGGTATTTCA ACACCGCCGT TCCCGGCCCCG GTNCGCGGAG AGCCCCGCTT	180
NATCTNANTG GGCTACGTGG ACGACAGTCA TTTGTGCGGT TTCGACAGGA ACGCCGNGAG	240
TTCCGAGAAG GGGAGCCGCG GGTCTCGTTG GGTGGGAGCA GGAGGGGNCG GAGTATTTGG	300
AANCNGGGAG GACAACAGNA GTTACAAGNG CCCAGGT	337

(2) INFORMATION FOR SEQ ID NO:738:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 70 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:738:

GGAANAGAAT GGTCTGCACC ANTAAAACCA GGNGCACCCA CACCCTGGAA CCTCTCCANG	60
AAGACTCTCG	70

(2) INFORMATION FOR SEQ ID NO:739:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 277 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:739:

CAGCAAGACG TCCCAANTAA GTTTAAGTAT AAGGAAGGCA CTCTNAAGGT CGCGCCAGAC	60
TGGGCAAGAC CTCAAANAGG AGCATCCTGG GTCGGCTACA CTGCCCCCTT CCTTGAATNC	120
ACTCTGCCTG TTTANNAACC TGGGAGTGCT GGNCACCCTG CAGCAGTNCA GCGAATGGAG	180
CTTCATGCAG GCTCTATNCT GTGAACCTGT GAAGCCCTTT GCCTGGCCCA GGTNGACAGC	240
TTTANGTATT TGAAGGNTCA GGGGTGGAGT NAGGCTG	277

(2) INFORMATION FOR SEQ ID NO:740:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:740:

TGAGCCTAGG NGCTAGGTTG CAGTGAGCCA GATGGCCCAT TGCACTCTAG CCGGGCAGCA	60
GGCNGACC	68

(2) INFORMATION FOR SEQ ID NO:741:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:741:

AGGAGCTGTC GGGAAGATCA GAAGCCAGTN AGGATGACCA GCGCGACCTT ATCTCCANCA	60
ATNAGCAACT GCCATGCTGG CCGGCGCCTG GGGCCCGGAA GAGCAAGTCC AGCGCGGANCA	120
CTTGTACACA GCTTTTCCAN CTGGTGACTT NCTCTCGN	158

(2) INFORMATION FOR SEQ ID NO:742:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:742:

GGCAGAGNCT TGCTCTNCCC AAATTAAATT TGCAGTTTTT AACTCTTNAT GACTACCTGC	60
TAAGTGA CTT TAACCTCTTC CGCTTAGAAT CAACTTATGA AATTCGTCAG GACATTGAAG	120
ATAGTGTCAG CAGAATGAAG CCATGGCAAT CTGAAATATG GCGGTGTAGT GTTTGGTGGT	180
TGGGCGCGAA TGGCCCAGCC CATTGTGGCT TTNACTGTCTG TAGNAAGTGG CCAAACCCAA	240
CATAGGTGAA AACTGGCCAA CCCGAGTTCG TGCCAGATGT TACCATAAAT CTCCAATGTC	300
CAGAGATCCA CATCAAAGNT GANTGGGAAG GNCTTCGTNA GCATGATGTA TGCTTTTAA	360
ATTACCGTAC GNTCCCACAA AACCTT	386

(2) INFORMATION FOR SEQ ID NO:743:

(i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:743:

GGCANAGGET TGCTGCTGGG GAAGATCTGG AGGTCCAAGT GCTGCANGGC ATCTCTGGGA	60
AGAGCCAGAT CCTGTTTGCT CTCGTCTTCA CCACCAGGTA CCTGGACCTG TTCACCAACT	120
TCATCTCCAT CTACAACACA GTAATGAAGG TGGTTTTTCT CCTCTGTGNC CTATGTTACA	180
GTGTACATGA ATATATGGGN AAATTCGTA AAACTTTTGT ACAGTGNAGA ATGAACACAT	240
TCCGCCTGGG AGTTTCTTCT GGTCCCAGTT CATTGGCCTT TTCCTTCCTT GAAAACTACA	300
GTTTTCACCTC TGCTGGGAGA TTCCTCTGGA CTTTTTCTAN GCTATNNGGG AATTCATGGG	360
NNATCCTGTC CCCAG	375

(2) INFORMATION FOR SEQ ID NO:744:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:744:

TCGGACGAGT CATGGGCTCC CGNAACAAAC GTGAGGNCTG NCAGNGTCAA ATTTACCCTN	60
GTCCAAGATC CGCAAGTCCG CCCGATGAAC TGA CTGACGC TTGATGAGGA AGGNCCCACG	120
GCGTCTNGTC GAANGCAACG GCCTGTCTAN CGGAGGG	157

(2) INFORMATION FOR SEQ ID NO:745:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:745:

GGCANAGCTA CAACCAGCTG AGCCGTGCCG TGCCTAACTG GCGCGGCNCT TGCCCAACCT	60
GCCCGAACGC AACCAGTTCC GCGTGCCNCT TCGGCCGGCT GCTGGACAAG CTGTATGCTC	120
TCGGCTTGGT GCCCACGCGC GGTTGCTGG AGCTCTGCAC TTTNCGTNAC GGCCTCGTCC	180
TTCTGCCGCC GNCGGCTCCC CACCGTGCTC CTNAAGCTGC GCATGGGGAA CNCTTTCAGG	240

GCTGCCGTGG CCTTTTTGGG AGCAAGGGCA CGTAACGTTT TGGGGCCCTG AACGTGGGTT 300  
TACCGAACCN CGGNNTTTTC CTTGTTNAAG GGGGNAAAT 339

(2) INFORMATION FOR SEQ ID NO:746:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 358 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:746:

AGGCCTGTAC TACCACCGGT ACCTCCAGGA GGTCAATCGAT GTACTGGAAG ACGGATGGGC 60  
ATTTCCAAGA GAAGCTGCAG GCTGCGCAAT GCGGAGGAAC ATCANGAAGC GGGAAAGCTG 120  
AGCCGAGAGC TGGNACTTTN TNAGCCACCA CGTCCGCACC AAGCTGGNAT GAGCTTCAAG 180  
CGANCAGGTA GGTGTTCACG GACTGCGGAT GTTTGCTTCA AGGCCAAGNA TGGACGCCGA 240  
GCAGGGATCC CAATGTGACA GGTGGNATTC ATCTGGAATC TGCCTGGAAA CAGTTTTGGA 300  
ACACCTGGNA CCCTTCAGGA ACCAGCATAC ATTTTCGAGNG CCCGNGAACC TGGNAGTT 358

(2) INFORMATION FOR SEQ ID NO:747:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 306 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:747:

GGCAGAGCTC AGACATGCAA GANGTCATTG GCTCANCCAT TGCTATCAAT CTCCTGTCTG 60  
NAGGAAGAAT TCCTCTGTGG GGTGGCGTTC TCATCACCAT TGCAGATACT TTTGTATTTC 120  
TCTNCTTGGA CAAATATGGC TTGCGGGAAG TAAGNNAGCA TTTTTTGGCT TTCTCATCAC 180  
TATTATGGCC CTCACATTTG GNATATGAAG TATGTTACAG TGAAACCCAG CCAGAGCCAG 240  
GTTACTTCAA GGGNCATGTT CCGTNACCAG GCTGTTTCAG GCTGTTTCGNA ATTCCACAGA 300  
TTGNAN 306

(2) INFORMATION FOR SEQ ID NO:748:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 454 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:748:

GGCANAGCCA CTGTCTCCTT TACCACAGGG AATATGTCAG TGGATTGGA AAAGCTATGA	60
GGATGCCCCAT GTGGAGTTCA TACACAGTCC CCCAGTTGGG AGACACATCG CCTCTGCCTC	120
CCACTGTCCC AGACTGTCTG CGGGCTGATG TCAGGGTTCC TCCTTCTGAG AGCCAAAAAT	180
GTTCTTCTA TTTAGCAGAC AAGAATATCA CCCACGGCTT CCTCTATCCT CCTGCCAGCA	240
ATAGAACATC AGATAGCCAA TATGGTGCTT TAATTACTAG CAATTGGTA CCTATGTATG	300
AAGAATTTC AAAAAATGTG GGACTACTTC CACAGTGGTN CNTNTTGANA AAACATGGCC	360
ACAGAAAGGA AATGGNGTTA AATGTGGGT TAGTGGGACC ATNATTGGG TTNTAATTAT	420
GATGGGNCNT TTGGTGTTCC AGTGAATTTA CCAA	454

(2) INFORMATION FOR SEQ ID NO:749:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:749:

GGCAGAGCC GCCTGCAGGG AGGAGAATGT ACCCACTGG NACCTGNAGC TCCTGGTCCC	60
TCAGCCAAGA CCTGAANGNG TCCCCAGCCA GCCTGCTGCT GGGGACCCTG TGGCTTGCTG	120
TCAGTGATG GGGCCTCTTG GCCTTCCCCT GGGGAAGTTC ACCCNTGTTA CCCCAGCTTG	180
CCTTGCCCCT GGGNCCTTTT NCTGGGCCCC AGTGNCTTCC TGCCTTTGAC ATNAGAACTT	240
G	241

(2) INFORMATION FOR SEQ ID NO:750:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:750:

CCACCTGGTN CTGCAAGGAC CAAGNGGTCT GTCCATTCAA GGAATGCCCC GAATGCCAGN	60
AGAAAAAGGA GAGAAAGGAG NTACTGGNCT TCCAGGTCCA CAGGGTATCC CAGGAGGCGT	120
TGGTTCACCA GGNACGTGAT NGGCTCACCA	150

(2) INFORMATION FOR SEQ ID NO:751:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:751:

GGCAGAGGTA CACGTGCCTC GAGCTGCCAC CTCCGGAGTG GGGCTGGAGA ACGGCATCCC	60
ACGGGGACCT GATCCGGGGC ACGGTGCTCA CCTACCAGTG CGAGCNTGGC TACNAGCTGC	120
TAGGCTCCGA CATTCTCACT TGCCAGTGGG ACCTGTNTTG GAAGCGCCGG CCGCCCCGNT	180
GCCAAAAGAT CATGAACTTG TGCTGACCCT GGCGAGATTN CCAACGGGCA CCCCACNGCC	240
TTCGGAACGC CGGCTTCCCC GTTGGNTCCC ACGTTNCAGT ACCGCTGCCT GCCAAGGTTA	300
CAGCCTTCGA GGGGGCAGCC ATGTTACCT GNTTACAGCC GGGGACAAAG GCACANCCAA	360
TGGNAGNATT AGGGTTCCCC AATGGGGCTT TGAATAAGGA GCCTNGCCTT AAACCGGGGG	420
TTNCGAGAAT GGTACCAAA GTTTTANAGA ACATTACCAG GGGGGGATTT TTGGGTTTTT	480
NTGNTATTAG GGTTTTAG	498

(2) INFORMATION FOR SEQ ID NO:752:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:752:

GGCAGAGGNN NNCACCCACA TTACCTGCTT TCTTCTTGGG TAGCTTGTCC ATCAGCTCCA	60
CCCCTTGTGA ACACCTTTCT GAAAGCTGGA GGGCTGGGAG AAGGGGGTTG TATTCATCAA	120
TGGCCAGAAC CTTGGACGTT ACTGGAACAT TGGACCCAG AAGACGCTTT ACCTCCCAGG	180
TCNNCTGGTT GAGCAGCGGG AATCAACCAG GTGCATCGTT TTTGAAGGAG ACGATGGCGG	240
GGCCCTGCAT TACAGTTCAC GGGAAACCCC CCACCTGGGG CAGGAACCAG TACATTAAAG	300
TGNAGCGGTG GCACCCCTC CTGCTGGTGC CCATGGGAGA CTGCCGGCTN CTNTTGACCT	360
GAAAGNCTGG TTGGTTGTTG CCCCAACCTT CATTGCAAAA GCATTTNCTT AANTAGNAAC	420
TTCAGGGATT GGGGGTTAAA ATTTGCCCTG TTTTAGTTNA AAACCTAAGC TTN	473

(2) INFORMATION FOR SEQ ID NO:753:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 434 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:753:

GCACCCCAAC ATCGACACGG CCAGTTTNTT CCGCTGGCGG CATCAGGCCC GGGTGAACG	60
CATGGNGCAG TTCCAGAAGG AGAAGGAGGA ACTGGACAGG GGCTGCCCGG AGTNCAAGCG	120
CAAGGTGGCC GAGTGCCAGA GGAAACTNAA GGAGCTGGAG GTNGCCGAGG GCGGCAAGGC	180
AGAGCTGGAG CGCCTGCAGG CCGAGGTACA GCAGCTNCGC AAGGTGGAGC GGNGTGGGNA	240
GCAGAAAGCT GNNAGGAGAT TGC GCAAGAT AGGNGNAAGT AGCATGCCCT GGTAACGTGG	300
GACANGCTTC NGCAAAGACG GCTTTCAGCA AAGAGCCATG GTTAAATTAC CAAGCCCCNG	360
TAAGTACGGT GGTAGGNATT CAAAGGTGGT NTAGGGTAGC CAGAAACACA AGGACTTTCT	420
TGGNAAANAT TACG	434

(2) INFORMATION FOR SEQ ID NO:754:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 375 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:754:

GGCANAGGNA CTGTAAAAAT GAAAGTCCTA ATGGGAAACC CTCTTCTCCC CACACCCCAG	60
TTGTTGGGCT CAAGTCTGCT CTGNAGTCCT GATCTCCCTT GAATTGAGTC TCAGCATCTT	120
CNNGTTGCCT CCACCTGCTC GTCTGTNAAT CCCATTCCCT GCAGACAGTG GAACAAAGTC	180
ACTGGTAATC TTCCTCAT TG CCCTGGGACT GCTCCAGAC ACAGCTATTT GGGACCCAGA	240
TCTTCCCCAC CAAGCCATGG GCGANATCTT GTTGAGTAAG AGTTTCAGTC CTGGGGTCTT	300
ATTTCCCCCA AACGTGGTAG GGGATCTTGG ACCCNATGT CTCTGNTTTT TTCCTAAGGN	360
CACAGAGGNT GTGGG	375

(2) INFORMATION FOR SEQ ID NO:755:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 301 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:755:

GGCAGAGCAG AGTTTGACAG GGAGATAGAC CGGGGATCCN GGANCCCTTN TNAACAGCTG	60
TTTGAGAAAG ATGGTCAGTG GCATGTACTT GGGAAGAGCT GGTTCGACTG ATCCTAGTCA	120
AGATGGCCAA GGAAGGGCCT CTTATTTGAA AGGGCGGATN ACCCCGGAGC TGCTCACCCG	180
AGGGNNAGTT TAACACCAGT GAATGTGTCA GCCATCGAAA AGAATNAAGG NAGGCCTCCA	240
CAATGCCAAA GAAATCCTGG ACCCINNCTGG GAAGTTGGAG CCNTTCCGAT TGATGGACTG	300
T	301

(2) INFORMATION FOR SEQ ID NO:756:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:756:

ACCCTCCTTT CCTGCAGCTC CAGCTTTNTG CTCTGCCTCT NAAGGAGACC ATGGCCCAGC	60
ATCTAANTAC CCTGNCTGCT CCTGCTGGCC ACCCTAGCTG TGGCCCTGGC CTGGNAGCCC	120
CAAGGAGGAA GATAGGATAA TCCTGGGTGG NCATCTATAA ACGGCGAACC TNCAATGAAT	180
GAGTGGGTAC AGCGTGCCCT TGNACTTCGC CATCAGCNAG TNATGAACAA GGNCACCAA	240
AGATGGACTT ACTNACAGAC GTCCGNTTGC GGGTTACTTA AGAGCCAGGC AACAGACCGT	300
TGGGGGGGGT GAATTAATTN TTCGACGTGG AGGTNGGCCG AACCTATGTT ACCAATTCCC	360
ANNCCAATTG GGACAANGTG	380

(2) INFORMATION FOR SEQ ID NO:757:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:757:

TTTTGCCCCG TTGGGATTGT NATGGGTGTC CCATTGAAAT AAAAGTATTA TCAGAACTTG	60
GTAGAGAAGC TCAGAACTT TCAGCTATGG AAATTAGANN GAAAGCTAGA TCATTTGCTA	120
AAGCAGCCAT TGAGAAACAG AAATCAGCAT TTATTCGTTG GGAATAATG GCAGATTGGG	180

AATAATTGGC TACTATGACA TTTGAATGGG NAAGTNTGAA GCCAAACAGT TGAGAAACTT 240  
TTTACCAAAT GTATGATAAG GGCTTGGTTT ATCGTTCTTA CAAACCTGTN TTTTGGNCTC 300  
CGTNCATCTA GGACGNCATN GGCTGAAGCA GAACT 335

(2) INFORMATION FOR SEQ ID NO:758:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:758:

AGTAGAAAAA TCAACAGAAC AAAGGAAGAG TATGGCTCCT GAACCTACAC AGAGCTCTAC 60  
AGTAGTCGCA TCTGCCCAGC AAGTGAAGAC AACGCAAAC TCAATGCTC CTGAATGTAA 120  
ATGAATGCAA TTNTGAAACT GATTCCAATG AATTTTGAAT GTTAAGGGAA ACCTCCCATC 180  
CATTTAGTGG ATTTCTNCAT CTAGATCTAC ACATATGTGA ATGACATTGC ATGGCTAAAA 240  
GAAAAAGAGT CCAAACAGAC GTATTACTGG AGGGGCCAAT GCCAACTTNT CTTTTNACAC 300  
AGCTAACTAT AGGNTTATTT NTNCCTTATC C 331

(2) INFORMATION FOR SEQ ID NO:759:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:759:

ACTGTGGACA TGATGTATGG TGGCATGAGA GGCATGAAGG GATTGGTCTA TGAAACATCA 60  
GTTCTTGATC CTGAATGAGG GCATNCGTTT CCGAGGCTTT AGTATCCCTG AATGCCAGAA 120  
ACTGCTACCC AAGGCTAAGG GTGGGGAAGA ACCCCTGCCT GAGGGCTTAT TTTGGGCTGC 180  
TGGTTAACTG GGACATATCC CAACAGAGGA TNAGGTATCT TGGGCTCTTC AAAAGAGTGG 240  
GCAAAGAGGG CAGCTCTGCC TTNCCATGTG GTNNACCATG NTGGGACAAC TTTCCCACCC 300  
AATCTACACC CCATGTTTTT AGCTCAGTGT CAGTGTTTAC ANCCCCTTCA ACATGGAAAG 360  
TTAACTTTNN CCCGNGCATT ATGGCACCAG GGN 393

(2) INFORMATION FOR SEQ ID NO:760:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:760:

GGCANAGGAT TTTGTGCCCG GCTGGGATTG TCATGGGTTG CCCATTGAAA TAAAAGTATT	60
ATCAGAACTT GGTAGAGAAG CTCAGAATCT TTCAGCTATG GAAATTAGAA AGAAAGCTAG	120
ATCATTTGCT AAAGCAGCCA TTGAGGAAAC AGAAATCAGC ATTTATTCGT TGGGGAATAA	180
TGGCAGATTG GGAATNAATT GCTACTATAC ATTTGATGGG GAAGTATGAA GCCAAACAGT	240
TGAGNAACTT TTTACCAAAT GTATGATAAG GGCTTGGTTT ATCGNTCTTN ACAAACCTGT	300
GTTTTTGGTC TCCGTGCATC TNAGGGACTG CCATTGGGCT GGAAGCAGAA CTTGNATTTN	360
ATCC	364

(2) INFORMATION FOR SEQ ID NO:761:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:761:

AAAGCTATGA GGATGCCCAT GTGGAGTTCN TACACAGTCC CCCAGTTGGG AAGACACATC	60
GCCTCTGCCT CCCACTGTCC CAGACTGTNT GCGGGCTGAT GTCAGGGTTC CTCCTTCTGA	120
GAGCCAAAAA TGTTCTTCTT ATTTAGCAGA CAAGAATATC ACCCACGGCT TCCTCTATCC	180
TCCTGCCAGC AATAGAACAT CAGATAGCCA ATATGAATGC TTTAATTACT AGCAATTTGG	240
TACCTATGTA TGAGGAATTC AGAAAAATGT GGGACTACTT CCACAGTGTT CTTCTTATAA	300
AACATGCCAC AGAAAGAATG GNGTAAATGT GGTTAGTGGA CCATATTTGN TTATAATTAT	360
GGTGGGCCAT TTGNNGCTCC CGATGGAATT ACCCAACCTT TGGGCCAACA NGGTGTT	417

(2) INFORMATION FOR SEQ ID NO:762:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:762:



TTAAGAGTTC CCAGAAATAC ATTTGCCACC AACAGAGTAG CCAAATTTAT AAGGAAAAAT	60
GATTCCCAAT GGATATTTGA TGTTTGAGGA TGAAAATTTT ATTGNGTCTT CTGTTGCCAA	120
ATTAAATGCC CTGAGGAAAA GTGGCCAGTT CTGTGAATGT TCGACTTCAG GTCTGTGGCC	180
ATGAANGTTA GCACACAGAG CAGTGCTAGC TTGCTGCAGT CCCTATTTAT TTGGAAATCT	240
TTAATAGTGA TAGTGGTCCT CATGGAATTT CTCACGTTGA AATTTTGATG ATCTCAATCC	300
CAGANGCTNG TTGGAAGTCT TGGTTGGNAT TNTGGCCTAC ACTGNTCCAG TT	352

(2) INFORMATION FOR SEQ ID NO:763:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:763:

GGCANAGCTC GGCATGTGNC GGGAACCTGA GGGACTTGTC GGGCCTCAAT NATCTGCTCA	60
ACGTGCTGCA GAGCCTGCTG CTCCCGTTTCG CCGTGCTGCC CATCCTCACG TTCACCAGCA	120
TGCCCCACCT CATGCAGGAG TTTGCCAATG GCCTGCTGAA CAAGGTCGTC ACCTCTTCCA	180
TCATGGTGCT AGTCTGCGCC ATCAACCTCT TACTTCGTGG TCAGCTATCT GCCCAGCCTG	240
CCCCACCCTG GNCTACTTCG GCCTTGCAGC CTTGCTGGCC GCAGNNTACC TGGGCCTTAG	300
NACCTNACCT GGT	313

(2) INFORMATION FOR SEQ ID NO:764:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:764:

GGCACGAGAG AGAAAATCAT CAAAGAAGAT TCTTTGGGGA TCCTCTTCCC TTTTAGAGAC	60
CGGGGTAAAT TTAAAAACAC TGCTTGTAAC ATTTGTGGCA AAACATTTGC TTGTNAGAGT	120
GCCTTGGNAC ATTCACTATA GAAGTCATAC CAAAGAGAGA CCATTTATTT GGCACAGTTT	180
GCAATCGTGG CTTTTCCACA AAGGGTAATT TGAAGCAGCA CATGTTGACA CATCAGATGC	240
GAGGTNCTGC CATCCCAGCT CTTTGAGCCC AGTTCCAACC TTGGCCCCAN TCAGAACTTC	300
AGCGGTGATT TCCCGNCAAN TCGTTGTTCA TCTCTTCATT CAAGACAGAG GGTCCAACGG	360

GNTTTCGTGG CCAGTTTTTT TCCNCCAGGG CCCGTTAAAG GGCCANCCCC CA

412

(2) INFORMATION FOR SEQ ID NO:765:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:765:

TTGTGCCCCG CTGGGATTGT NATGGGTTGC CCATTGAAAT AAAAGTATTA TCAGAACTTG	60
GTAGAGAAGC TCAGAATCTT TCAGCTATGG AAATTAGAAA GAAAGCTAGG ATCATTTGCT	120
AAAGCAGCCA TTGAGAAACA GAAATCAGCA TTTATTCGTT GGGGAATAAT GGCAGATTGG	180
GAATGAATTG CTACTATACA TTTGAATGGG AAGTATGAAG CCAAACAGTT GAGAACTTTT	240
TACCAAATGT GATGATAAGG GCTTGGTTTT ATCGATCTTG ACAAACCTGT GTTTTGGNTC	300
TCCGTTTCATC TGAGGACTGN CATTGGGCTG GAAGCCAGGA ACTNGNAATN	350

(2) INFORMATION FOR SEQ ID NO:766:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:766:

GGCACGAGCC AAAGGCCATG TACTCTGCGG GCAGGATGTG GAGAGGGGCA CATTTCAGTNA	60
CCGGCACCAT GTTCTCCATG ACCAGGAGGT TGACCGCAGA CGTGTGTNCC TATAANTCAT	120
CTCTGGCCTG ACCAGGCCCC GTACACCGTG TGCAANAGCT CCCTCTCGGA GTACGGAGTC	180
CTGGGCTTTA AGCTGGGCTA TGCCATGGCC AGCCCCAATG CCCTGGTCCT CTGGNAGGCC	240
CAGTTTGGGG ACTTCCACAA CACGGCCCAG TGCATCATCG ACCATTTCATC AGCACCGGCC	300
AGGCCAATGG GTGCGGCATA ATGGCATTGT GCTGCTGTTG CCCCCTGGGA TGGAAGGCAT	360
GGGCCCAGNG CATTTTTNAN GAAGGCCNNA AGTTTCTGCA GT	402

(2) INFORMATION FOR SEQ ID NO:767:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:767:

GGCAGAGCCT CTCCGCACCA CCTCAGCGGG CAGGAGGTCC CACCATGTGN ACAGACATAG	60
CCCAAGGAGG CACCACAGGT CTATGTGTGC TGGGGGATGT NAGGTGCCAC CCAACGCTGT	120
CCTGGTGGTA TTTACAATGA ACATCCTCCT CCTCCATCAC TCCAGGGGTG GTGTCTCGGC	180
CGCCCCTACC AGCTGGCTGA GCCCCCTGGC CTCCTGCGNT TCCCTCACTT CCCTCAGTTC	240
CCAAAGCTGC CCAGTCCATG GGGGACAGAA CCGTNACTCA GANTCCACAT TCAAGTGTGG	300
CCCACCCTGC AGTCTTCATC CTTTCATTCAG CTGCTGCCTT NTGGAGGTGN CTTTGGGGCC	360
ACATGTGCTG TGGTGTGTTGT TTTCTNGGA CAGGAGNCTT TTCCANCAGN AGGTTGGGTT	420
CCANGGGTGC GTTTGAAATT CTTCTTTGG GANCTTGGTT TTCCGGNGAA CTTTCTTTGG	480
GGCCTGTTTA AGAAGGTGGT GCNG	504

(2) INFORMATION FOR SEQ ID NO:768:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:768:

GGCANAGCAA AGAGAGAAGG TCGGGTACTT CAAGAAGAAA TGAAAGAAGG GACAGACATG	60
TTCATCATCA AGGCTGTNCT GCCTGTTGCT GAANCTTTGG TTTTCCTGAT GAAATCAGNA	120
AGAGGACAAG TGGCCTGGCC AGCCCACAAC TAGTATTCAG CCATTGGGAG ATCATTCCCA	180
GTGAACCCCT TCTGGGTGCC AANNACTGAG GAGGAATACT TGCACTTTGG GGAGAAGGCT	240
GACTCTGAGA ACCAAGCCCG GAAGTACATG AACGCATACG GAAAGCGGAA GGGGNTTTTA	300
TGTTGGAAGA AAAGNTTTTG GGGCATNCCA GAAAAAGCCA GGGGNCCCTT NGGCAAAATT	360

(2) INFORMATION FOR SEQ ID NO:769:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:769:

GGCAGAGGCT CCAACGGCTT CTCAGACCCC TACGTCAAGA TCTACCTGCT GCCTGACCGC	60
AAGAAAAAGT TTCAGACCAA GGTGCACAGG AAGACCCTGA ACCCCGTNTT CAATGAGACG	120
TTTCAATTCT CGGTGCCCCT GGCCGAGCTG GCCCAACGCA AACTGCACTT CAGCGTCTAT	180
GAACTTTGAA CCGCTTCTCG CGNCAGGACC TCATCGGNCA GGTGGTGCTG GACAACCTCC	240
TGGAGCTGGT CCGAGCAGCC CCCTGACCGN CCGNTCTGGA GGGGACATCG TGGAGGGCGG	300
CTTCGGGAAA AAGCAGATCT TGGGGAGCTT CNNCTTNTGC ACTNTGGTTA CCTNCCAAG	360
GGCCGGGGGG CTTCACCTGG A	381

(2) INFORMATION FOR SEQ ID NO:770:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:770:

GGCAGAGNAG CAGGCACTGG NGGAGGGGGC TTNAAGGAGG GAGTGCCCCC TCAAACCTCCC	60
TGCTTCCCTG GANCTTCAGG NAAGCTCAGC CTCAGCCTTC AGGCCTGAGC AAGTGCAGGG	120
CGGANTAACC AGCCCAGGTT CAGATGTTGG GGTGTGAAAG CCTCAAGTGA ACTCAGCCTG	180
GTTGGAGAAC TGCCCCACCC AGTATCTTCT GTGCCATGGT TCCCACATTC GCACTCCATG	240
GCCTCCTGTC CTGGNACCCC ACGTTTTGNA ANGTAACCCC TAGGNACCAT GGGATTACCT	300
CTGTGAATTC ACGNTTGAGC CCAAGTTCCC CACAATGGAA AACTGGGGAA ATGGCCAGTT	360
GTGTGTTCCC AGGAATTNCT TCCCTTANTG TTNCCTTGAA GTGCCCAGC ATGTAGGGCA	420
AGAAGGAAGG TTGAAGCGTT TTCCTAGNG GAATTTTTCC TTCAGGGGGG CTCNATTTTT	480
GNCCAT	486

(2) INFORMATION FOR SEQ ID NO:771:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:771:

GGCAGAGNCA ACGNGNGNCT TCCTGGAGAG CAGCAACAGC ACGGACTACA TTGCCATGCA	60
CGACGTTGAC CTGCTCCCTC TNANCGAGGA GNTGGACTAT GGCTTTCCTG AGGCTGGGNC	120

CTTTCACGTG GCCTTCCCGG AGCTCNACCC TCTCTACCAC TACAAGACCT ATGTCGGCGG	180
CATCCTGCTG CTCTCCAAGC AGACTNACCG GCTGTGCAAT GGGATGTCCA ACCGCTTCTG	240
GGGCTGGGGC CGCGAAGGAC GGACGAGTTC TACCGGGGGC ATTAAAGGGA GCTGGGN TTC	300
AGCTTTTTTTT CCGCCCCTCG GGGAATTCAC AACTGGGTNA CAAGACATTT TCGCCAACTG	360
NCACGANCCA GNCTGNTGGA AGAGGGACCA GAAGCGCATT GNAGTTCAAA AACAGGNGCA	420
GTTTCAAGGT GGACAGGTNG GGAAGGCTGA ACATNTTAAG TTACCATGTT GGTTTTCCGG	480
ATTGCCTGTT	490

(2) INFORMATION FOR SEQ ID NO:772:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:772:

GTGTGGGGTG CCGNGGTGAC CGNAGNCAAA NAGGNGGTTG TGGCTCAGTG CATCCACTCT	60
GGGAGAGCGT GGACCTGGTT CCTGGGGGCG ATCGACAGTC ACNMNTNAAC ATTCCGTGGA	120
GGGACAGTGT TTATGATCCC GGCTTAAAC CACTGACCAT CTCTTATGAC CCNGCCACGT	180
GCCTCCACGT CTGGAATAAT GGGTACTCTT TCCTCGTGGA ATTTGAAGAT TCTACAGATA	240
AATCAGCTGC ACTTAGTGNA TTGGAACGCA NCAAAATTGA AAAC TTGAG GATGCAGCAC	300
TGGAAGAAAA TGGTTTGGCT GTGATAGGAG TATTTTAA GATTTCGGGA AACTTCTGGC	360
AGCCCAAGTGT CTA CTGGAAG GCCCAAGCCG NTTGCCAGAA AGTGGGGCCC GCCCAAAAAG	420
ACTGGGTTTT GCAGTCCAGG CCTTNCTNAG TTNCCAGTNC CAGGGAA	467

(2) INFORMATION FOR SEQ ID NO:773:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:773:

AGGCACGCAG CCTACTAGGT GTGGCGGCGA CCCTGGCCCC GGGTCCCGT GGCTACCNGG	60
NGCGGCNGCN CCCN	74

(2) INFORMATION FOR SEQ ID NO:774:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 370 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:774:

ANACCACCTG TGGTCTCACT AACCCCAAAA CTGCGCTCNA CCCGGCTGCN TCCAGGGTCT	60
CTAGTCCCCC CACTAGAGAC TGANAAGTTG CCTCGCAAAC NAGCAGGGGC CCCATTTGGT	120
GGGAGTCCTG GGCTGGCAAA GCGGGGCCGC CTACAGCCCC CAANTCCCCT GGGGCCTGAG	180
GGTTCANTAG AGGAGTNTNA GGCTGAAGCC TTAGGTGAGT TAGGAGGAAG GGGATGGGAC	240
CCCACGGCCG ACNTCCTGGC CCCCNCGGC TTGTTGGGAC CACCAACCAA GGGGACCAGC	300
GNATCCTTGG CAGAAGGNCC CTTCTTCCT TGGTTGNCC TGTTTTTAAN TCAAAAGGGG	360
CCNAAGGCAA	370

(2) INFORMATION FOR SEQ ID NO:775:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 370 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:775:

GGCAGAGCGA ATTTGTATGA NATTAGCCGG CCGTGGATTC ANAATCGCTC TTTGTGTGAT	60
GGGTCCCAGG GGTTCCTTTT NACCACAGAG CCAGCCTGAA ACTACCCACG GGTGCTGTGG	120
ACCCCTTGAA TCATGGCGGG ATGGAAATGG GCTGTGCCTN CAGCCGGGNA CTCAGGACTG	180
NAGCATGTNT GGGCAGCAGC CTGGTAAGCT GGCCAGCCTC GCGCCCTTG GGGACAGCCC	240
TTGAANACTC TGGCTTCGGT GCCCTGAGTG AGGGGGCGCC ACCCTGGGCT TCCCTGGGAT	300
GCGAGCAAGA CCCAAGNCAG GNTGNTGGAA CCGGGACAAT TCGNGTCATG TTGCTGTTGT	360
NCCCTTCCTG	370

(2) INFORMATION FOR SEQ ID NO:776:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 521 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:776:

ATCCCCCGGG NCTGCAGGAA TTCGGNACGA GAGTTAAACA CTTNATTTCC TCCCAACAAC	60
ACTAGAGCGT TGGCNATNAT AACCCCCATT TAATGGATTA GGAAACCAAG GAACCATGAA	120
ATTAAAAAAC TTGCCCCAGG ACATACAGCT AGGTTTTCCC AGGTCCTGCT GCAAGGAGGC	180
GGCCAGGTCC TGCTCGGTTG GACACTCCAT TACTTCCCGT TTTTCCTGAT GGGCCGGGTC	240
CTCTACTTCC ACCACTACTT CCCAGCCATG CTCTTTTCAA AGCATGTTGA CAGGNCTTCT	300
TTGGGNACAC CCTCCTGAGG GCTCTTTGCC CTGGNGCTT GGNCTCCATG GGCCCTGGG	360
CGAAGGGGGC ATTNACANTG GCGGGGGGAN TCCTGANGCC NGNTTCCTGG GGGAAGTNC	420
CTNACAGTTT TTAAACNTT TNCCAACCTT TGGGTTTTAN GGGGATGGTT TGGTNCCCTG	480
GGGCCCAGGA CCCCCCAAAT TCCCATGGGN AGGACTAAGG T	521

(2) INFORMATION FOR SEQ ID NO:777:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:777:

TATCCATAGA TTCAGTGCAA TTCCAATAAA ATCCCAGCAG GCATTGTTGA AGAAAATGAA	60
CAAGCTTATT TNCAAATTCA CGTGGAAATG CAAAGAAGCC AAATTAGTCA AAACGGATTT	120
GAAAAAAAC AAAGTAGTGA CTTAACGTTT ACCTGACTTT AAGNATATAT TATNAAACCT	180
ACCTTACTCA AAACAGTATA GTAGTCATAT AAAAGATAAT GGGAACAGNN TTAGAGAACC	240
TAGAGGTAGG ACCCGGCACA ATTATGGACA ACTGCTTTTC CAACAAGGGT GCCAAAGGCA	300
TTCCGTGGGA AAAAGGAAAG TTTTTTCCAA CAATGGGTNT TCCTNTGTAA AATGGACNTT	360
AAATTCCTTC CCCTGTNTTT TNGGCCAAAT TGNCCCCACT GGGGTTTTCG GTCTAATGTA	420
AACCNCAATT TTAACCTCCT TGGGGAAAGG AACGTNGGGG AACCTTGTTN CCCGGGNTTG	480
GGGNACGTTT TAGGTTTGGG TCCA	504

(2) INFORMATION FOR SEQ ID NO:778:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:778:

AGGGGCTTGT TTTTATAT AGTGTGTTT GGGGAGGGG GACGCGGGAG GNTGCATGTT	60
TTGGGAAAAG GGGGTGACAG ACAACTTTTA AAAGGGCAGC ANACTCCCTC AGCCATGAGA	120
AACCAGCTTT GGGGAGGAAG GCCGGGAAAT CAAAGCGAAG TCCAGTTAAT CTCCCCTGAA	180
CANTTTGGGA AGTTCATTTT NCCCTCANTG CCAGCCAAAT CCGGGCANGA CCCTCGAAAG	240
AAGNACCGAG GGTCCCAAAG GACCAATGCT ACAACCAGCA AATGCTGCCA CATCTTTNNN	300
CTGATTGGGG GGTNGGGGAT GGGTTGGGGG GGATTGGGAC TNGGGGCCAA AGGGTTCCTGG	360
GGTGGGGCCA TTTTAAAC TTTGGGNGGN CTTTCCATT TTTTGGTTN AGGGCCAT	418

(2) INFORMATION FOR SEQ ID NO:779:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:779:

GGGCACACGT GGAGCTNAAC TTAANGCCAG CGGGGAGNCG GGGAGGCACT GCCCTCATTN	60
TTGCANTNCC TTNATTCTTT TGAGGGCACT GCCAGCCCGG GAACCACTCA ATCTNCTTNT	120
GGTTGAAAGG TTTGGTTCAG GAAGGNTGGT CTCCTGGTTC CCNTTGGGGT GCTTAATGAT	180
GCACTTNAGG GGCTTGCNAG GGGTGAAAGT CCTTGNAGGC CCTGATNGGT CCAGCTTNTC	240
CACAGGGTGA TNNTTGTTGT AGTCNAGCCG GGTCAGCAAN GTTNAGAGGC AGCAGGCCCT	300
GTTTTTTNCA GGTGTTCT CTGGATCCT GGCAAAGNTT TTTGGGTGAT TGATGGCCCC	360
GGCCCCAAG TTGGCGAGNT TCAAAGCTG TATGTTCCCG GTTTNGAAAC CTTGNCCTAA	420
TTTGGTTTC CAATNACCAN CCACTGATGC CAGTTTTTTT TAATAACGGG G	471

(2) INFORMATION FOR SEQ ID NO:780:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:780:

TTCCCGNTGT GGAGCGAGTG GACTCCTGCC CCTCCATGTA CAGCCGCTCC ATCCAGGGCC	60
ACCATGTCTG CCTCCTGGTG AAAAAGGGTG AGAACTCTGT CTNAGTCGAC GGGAAGTGCC	120



AGTGAAGCTCC ACGCTNACTG AAGCAACTTG TTAGNAAGAG AATGAAGGCG AACGCTGGCC	180
AAGTGTGAA AGCTGCCTGC AAGCCCCGCA CCACCCGAG GAGCACGTNA CCCAGGGAAC	240
CGCAGCCCTG ACGTGTCTCG CCTCTCCTGN AGTCGTGTGT ACTGTTACCC ANGCCTGNNG	300
TGTTTAATTT NAACTCTAAT GTTTGTNCCG NCGTTGTTNG GACATCCGAG GGTCCATTNG	360
TTNGGGGTTT GAAATTATTC TGGAACNTC CTTTTTTAAC GTGGAATTNT TANCCCTTTC	420
TTTTTNGGGG CAAGAAGTTC CCTTTTTTGG NGCCCCAAAA CCAG	464

(2) INFORMATION FOR SEQ ID NO:781:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 112 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:781:

AAAACGGGNA GTAAGGCAGT GGTGGAGATG GAGAGCCCTG AGCNTCCACT NTCCTGGCCC	60
CCAGTNTTCC TACATAAGGC CACGGCCCCG NTAATGGCGG GGCNAGCCC CA	112

(2) INFORMATION FOR SEQ ID NO:782:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 129 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:782:

CGNATGGCCC TGTCTNAAA ACGGGGAGTA AGGCAGTGGT GGAGATGGAG AGCCCTGAGC	60
NTCCACTNTC CTGGCCCCCA GTNTTCTAC ATAAGGCCAC GGCCCGGNTA ATGGCGGGGG	120
CNAGCCCCA	129

(2) INFORMATION FOR SEQ ID NO:783:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 320 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:783:

GGCAGGAGCA GGCACGGAGC CTNAGCCCAT CGCNATGCTG GTCCTAAGGG GCTCGTCCTN	60
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GAGGGGTCCT GATGCTGGGT GCCTGAAANA AGAGCTCGGG GAGCCCGCTG CAACCNAAG	120
GCCTGCCCAG CCGGGAAGCT GCCAACCCCC TGGTGGTGGG AAGCCGTGGC CCTCCTGGGA	180
CCTCAGCCTG GAATTCCTGT TCTCCAGCT CCTNACCTGA GGCTANTTCC TGGCCTGGTT	240
CTGGCTTTGG TTGCNTGCCT CTTNACCCT TTGAACCTGC CTTTTTTTC TTCTCCTNTT	300
CCTGGGTGTN TTTTTTCCA	320

(2) INFORMATION FOR SEQ ID NO:784:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 431 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:784:

GGCAGAGTG GCAGCAAGCC TCTCCTGCCC TTCCAAATTA GCCCATCGAA TGGTAAGGTT	60
CCTNAACTTT GGGCAGGTNA AGANCTGTGA AGGTGGAGCA GGTAAGGGG GTCACCTACT	120
CCCTGGAAGT CGTTCCTGGG CCCGCTTATG TGCCACAGAG GACCTGCCCT TCCCACCAGC	180
CGNGTCGTGT GAACTCCTTC AAGAACCAGC TGGTCACCCG GGAAAGGGGA ATGAAGCCTC	240
TATTNACTGT NTTCATCTTA CCTGGGCCCC TGGGGGACTA CCACTGGTTT NACTNCCCC	300
ACCGGACTGG NACTGTNTCC CACCGGGGGG NCAATTTTCC AGGGTTCCTG ATGTTCANTG	360
AAAANCCTGG GNATGGGTTG GTTGGTTTCA AAGAGGTTTT TTTGNCCATA AAGGAGGNGG	420
GTTGGGTTCT T	431

(2) INFORMATION FOR SEQ ID NO:785:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 122 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:785:

GGNANAGNCG TNAAACTAC CCCTAAAAGC CAAAATGGGA AAGGAAAAAG ACTCATATCA	60
ACATTGTCGT CATTGGNCAC GTTGTNTTCG GGCAANTCCA CCANTACTGG NCCATCTAAT	120
CT	122

(2) INFORMATION FOR SEQ ID NO:786:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:786:

GGCACGAGAG AAGATAAAAA AGTGAGGTGG ATTAAAGGGC CCATAGAGGA AGCCACCTGA	60
ACCCCCGGCC TGGCCTCCTT NTCGGCTCTT CCTCTCCGGG GGCCCAATAG GGCTGTGCGT	120
TTAANAGGCA GTTGGGAGAC CCTGGTGGCC GGTTTTGGTC GGTCACCTGGG CACGCGGCTG	180
GAGCCAATCA GAATCTCCCG GCAGTTGGTT CCCGGGAGGC AGAATCTGTT NAACTGACA	240
AAGCCACAGT TTCCGGGTCC CTGTTTCGGG GAGTCGGGGA CTNATTGGGT CACCCCGGGT	300
TAGTTCGAGA CTTTAGACTN GAGCTGTTTT NGGTNCACTC AGGGAGGCNA GTT	353

(2) INFORMATION FOR SEQ ID NO:787:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 120 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:787:

CACGCATNCA ACAAGGGCCC CTCGTACGN CTGTCGGCCG AGGTCAAGAA CCGGCTCCTG	60
TCCAAATATG ACCCCCAGAN GGAGGCAGAG CTCCGCACCT NGTATCGNGG GANCTCACCG	120
	120

(2) INFORMATION FOR SEQ ID NO:788:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 111 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:788:

GGCANAGAAA AGCCAAAATN GGAAAGGAAA AGACTCANAT CAACATTGGT CGTCATTGGA	60
CACGTAGATN CGGGCAAGTC CACCACTAAC TGGCCATCTN ATCTATAAAT N	111

(2) INFORMATION FOR SEQ ID NO:789:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 82 base pairs
  - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:789:

ACGATTCACA CCGTAGCCCT GGGGNAGACA NTGATTTGAT TACAAAACCA CCCAGACCTT	60
CCGGCTTGCC ATCATGNNTG TG	82

(2) INFORMATION FOR SEQ ID NO:790:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 124 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:790:

CATTCGTACG CGGGTGTGGT GTCAGTACAG CCACAGCCAG ATNCAGGAGC ACGTGANGCC	60
TGCNCANCCC AGCATCCGNG AACGTGCAGG AGCTCAAGGA AGCCATCAAG AGCCTGCATT	120
GGAT	124

(2) INFORMATION FOR SEQ ID NO:791:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 276 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:791:

GGCANAGTGA GTGACCGGCC TTTNAAGTGC GGCTACTGTG GTCGTGCCTT TGCCGGGGCC	60
ACCACCCTCA ACAACCACAT CCGAACCCAC ACTGGAGAAA AGCCCTTCAA GTGCGAGAGG	120
TGTGAGAGGA GCTTCACGCN GGCCACCCAG CTGAGCCGAC ACCAGCGGAT GCCCAATGAG	180
TGCAAGCCAN TAACTGAGAA GCCCAGAATC AATCGAAGTG GGATTAACGG GNTTGACTGG	240
TTGGNATTAA AACTGCAGGA GAAGTCCATG NTTNAA	276

(2) INFORMATION FOR SEQ ID NO:792:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 161 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:792:

AAGACCGGNC TTCNTAATAA NCTTAATTAA TTCCCCCGGN AATGTGGATT TTTCCTNGGA	60
AGGACGAGCA GGAGCTTTGC ATCACCATCA AGTAAACTGC AATCTCCTTT TTTTANGAAN	120
NTCTGGGAGG AATGAATTG AACTTAATNA AGCAGNACAC G	161

(2) INFORMATION FOR SEQ ID NO:793:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:793:

GGAGAACCAC GTGGNACAGC ACCATGAACA TTTTGGGCGG GGNAGGCAGT NCTGGCCGGT	60
AAGCCCCTCA AGTCGGGTAT GAAGGAGCTG GCCGTNTTCC GGGAAGAAGG TCACTGAGCC	120
AGCACCGGCA GATGGGCCAA GGNTGGCAAG CATCACCTTG GCCTGGAGNT AGCCCAANAA	180
GCTNCGAACC ACCCCCTGCN AGGACTCCCT GGCCAACAGG GAACTGG	227

(2) INFORMATION FOR SEQ ID NO:794:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:794:

GGCANAGCTG AAACGGGCAG AAGACAAAGC AAAGCTAAAA GAGCTGGAGA AACACAAAAT	60
CCAGCTGGAG CAGGTGCAGG ANTGGAAGAG CAAAATGCAG GAGCAGCAGG CCGACCTGCA	120
GCGNCGCCTC AAGGAGGCAG GAAAGGTAAG CCAAGGNAGG CGCTGGAGGC AAAGGAAACG	180
CTATATGGAG GAGATGGCTG GATACTNGCT GATGCCATTG AGAATGGCCC ACTTTGGGAC	240
AAGGGAGATT GGCTTGAAGA GCGGGGTNGA GTTCCCTNGC ANGCAAGGGA GGTGGGAGGG	300
CACTTNN	307

(2) INFORMATION FOR SEQ ID NO:795:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:795:

GGCAGANNCT TTGGATGACA ACGTCTGCAT GGCCTTTCCA GGTCTNCACC GCCGATGCAA	60
GGNTAGTNAT CAACAGGGCC CGGGTGGAGT NCCAGACCCA CCGGCTGACT GTGGAGGACC	120
CGGTCACTGT GGAGTACATC ACCCGNTACA TCGCCAGTTT GAAGCAGCGT TATACGCAGA	180
GCAATGGGCG CAGGCCGTTT GGNATCTNTG CCCCTCATCG TGGGTTTCGA ACTTTGAATG	240
GCGCTCCTAG GCTTNTATNA GACTGACCCC TTCGGGGCAC ATAACCATGC NTGGTAAGCC	300
ANATGCCATA GGCCGGGGGG TGCCAAGTTC AGTGCGTGAG TTNCCTGGNN GAAGGAATTA	360
TAT	363

(2) INFORMATION FOR SEQ ID NO:796:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 225 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:796:

GGCANAGNCT CAAACAGTGC AAGATGTCTC TAAACGGGCA GCGTGGNGGA GTNCTGGTGT	60
GTAAACCCCA ACACCGGGGA AGCTGATCCA GGGAGCCCCC ACCATCCGGG GGGACCCAAG	120
ATNTNAATCT CTTCTACAAT GAAGGCAGCA GGTGGCTCGC GGGGTGCACA CCCAGCGGNA	180
TGCAGTAGAA CCGCAGCCAN CCGGTGCCTG GNGCCCCTNA NCCCC	225

(2) INFORMATION FOR SEQ ID NO:797:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 295 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:797:

AGGCACACAG GACCATAAAG GTNCTTCTCC TNAAAGGGCT GGGGGCCCTT TNCTTNCGCC	60
TATAATTGGN ATGANAACTT CAACCCGNGT AAGCACCTGG AGTTGAAGGG AGGNAGAAAC	120
CGGGCCAGCT GTCCTGTCCT CCGCCCANAG TGACCACCCC GGNTATGGCC AGCNAGCCTC	180
CNGGGAGCGA GAGTCCTGCT GAAAGGGGCC ANGNTGGTTT TGGTGAGNAG CTGGCCTATC	240
ATTAGGGNGT TTGGGCTTCC ANCTGGTNGT NAATGCCCAA CTTAGGGGTT TCCTT	295

(2) INFORMATION FOR SEQ ID NO:798:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 232 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:798:

GGNANAGTGG ACAAATTCGN GGAGACCGCA TCAATTAAAA TCCAGATCAT TAACCGTCCG	60
GNTCCACCCC AAATTNTGAA AGATTAAAGGA TGTCTGGGGA GAAAATNTCG CTCTCANATG	120
GGNCTCCACC AAAGGAATGA TGGNAAATGC CTGCTTATCA NAGGCTTTTN CCATTNAAAA	180
GGCTGACAAA AGAGGCTGGA ATGGTTTTAC TGTNNATTGA AGCTTTNTTC AT	232

(2) INFORMATION FOR SEQ ID NO:799:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 407 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:799:

GGCAGAGNAT CAAATATTAT TTTATTATTT ATTTAATTAT TAATCAAATG TTTGTGTAGG	60
TCTATTTCTG GGATCTCTGT TCTATTTTCT TAATCTTGTG TCTGCTCCTC TACCAATACC	120
ACACTGTCTT TATTACCGTC GCTATATGGT AAGCCCTGAC ATCATGGAAT TTNCTTCTNT	180
TTCATACGTT TTGGCTATTC TAGTGTCTTT CCCTTTCCAT ATAAATTTTA AAATAAGCTT	240
GTCTATGTCT ACAAAAAAAT CTTTGCTGNG NATTTTGGGG NAAGGAATTG GCATTTAAAG	300
CATCNCGGGT CATGGTGGGC TTCACGGCTG TAAATCACAG CACTTTNGGA GGGCTGAGGG	360
CAGGNAGGGT TGTTTGTGGG GCCAGGTGGG TNNTGGAACT CCCGGNT	407

(2) INFORMATION FOR SEQ ID NO:800:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 471 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:800:

GGCAGAGCAA AAAGCAGGTC AGACAGGGCC AGGTTCAAGA GGTATACATC TTTAATGCTC	60
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CTCANCTTCT TGCAGACCAC AAGGACCAGG ATGACCAGGC TGTTCCTCCNG AAGATTGANT	120
ACAAACAGGA GGCAATAAAA GACAGCAAGG NGCAACTTGC CATTTNNTTTG ATTAAGTNCC	180
GCATCACAGG GGCTTGAGAA AGATATCAGG GTAGTAGTAG TCGGTCCTG TTGTCACACT	240
GAGGTCAAGT GTATAATCCA TCAAGGCAGC GGGACCTGGT CACNGAGGAC ACATAAAAGA	300
CATTCCACTC CTTAAAAACA TTTTTTTTTT TTAAAAATTA GGGGGATGTT ATGGGACTGA	360
ACTGTGTNCC TCCCAATTC CAGTTTTGAG GTGCTCAACC TCCGGTGTGG GTGTGACCAT	420
TGGGGTGGGN NNGACTATTT NGGNCCTTA AAGTTGTAAT TAAGGTAA T	471

(2) INFORMATION FOR SEQ ID NO:801:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 131 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:801:

CTGGTGGGGN TGCTGGAGAT GCCTTTGAAT GGCTTTGAAT TTTGGGNGTT GATCCTNGTG	60
ACCAGTTTTT CCCATCCCAT NNTGGCATGC GGTTCAAGTTC CTGGGACCAT GACCNTGGTA	120
AGTTTGAGGG C	131

(2) INFORMATION FOR SEQ ID NO:802:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 139 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:802:

CTGGAATTTT AGGCCANTNA GCCCAGGGTC TGGNAACGCA AGGCCTAACA ACCCAAATTG	60
GGGCACATTT TAAGGAGGTN TNAGGAATTT TAAGTCCCGG GGACAAGGGG GGGTTACCNC	120
ACGGAAAAAT TGGTCNNTT	139

(2) INFORMATION FOR SEQ ID NO:803:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 353 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:803:

CAATTCTCCT ACCGCCAGTG GTNTGACCAA AACGCGATTC CCAAAANTTG CGCCATGATT	60
NTCGCCGCCG ATGNANTTCA TTCCTGGCAA CGGTATTCCG GTCGATAGCN TGGTTATTGA	120
CCGCAAAATC AATCCGCTAC AGATCAAACA AGACGGTGGC AAAGNCTTNA AAACNCTGG	180
TGCTGTGGCG TAGTGATGAA GATGCGCAAA CGTNTGGTTA TGGTGAAAGA NTTCAACGAA	240
CTGTGCCACT CACACGGTCT GGTAAGCATC ATTGAGCCAT NCGTCCGTCC ACCGNGTCGT	300
GGCGATNAAT TTCGATCGGN AACAAGCGAT CATTCGATGN CCGCCAAAAA GTT	353

(2) INFORMATION FOR SEQ ID NO:804:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:804:

GGCAGAGCA GCCCCAATT TTTCCCTCCG GCCTGGGCGG CCCCTGGTCC NGGNGGCNAA	60
TGGAAGANCA AGGGACCTGC CCGGGGNC	88

(2) INFORMATION FOR SEQ ID NO:805:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:805:

TGTTGTTTTG TNGTTTCATT TTTTAAGACT CCCAGNTGGA CATNTTAATT GCTTTGCAAA	60
TNACCTGCTT CAAGGATGTG GGAATTCCT AATTNTTNCT GTGAACCCTT TTNAATTCCC	120
CCACCATGCG TNTNGTGAAC ACCTTCACCA ATAACATAGT CATGTATTTC CCTGCTGCCA	180
TATTTGGTTT TTTTCCACC TCGGGGATC CTTTTTTNTN ACTATNAAAA TNGGNTTCCT	240
CCATTCTGAA GGGT	254

(2) INFORMATION FOR SEQ ID NO:806:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:806:

TGGTGGCCAT CNTAGACCCC CACATCAAGG TGGACTNCGG CTACCGANTT CACGAGGAGC 60  
TGNGGAACCT GGGGCTGTAT GTAAAAACCC GGAATGGCT CTAACATAA GGGCTGGTGC 120  
TGGCCAGGCT CAGCTGGTTA CCCTGAACTT CACTAATCCN ACGATGAGGG CCTNGTTGGN 180  
TAACATGTTN CAGNTAATG 199

(2) INFORMATION FOR SEQ ID NO:807:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:807:

CCCANGGTGT NANCACATT GAGGAGGGTT TATTAAGTGN CCGTGGTCAT CGACCCCTTG 60  
AACAAGAAGA GAGANGTGGC TCACGGCCTG AGGCCTAACC NACCGACCNT CAGTGGAGGT 120  
GGCTATCGGG NTCGTCC 137

(2) INFORMATION FOR SEQ ID NO:808:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:808:

CTCTTCAGCN TCGAGGTCAC CTCCACCTTC TTTGCAGTGC GGGNACTACT NGCGGGGGCT 60  
TCTTNGGTTG CCCCCTTCAG TGGCCTTNCA TCTTCCGGGT TTTTGGGCGT CTNNGG 116

(2) INFORMATION FOR SEQ ID NO:809:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:809:

TTACCAACNT GANGCTGATT GAGTATTGNG GGAGCTTGG TTCGGAGACA GGCAAAGGAG 60

NCATGTTTGG TGAGNTTGGT TTTTCAGTAC TTCCAGAACC GNGANTGATT ATGGAAAGGA 120  
CCTNATGGAG AAGGT 135

(2) INFORMATION FOR SEQ ID NO:810:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 377 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:810:

GGNAGAGGGC AAAGGTGCTA TTAACCACTA CGTAANACCT GTAAAGCCTG GCCGCCTTGT 60  
TG TAGAGATG GGTGGNCGTT GTAAATTTAA AGAAGTNCAA GGTTTCCTTA ACCAGGTTGC 120  
CCACAANTTG CCCTTCGCAG CAAAGGCTGT NAAGCCGCGG GAANTCTAGA GAAGATGCGA 180  
AAAGATCAAG AGGAAAGAGA AACGTTAACA NCCAGAACCC CTGGNACATT TNAGCCGATT 240  
TAGCCACTGC CCAACATNCT GGGGCTTACG GGAAAGTTAC TTGGGCCCCAT ATGAATTTGA 300  
CCCACAAGGG GGAANTACTG GGGGCAAGTT NCTTACATGC CCCAAANGTG TGTAGTGNGT 360  
TTTAGGGGGT TAANTGT 377

(2) INFORMATION FOR SEQ ID NO:811:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 384 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:811:

AGGTGAAATG GATGANAATT CANTNTCCCC AAAGGCTTGT AACGANTTTA AGATCANTGG 60  
CTACCCCAAA CGGGGNCAGN AAACGGAGAA GCACAAACNA AACTNAATGC NTCCAATATC 120  
GAGGATCANT NTGAGANCAG AAGCCAATGT NAGTTTTGCA AGTTGGGATG TTGAGAAAGA 180  
CAGCCATCTT TGNCTTTCAA TATTTCCAC GTCAGAAACA AGGTTGCGATT CCTAGGAACT 240  
CCTTCCAGCT CTTACAACTN TGAACGGTTT CACAACAGAT ACTTGATCGN TTCTGGAAAT 300  
GAAAGNTGGC TTCTTTAAAA TCCAACCAAA GNGGGGGGTC CGCTACCTCC ACTTTCACAA 360  
GGAGGAGCCC GTGGGTGGNA NCCC 384

(2) INFORMATION FOR SEQ ID NO:812:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:812:

CTGGGAAAAG ATTGTCAGGN CATTGCCATT AGGGAGCTAA ACAGAGCGGG CTTTACTTTN 60  
TTNAACCCCTC TGNGAGATTN ACCGGCATT C TTAGTCTACT GTGAAATTCG NTGGGTCTGG 120  
G 121

(2) INFORMATION FOR SEQ ID NO:813:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:813:

GGGGGCCTGA TGTGCTCACA GCNACAGTTA GTGGGAAGCT GCCTACACAG AGCATNACTT 60  
TCCAAACGGA GTCCAGTGTG GCAGAGCAGG AGGCGGAGTT CCAGAGCCCC AAGTATATCT 120  
TCCACAACCTT CATGGAGAGG CTCTGGGNCA TACCTGAACT ATCCAGCAGC TGCTGGAGNC 180  
AAACTGTTTC CGCATCCAAT GCTGATCCAG CAGGCCCTCC GGNAACCAAG CGCTGNAATT 240  
TNTCCACTTG CCTACAGCTT TGTNACGGCT CTTNACATCT TTGGTTAGTT CACCAAACCC 300  
GGTTGACCCA AGAGGCAGTT TTCAAGTTTG NTTGNNGAAG GCCC 344

(2) INFORMATION FOR SEQ ID NO:814:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:814:

ACCTGACTTA ATTCGTTTCGN ATACCACCTG TTTCTGTNCT TCATTTAACA CAGGAGGTCG 60  
ACCAAAACGT TTCCCTGCGC CGCGGGCTCT NACTATCCCG GAATGAGTGC GTTCAAGTAA 120  
AAGGTCTCGT TCAAATTCAG CGACTGCTGA AAATTAATTG CATCATCATT TTTCCTGTNG 180  
GGNCTTGGTC AGGTCAATGC CCACCCCAAT GGTAAAGGCA AATGCACTGN NGATNACC 238

(2) INFORMATION FOR SEQ ID NO:815:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 295 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:815:

```
GGCANAGGGA AATNAGTTTT TGGCTAAACT TGGAACGTGC GTNATACCGC ATCCAGGAGA      60
AACGGGAGAG CCCGGAAGTT CTCCTGACTC TGGATATCTT GNAAACATGG CAAGCGCCTT      120
CCATGCCACC GTNAGTTTTG AACACTGAAC ACAGGTCTAA AACAGGCTTT GGGAAACTGT      180
GAAATGAACT ACAATCCTCT GAATGAAAGN TTTCCCTCTG AAATGGATTT GCTGTCTGCC      240
ACGGGGCTGN NACAAANTAA GACAGGCGCT TGTGTCATT TTCACACATT TNAGG          295
```

(2) INFORMATION FOR SEQ ID NO:816:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 332 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:816:

```
GGCAGANAAG GTTCTGTGGG CTGCNTTGCT GGTCACATTC CTGGNAGGAT GCACTCNAAG      60
GTGGAGCAAG CGGTGGAGAC AGAGCCGGAG CCCGAGCCTG CGCCANAACN CGNAGTGGCA      120
GAGCGGCCAG GCTGGGNAAC TGGCACTGGG TCGCTTTTGG GAATTACCTG CGNTGGGTGC      180
AGACACTGTN TNAGCCAGGT GCAGGAGGAG CTGCTTCAGC TCCCCAGGTT CACCCAGGTA      240
ACTGAGGGGC GCTGATGGGA CGNGAACCAT GTAAGGAGTT TNGAGAACCA AGTCTNNAAC      300
CAACATGGTG GAAATTCCCC GTTTTTTTAT NA          332
```

(2) INFORMATION FOR SEQ ID NO:817:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 274 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:817:

```
GGCACAGCTT GGCCTCCCAA AGTNCTGGGA TTGCGGGCTG GCTGCACGGG GGCAGGAGCC      60
TGNCCCTGAT TCAAAGGTTT CTGAGAGACT CGGTCTCTGG GGCAGAGGCC TGNGCAAGGG      120
```

GACCTCGCTG GGGTGTCTCT NTTTTAGCCA CGCTNCGGTG TTTCTGGGTC CTGTAACCCA 180  
CGTTTAAGCA GCCTGTGGTG CTGGTGGCAC AGGNGAAGGA AACCGAGGTC AGGGNAGCCT 240  
TTGGGGGCTG CTTTGNAGGG NACAGGCAGN TCCT 274

(2) INFORMATION FOR SEQ ID NO:818:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 288 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:818:

GGCACGAGGC GGCAAGAGCT TCANCCACAG CTCGCACCTN ACCGCGCACC AGGCATNCCA 60  
CCGTGGCGTG CGGCCCTACC ACTGCCTCGA CTGCGGCAAG AGCTTCAGCC GGCTGAGCCA 120  
GTTCGAACCC CGGNATGCAG CTCCGCNAGA CCCCAGTTCC CACGGAGCCC CAGGNAGTTA 180  
CCGTNTCCCG GAGAAAGCCC AACGAAGGAG GAGAAGGGCG CCCCGBAAGA GTNCGGAGGA 240  
GGGCCTGGNC CCTNAANAGT NAAGGTGGGG CAGGAAGAGC TTACCGGT 288

(2) INFORMATION FOR SEQ ID NO:819:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 101 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:819:

GGGGCTGGAC GCANGTGCAC TAANCATGGG TGAACCCAG GGATCCATGC GGGNTCTAGT 60  
GACAGGGGGT CTNGGCTTGT AGGCAAAGNC ATCCCAAAGG T 101

(2) INFORMATION FOR SEQ ID NO:820:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 213 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:820:

CATTGNATGT GGTTACCACC TTTNGTNNAT CCACTCATCC ATCGATGGNC ACGTGGGTTG 60  
NTTCCACCTT NAANCTGCTG TGAAATAGTG CAGTGTACCC TNTAAACATG GGTGTACTGA 120

AGAGCTCTTA TCAAGTGCCT TGANAACATC ACTGGAAAAT GTCCATGGGA CTCTGAAAGG 180  
TTGCCANAAG AATGGCNGA GGCTCTATNA CGA 213

(2) INFORMATION FOR SEQ ID NO:821:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 373 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:821:

GGCAGAGNCA CCCTTTCACC CTTCCCCCTA TCCAGGACAG TTTCACCGAA ACCCCGGNGC 60  
CCCGGNGGTA TCCTTGAGCG GAGAGGGCGG GCGGGGAGCA GGAAGGCCGC GCTGTCGGGA 120  
AGGGGCGGGG ACCTGCCCCN TTGGCCCAGG TTTTGGACAC CTGGGCGCCC CTGGCCCTTC 180  
GGCAGAACAC GGTGCCGGAC AGTAAGAGGT CCAGCGGTTA GTGGGCGCGG NCGGCGGCAC 240  
GTAAGGCTGG AGCCGCCTGC ATTTTCCAGC AATGAACGGC GCCCTTTTCC CCTTGCCCGC 300  
AAAGGTCTT TNCAGGNCAA CTTTCGAGGC CCTNAATGGT GGGTTTTCCC TGGTTGNTTG 360  
GGGTTTNCCT GGG 373

(2) INFORMATION FOR SEQ ID NO:822:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 323 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:822:

GGCANAGACG CGGAGAATNA GGAGGAGGAT GACGTTCTTG AAATNAACAG CAGCTTTACA 60  
GCCGTTACTG GTGAACAAGA GGAGCACACT CTCCAAGAAA CAGCATTACC ACCTGTGAAA 120  
TAGTAGCATC ATCGCTGCTC CCATCACGGA CCCTTCTCAG AAGTTCCCTC AATACCTACC 180  
TCTTTCTGCA GAGGATAATT TAGGTCCTCT ACCTGAAAAC TGGGAGATGG CCTATACTGA 240  
AAATGGAGAA GTCTATTTTA TAGAGTAAAA GTATNACCAT TATTTNTACC TNAAATCTCT 300  
NCTACTCTTT GTTTTANCCT TGC 323

(2) INFORMATION FOR SEQ ID NO:823:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 351 base pairs  
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:823:

GGCANAGNCA GACGATCATC CACTCTGGAT GTCATCCAAA TGGCTTTCCA TGANTGTTTT	60
AATGCTAGAT GAAAAACGTG TTATGGTGGA TGCCAATGAA AGTTCCAATT CAAAANATGT	120
TTGAAAANGT GGGTATCACT ACCATTAAAG TTAACATTCG TAATGCCAAT TCCCTGGGAG	180
GAGGCTTCCA TTGCTGGACC TCGAATGTC CGGCGNNGNG GCACCTTACA GTCCTACTTG	240
GACTGAACAG GCCTGATGGA GCTTNTGGCT GGCCTCAGAT ACACCTNAGN AAGCTTAGGG	300
GCAAGGTTCA TTCTNTGCTT TNAAAAAGTG GCATGGAACT GTAGTGGCTT T	351

(2) INFORMATION FOR SEQ ID NO:824:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 216 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:824:

GGCAGAGNCA AGAGCGAGTA CTCAGTCTCA AAATAAAAAA AAAAGGGTGA ATTTTGCCTG	60
ACTCTTATGG CTGTGGTTTA AAAGAATCAG AGTTTAGNTC GGGCATGGTG GCTCANCCCT	120
GGATAATCCC AGCACTTTGG GAAGGCCGAG GTGGGAAGAG CAAAACTCCG TCAAAAAAAA	180
AAAAAGGGAA AAAAAAACC CNGGNNCCNG GAAAAA	216

(2) INFORMATION FOR SEQ ID NO:825:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 382 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:825:

AGGNNAACCC TTCGAGCAGA CCAAGTACCT GGNGGGCCCG GAGCGGCCT TNNTGCCTA	60
CTCGCTGGGC ATGACCGAAA GCCAGGTGAA GGTCTGGTTC CAGAACCGCC GGACCAAGTG	120
GCGCAAGNGN CATNTTNGGN AGAATGGCGT CGGCCAAGAA GAAGCAGGTA NTCGGAACGC	180
CGAGAAAGCT GAAGGTGGGN GGCTCNGNAC GCGGNAGGAA CGACGGACGN AATTACAACC	240
GGCCCCCTGGN ACCCCAACCTT CGGNACGGAC GAGAAAGATT CACGCGGGCT GCTNCAGGAA	300



AGCACAAAAC CCTTCGAAAC TTGGGCGCTG GTTCANCCCC TTCGGNCGGC GGTGCGGGGG 360  
GNACGCCTTT NTTTAGGTAC CC 382

(2) INFORMATION FOR SEQ ID NO:826:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 280 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:826:

GAAGGAAGCN GGGGACAGGN TGAAAGCAAC AACACCTTTN CAGACAGTNG ACCGGCCCCAA 60  
GGACTGGTAC AAGANGATGT TTAAGCAAAT TCACATGGTG CACAAGCNGG ATGATGACAC 120  
AGACATGTAT AATANTCCTT ATACATACAA TGCAGGTTTG TNCAACCCAC CCTACAGTGC 180  
TTCAGTCACA CCCTGCTTGC AAAAGACCCA AAACCTNCAG GCCTTTTTTTT CCAAAAAGGC 240  
CANTTCCGGN CAACAGNCCC CAATTGNTTT TTTAAGGGTT 280

(2) INFORMATION FOR SEQ ID NO:827:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 410 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:827:

GGCANAGGGA AAGAAGGCAA TGATGTAGAT GAGGCTTCCG ATCAGAGCTG CAATGTTGGT 60  
GTTGTTGAAG AAGACACTGA TAAGATAGCT CATGGCAATA ACCGAGAAGC TGTAGTCCGA 120  
AAAATACAGG AACAAAATGA ACCCATTTNT TTTAGGGAAG AATATTGCCA AACTTGAGTA 180  
TAATGATGAG GATCACGATG GTAACCAGTN AAAAATCCAA CACTCTCTAT AAGCCAGGCA 240  
AAGAAATGGC TGCAGGAGTT CACACCCATC ATCTTTCATG TACTGTAGGA AGGAAAAATG 300  
TGAGGCACTT GTTATGCTGA TATTCTTCCC AATTAAAATT ATTTCCCGTG TTGTGTTCAA 360  
AATGTNCNGT TAGTCCTCCG TATATGGANN AGGGCTTTTT NATTATTTTG 410

(2) INFORMATION FOR SEQ ID NO:828:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 365 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:828:

GGCANAGCGG CACGAGCGTN AAGGTGACCC TCCGACTGGA CACCCACCCT GCCATGGTCA	60
CCGTGCTGGA GATGGGGGCT GCCCGCCACT TCCTGCGCAT GCACAGCTGG CCAAGACCCG	120
GAAGGAGCGC GCACAGCTGC CTGCAGCCCA CGCTGGNAGA TCAACCCCAG GGCACGCGCT	180
TCATCCAAGA AAGCTGAATG CAGCTGCGCG CAANAAGGCC TGGGCCTGGT TCCAGCTGCT	240
GGTGGTTCCA NATATACGAG AAACGCCATG GATTGCTGCT GGGACTTGTT GGACGGACCC	300
TNGGGGCCAT GGTGGGGCCC TTTGNANTGA GCTGCTTTGT TCAAGGGCCN TGGGAGNGGA	360
CAATG	365

(2) INFORMATION FOR SEQ ID NO:829:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:829:

GGCACGAGCT CGTCNANGGA ATCGGCGTTT ACTGGGGGCC AGGCCGTNGT TTAAATGTAG	60
GCATTAGACT TCTTGGGCGG CNGACAGACC AAAGAGCGGA AATTCATCCT GCAAAGCCAT	120
TGNAACAAGC AAAGACTCAA AACATCAATA AACTGGTTCT GTATACAGAC AGTATGTTTA	180
CGAATAAATG GTATTAAGT AACTGGGTTC AAGGTTGGAA GAAAAATGGG TGGTANGACA	240
AGTGCCAGGG AAAGAGGTGA TCCAACAAAG AGGACTTTGT GGGCACTGGN GGAGGCTTTA	300
CCNNGGGGTT GGACATTTNG TGGATGCCNG TTCCTGGTCC TTTCGGG	347

(2) INFORMATION FOR SEQ ID NO:830:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:830:

ATGAAGTCCA GCGGCTTCCT CCGAAAAATT CTGTACANAA GGGTGGCTGT TTGGGGCANC	60
AAGTAATGCG TTNAAGGGNA GGCAGGTGGG NGTGAAGGAG	100

(2) INFORMATION FOR SEQ ID NO:831:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 224 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:831:

AGGTATGGTC AANCTGACGG CGGANTGGAT AGAGCAGGAG GCGCAGTGCA CCAACGCGGT	60
GCGCAACCGG GAAGCTGGAC CTCCGGGGGT ATAAAATTCC CGTNATTGAA AATCTCAGGT	120
GCTACGTTAG ACCANTTTGA ATGCTATTGA ATTTTNCTGN ACAATGAAGA TCANGGAAAC	180
TNGGATGGTT TTCCTTTGTT GAGAAAGACT GTAAAAACAT TGTT	224

(2) INFORMATION FOR SEQ ID NO:832:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 258 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:832:

GGCACAGCTC AGTACAACAC TGAAATTAAA CTGCCTTGTN CATGCTTTCA TGTCTCAAAT	60
CAAGGCCTAA ATGAGTAAAA AGATGATTAC AGATTACCTA AAACCCTTAA CCAGTTTTGG	120
TTTTTGAATT ATGCATATGC TGTTGGCTTG CAATTGAGGT TTTTAAGTTT CTGTTTATGT	180
GAACTTGTTT GAAAACATTG GATTCGTCTT CTCTCCACA GTTTCTACTT GNANCCTTAG	240
TTAGCTTTTT NNNGGGGG	258

(2) INFORMATION FOR SEQ ID NO:833:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 379 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:833:

TTTTCAATAT CAGACCTGAC CTATAAGAGA TGCTAAGGGG AGCTCNTTAA TCTGAAAGGA	60
AAGGACATGA GTNAGCAATA NGAAATCATC CAAAGGTACA AAACTCACTG GTATCAGTGA	120
AGTNCACAAG ANCAGATTGG CTTGACACAC TAATTGCCGT GTGTAAGCCA TATTTTGAGT	180
AGGAAGACTA CAAAGCCTAT CAAAANTTAT NATTNCAATT TTTTAAGCGN TNAATATAAA	240

ANGNTNAAAT AGGAAACATT GGCCGGGCCA CGGTGGCTCA CACCTGTTAA TCCCAGCANT 300  
TGGGAGGCTG AGGCAGGTGG TTTCANGAGG TCCAGTNCGA GAACCANCCT GGGTTAACAC 360  
GGTGAACNTC CGTTCTCCA 379

(2) INFORMATION FOR SEQ ID NO:834:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 308 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:834:

TGAAATCACA GGCGCNTTGC TGGCCAAATT CATCAAACC ACCATGCCTA AAACAGTGTC 60  
ACACTGTNTT TCAACTTGAN TCCTTGTAAT ATAGTGATTT TTTTTTTTNN TTTTTTTTTT 120  
TTTTTCCCCT TAGAAAGCAG CCTGGGCGCG GNGGCTCAGG CCTGTNAANC CTAGCGTNTT 180  
GGGAGGCCNA GGTGGGCAGT TTGTTTGAGC TCAGGGGTTC GAGACCNGCC TGGGTAAACNT 240  
GGGCAAACC CCANCTTTAC TAAAAATACA AAAATTGGCC GGGCGTGGTG GCGCTGTCCG 300  
TNANACCC 308

(2) INFORMATION FOR SEQ ID NO:835:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 390 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:835:

GGCACGAGCT CGTCCNTNCA ACGACTGCAA TATGGCGCGT CAGTGCGAGG CAGCATCCTC 60  
AGCCTCTCGC TCTTGCGGGC GCCTAAAGCC CCGGACGCTA CTGCTGACAC GGGGCGCCAC 120  
GAGTTCACCT ATGCACTGAT GCCGCACAAG GGCTCTTTCC AGGATGCTGG CGTTATCCAA 180  
GCTGCCTACA GCCTTAAACT TCCCCCTGTT GGCTCTGCCA GCCCCAGCC CAGCGCCCGC 240  
CACCTCCTGG GAGTGCCTTT TCCGTGTCTT CACCCGCGGT CGTATTGGAG ACCGTCAAGC 300  
AGGCGGAGAG CAGCCCCCAG CGGCCGTTCG TTGGTCCTGA GGNTGTTATG AGGNCCAAGG 360  
GCAACCAAGT TGGGATTNGT TGGGNTGNAA 390

(2) INFORMATION FOR SEQ ID NO:836:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:836:

GGCACGAGCC TACACAGAGT GCTGCTGCCT GTATNGAGAG GCCTNNGGCA TGGNCTGCGC	60
CCTCTGCCCT GCGCAGGACT CAGATGACTT CGAGGCCCTG TGCAATGTGC TACGCCCCC	120
CGCATATAGC CCCCCGCGAC CAGGTGGCTT TGGACTCCCC TACGAGTACG GCCCAGACTT	180
AGGTCCACCT TACCAGGGCC TCCCATATGG GGCTNAGTTG TACCCACCAC CTGCGCTACC	240
CTACGACCCC TACCNACCGC CACCTGGGNC CTTGNC CGGAGGNTC CTTATGGGGC	300
AACCCGNTTC GACATTGCCA GACTTTGAGG ACGATGGT	338

(2) INFORMATION FOR SEQ ID NO:837:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:837:

GGCACGAGAA AAAAAGATAC CCAGATTCCA AGGACCTCAC GATGGTGCTG AAAACCTATG	60
ACACCAGCTT CCTGGACTTT CTCAGAAGGT GTTTGGTATG GGAACCTTCT CTTGCGATGA	120
CCCCGGACCA GGCCCTCAAG CATGCTTGA TTCATCAGTC TCGGAACCTC AAGCCACAGC	180
CCAGGCCCCA GACCCTGAGG AAATCCAATT CCTTTTCCC CTCTGAGACA AGGAAGGACA	240
AGGTTCAGG CTGTCATCAC TCGAGCAGAA AAGCAGATGA GATCACCAA GAGACTACAG	300
AGAAAACAAA AGATTAGCCC CACGAAGCAT GTTCAGCATT CAGGTGATCA GCAGGACTGT	360
TTCCAGCACG GAGCTTGACA CTGTTNAGCT GCCTCAACTT GGTAGACGGT CCAAGGAAG	420
TCAGAGGCAG TTGTCGGGGG CGGAGGTGT NCATGACCTT CCCAGGGCAG NGCAAAAATT	480
TTTCCTTCAA GGACACA	497

(2) INFORMATION FOR SEQ ID NO:838:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:838:

GGCACGAGGC AGGGTGCCTG TNATTCACTG TGTATTGTTGG TTTAAATCAA AGTGATTCTG	60
GGGGAAGCTA TGCTCTTTCA GTGGATAATA AAATTGGTAA CTCTATTGTA AAACATGTCA	120
ATGGTGTGTG AAGAAAAATC AACCAATCTG TAGGTGTTGA TAACTAGACA GTACTGTGTA	180
TGTNACGTGC CTGTNTGGGA TGTNCACTTC CAGCATGGTA TGTGTTAGCG ATGTGGNTCA	240
TGCCCAGAGN TCGTAGATCC TGTTTTGGGG TTGTCACATG GATCGTATGT TAAGCTNTTT	300
NCTTTTNCAT TAAATGAATT TT	322

(2) INFORMATION FOR SEQ ID NO:839:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:839:

AGTACATTCA AATGTGGGCA NCTCANC GCC AGAAATTCCT GTTCNCCCTG AGCCAGCATA	60
TCAACTGGGT NCGCTGTGCC AAGTTCTNCC CCGACGGCGG CTCATCGGGT CTGCCATTAA	120
TGACAGGNCT GTTAANGCTG TGGGGACAAG AGCCAGCCGG GAAATTTTTC CACTGGNNTT	180
NTAGGCATGG GGG	193

(2) INFORMATION FOR SEQ ID NO:840:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:840:

GGCAGAGAAG ACTTCAACTC TNTCGGATGC TCAACCTCAC TGACCGGCAA GTNAAAATCT	60
GGTTCCAGAA TCGCAGGATG AAAGAAAAGA AACTGAACAG AGACCGTCTG CAGTATTTCA	120
CTGGGAAACC CCTTATTTTG AAGAGCTCCA GGTAAGCGCC CTCACCCAG CCCCCTCAC	180
CCACCCTCCT TCCCACCAGC CTGCTCTCCG CAGCCCCACT GTCCCTTGGG TTTAATGAAC	240
GTCTCTTCTT CTGTGGGAAT TTCACGATTC CTTCCCACGG TCAACTCGGG GACCTTCCCA	300
GCGNACCATT GCAGCCTGCG GGANGAGGCC GGGGANTTGG CCGAGNNGGG TTCNTANTAA	360
GGGGGGAAAA TTGGGGGCCT GGGAGATTCC ACAAGGAGGG GCGGGGTTNA AGNTTNCCAA	420

AAGNCCGGGT TTTTNANCCA ANAGNCCGG GTTACCTTTT TTTTNCCAA AATGGGTTTT 480  
TNATTAGGGG G 491

(2) INFORMATION FOR SEQ ID NO:841:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 489 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:841:

CGGAAANTNT GGGTNCCCCG GGNCTGCAGG AATTCGGCAN AGGGGTACTG AACGCGGTTC 60  
TGGGAGCAGC AAGCCCACGG GTAGCAGCCG AGGCCCCAGA ATGGCCAAGT TTCTTTCCCA 120  
AGACCAAATT AATGAGTACA AGGAATGCTT CTCCCTGTAT GACAAGCAGC AGAGGGGGAA 180  
GATAAAAGCC ACCGNCCTCA TGGTGGCCAT GAGGTGCCTG GGGGCCAGCC CGACGCCAAG 240  
GGAGGTGCAG CGGCACTGGC AGACCCACGG GNATTAGACG GAAATGGAGA GCTGGGATTT 300  
NTCCACTTTT CTGTACCATT ATGCACATGG CAAATANAAC AAGAAGACCC AAAGGAAAGA 360  
AATTNTTCT AGGCCCATGT TTTGGATGGG TGGGGACCAA GGGAGGAAGG ANAAGGGTTT 420  
AACGGTTCAT GGGNGTTCC GAACCCTGGC GGNTTCCAAA AAANACTTNA ACGGGGGTTC 480  
TTTGGGGGG 489

(2) INFORMATION FOR SEQ ID NO:842:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 426 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:842:

GGCAGAGNAA GGAGCCCACC TGGAATTCT GGAAGTACCT AGTAGCCCCA GATGGAAAGG 60  
TGGTAGGGGC TTGGGACCCA ACTGTGTCAG TGGAGGAGGT CAGACCCAG ATCACAGCGC 120  
TCGTGAAGGT AAGCTCATCC TACTGAAGCG AAGAAGACTT ATNAACCACC GCGTCTCCTC 180  
CTCCACCACC TTCATCCCGC CCACCTGTGT GGGGCTGGAC CAATGGCAAA CTTCAAATGG 240  
GTGCTTTCAA AGGGGAGGAG ACCCACTGGA CTCTCCTTTC CTTGACTTC TTNATGGCCA 300  
TTGGGTCCC CATNATTTCT TTGTGGGGGG GAAAAATTC TTAGTNATTT TTGGATTNAA 360  
TTTTTGAAA TTCTTTTAAC CAGGCAAACC AAAATTAGGG GGAAACTTNC CCTNGGGGGN 420

CCCAAT

426

(2) INFORMATION FOR SEQ ID NO:843:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 386 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:843:

GGCAGAGGNN ACATCTCCGC CAGCAAGATG GAGAAGGCGG CACANCGNAG GGCCAGGGCC	60
ACGGCATCCA AAGCCACACG CTGCATCAGC CTGGGCTCTG GGACCTGAGG GGGCATGAAA	120
CCCGTGGGGA TGTCGCCAGC CACGCTCGAG CCAAAGNGCT TGTGGAGCTG NCCGAAGTGC	180
GACACGAGTN TGGCCACCAC GATNTACCAG CAGCTCCGTG GGNAGCGGCA CCCTCAGGCG	240
GTGTCGGTAG CGGTCTGAGA GCTTCTTCGC GGCTNGCAGC ACCGCCAGCA CACCGTGNTG	300
GTGGACCACG TCGCACAAGT TGGCCTGCCC GGTGCCNGCA AAAGTTTCAG CCATGTNAAG	360
GACCACCATG NCGGGNCCTT GTTGCC	386

(2) INFORMATION FOR SEQ ID NO:844:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 130 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:844:

TGGCACGNAA NTGGAGAGCC GGCAGCCAGG CAAGGCCACT GAATTGCCNG GGAGCCGGGG	60
NCCAATTCCA CNAACACCAG CCCAACTGA AAGTCCCTCT TCCTTCCCCT GNCTGGNGCT	120
GCTCCGCCCT	130

(2) INFORMATION FOR SEQ ID NO:845:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 181 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:845:

GGCACANTGA ATGATCCTGG GGGAGCN TTT GNCCACCCAG GGCCCTTATA ATTTTGGNTC	60
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GGGGGAAACG GCCCGCGGCA TACAGGACCT CATCCCGGTC CTGCTGCGGC ACNGTCTGTT 120  
TCCCCACCC AAGGAGACCT ATGCCCTGCA CCGNAAGCNG GCAGGGGCTT TCNTGGCCTN 180  
T 181

(2) INFORMATION FOR SEQ ID NO:846:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:846:

GGCTGNGTAG GGAACAGAGG AGGCCGAAAT CCCTCCCCCA TGATTCCTCA ACCNTTGTTG 60  
GNCAANGGCA TCTTTNATGG GTACAAGGGA GAGGCTTCTG GAAGAAGCTC CCTGNACACA 120  
NTACAGGTGC CCTTTTCCAA GGGCAAGAGN ANTTTGGGCT TCCATGG 167

(2) INFORMATION FOR SEQ ID NO:847:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:847:

GGCANAGCTC GAGGCTGTGA ATGCTCACAC AGCGCCTGGG AAAGGGGATN AACTCAGAGN 60  
TGCCTTTTGT GGTACTTTT GTNCTGAGGT AAGAGAGGGC AGCAAGTGA CCCCATGGG 120  
CTGCAGAAGC CGGTTGCGAN CAGGGACTGN TTACATAAGT TTTGGCAGTG AACCCCGGTG 180  
AAGTNTGGTG TTCCTTATGA AACCTGCTT TCCACAGTTG AGCAGAAGAC ACCACAAATN 240  
AAGNAGGGNA GCCCTCCCT TCACTGNAGT GGGAGTNTTC AATGGGGACG TTTGTGAACT 300  
CTGCCCTTGG GGACAATTTG TGA CTGCTTT T 331

(2) INFORMATION FOR SEQ ID NO:848:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:848:

TTAGAGTAGA GATGTAGCTT GANATTTTGA GAGGCTGAGG TGGAAGGATT NCTTGAGCTC	60
AGGANTTTAA AACCAGCCTG GGCAACATAG TGAGATGTTG TCTNNANTAA AAAAAAAAAA	120
AAAAAAAAAA AAAA	134

(2) INFORMATION FOR SEQ ID NO:849:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 207 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:849:

GAGCCCTTNA ATCTAACTTC GAAGCCCTCG GACTACGCTC TGGACCTNAG CACTTTCCTC	60
CAGCAACACC CGGNGCCTT CTAACTGTG AACTCCCCGC ACTCCCCAAA AAGANTCCGA	120
AAAAACCACA AAGNAAACAC CAGGGCGTAC CTGNTCGCCG AAGAGCTAAT GCCCCACTG	180
GGAACTTCCG AGGTCAACTT GNAACTN	207

(2) INFORMATION FOR SEQ ID NO:850:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 378 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:850:

GGCANAGGAG AAAGCAGCAT CAGGTAGACT ACATTCTTAA AACCTGGACC CCTCCTNAGG	60
TCCTTAAGGA TTACTACGCG GNAGGCTGGC ATCATCACGA CAAAGAATGG GCGGCCCCCTC	120
TACGTGCTCA GGCTGGGGCA GATGGACACC AAAGGCTTGG TGAGAAGCGC CTCGGGGAGG	180
TAAGCCCTGC TGAGAATTAC GTTCTCTCCA TAAATGAAAG AAGGGGCTAA GGCGAATGCG	240
AAAGAGGAAT TACAAAANTT TTTGGTCGGC CTATTCAGCT TCATGGGACC TGCCTGGTGG	300
GACTTGGGAA GGGCTGAACA TGCGCCCACT TTTGGGAGGA CCTGGTTTNA AAAGNCCTNT	360
TGGGGATTCA TCNNGGTT	378

(2) INFORMATION FOR SEQ ID NO:851:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 198 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:851:

TCTAGTGCTG ACTGGTCCCC AANGTCCCC TGGNTCTACT GGTGCTCCTG GCAAAGAATG	60
GNCTCAACGG TCTCCCTGGT CNCCATTGGG CCNCCTGGTC CTCGCGGTAG CACTGGATGA	120
TGCNGGTCCT GTTGGTCCCC CNGGGACCTA NTGGACCTGC TNGTCCCCTG GTCCTCCCGG	180
AGATGGTTTC GACTTNAG	198

(2) INFORMATION FOR SEQ ID NO:852:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 478 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:852:

TTCATTGCCT TTGCCCAGAA CTGGTGCATC AAGCGGCGGT CGCAGTCCAT CTACCTGCAG	60
GTGCTGACTG ANAAGCATGC CCCTGAGCAC TACAGGGTGC TGGGCAGTGT GTGCCAGTTT	120
AAGGAGTTTG GCCGGGCTTT CCACTGTCCC AAGGACTTCA CCCATGNAAC CCTGCCCCACA	180
AGTGTTCCGT GTGGTGAGCC TGGCTGCCCC CCTGCACGCC CCCACTGCCC CCGCACGAAT	240
NACCTCCTGG TGGCTACCGG GGCAGGCATG CAACCGGTGC CAGNCCCGTT TTNGGGNACC	300
ACCTGNTTTT CCAGCCCTTN CAGANCCGGT NCCNCTGNTG GCCCTTGAAT TTAAGAGGGG	360
CTNGGAAGCA GGTTAAGGTT GGGATTTTGG GGGGGTTTTN AGGGGAATTT AATGGGGTTC	420
CNAATTTTTG TTTTAAGGGG GCCAGANCTT TTGCAAAGTT GGNTTTTAAG GGGCCCAN	478

(2) INFORMATION FOR SEQ ID NO:853:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 265 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:853:

GGNAGAGGTA TCCGAGTGT NCTGGAACGG CCCTGTCTTG AGCAACATTA ACCGGATTGG	60
AGCAGACCAT GTCCAGAGCC TCCTCCTGAA ACACTGTGCC TCCTGTNCTG GCAAAGCTGC	120
GCCACCGGCC TGAAAAATNA GGAACGCCTA TCGGGCAGAA TTCGGGTCCC TTGGGCCCCCT	180
GCCTCTGCCT CCCNAGGTGG TCAAGGCTCG GGCCCCAGGC TGCTCTGCAG NCTNCAGCAG	240

GTNAACAGGA CCACTCTGAA CCATN

265

(2) INFORMATION FOR SEQ ID NO:854:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:854:

AAGTCGGACA GGGGCCATGA CAAGTCGGAC CGCAGCCATG AGAACTAGA CAGGGGCCAC	60
GACAAGTNAG ACCGGGGCCA CGACAAGTTT GACAGGGATC GAGAAGCGTG GCTATGAACA	120
AGGTAGACAG AGAGAGAGAT NTAGACAGGG AACGGGAATC GGGAAACGCG GGTATGAACA	180
AGGCAGACCG GGNAAGAGGG CAAAGTAACG GCGCCACCAT CGCCGGGNAG GAGCTGGCTC	240
CCTTATTCCC AAGAGCCAAG ATGGCAGTTA GNCGANAAGN TTGAAAGAGT TTAGACCCCA	300
TGGACCCTAG CTTCATACTT CAGACGGCCC CCCGGGGCAC GTNGTTCAAA CAGGANTCCC	360
CAAGCGGNAT TTAGGCCCAG NTTTGGGGGT TGACACCACA GCAGTTGGNC CCTTTT	416

(2) INFORMATION FOR SEQ ID NO:855:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:855:

GGCACCATAA AGGTTGTCCA ACTAATCTTN AAAGCTGAAT TTCCATTGGG AAGGGAATTC	60
TTTCCCGAGT TCATAAGTNG CCTTTCCATC TTCCCATCGA GTATTTGGNA ACTCTCTNAA	120
GGTTCCTCTCC ACTTTCCCAG GCTTTTCCAA TCTGGTCGGC GTATACCTTC TCCTTTGGAT	180
TTCCAAAAAT TGCTTCATAT ACAGCCTCTA GTGTGTATGT NGGGAAGATT TAATTGTGCC	240
TTGTNAATTA CATGGATACA AGTGGAATG TATTCTTGCC CNTGAACTTC TGACAGCCGT	300
TNATATCGCC TNTTCC	316

(2) INFORMATION FOR SEQ ID NO:856:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:856:

GAAGGCTTCG GNCACGCAAC GAAANTACAA GGTAGTGGNT CCTTCCTTGC CCACCCCCAA	60
NTCCAACAGG CGGCCCCCTTT ACCGCTTGAA AANTTTTTTCG CCCTAATCCA TGTGGTCNCC	120
AAGTCCCGNT TCTGAGTACT TTNTATCTAA TTTNAAAGAA GATGAAGAAG TTTTCAGGGG	180
NGATTNTTTT ACTGTGGGGC ANGTNTTTTG AGAAAGTCCC CCTGGGGGTG AAAGAACTTC	240
GGGATCTGGG NTGGCTATGA TTNCGGGGAG GGGGNACCCA CACTTGTTCG CGGGNATTAC	300
GGGGACCTT	309

(2) INFORMATION FOR SEQ ID NO:857:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:857:

AAACTAGTG GATCCCCCGG GCTGCAGGAA TTCNGCAGAA GTTTTACTCN CCAACTTNAT	60
CATCCAAATG CAAGTGANCA AANAGGCCCC CAGCTCTGGC CATCACGTAT AGCATCACCT	120
TCCTCCTCTT CCTCCTNATC CTTTTTGTCT GCTTCTAAAA GGACCTGAAT GAGGTGTGTC	180
CTGAAGGCCC CANGAATGCT GCACTGGCTG CCTGCACTGT NTGGCCTGGT GGCCACACGA	240
ACCAGGACTG AGAATAGCCT TGGGCACCGN CACCATCCTC CTTGTNTTTTG GCCATGGGCC	300
ATTAACCAGN CTGTNCTTTT TTNCC	325

(2) INFORMATION FOR SEQ ID NO:858:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:858:

GACCTATTGC TTTAANAACA AGGCCCTCTA TNANATCTCC TTCCCCACTC TAAAGCTAAC	60
CACACCAACC TACGGGGAAT CTGAANCCAC CTTTTTTNAG CNACCATGAA NTGGTGTNAA	120
CNCTGNCTT CCTTTTCCTT GGCCAGCTCC AATGCTGACC TCCGCAAGTN GGNCAGTNAA	180
CATGGTCCCC TTCCNACGTT TCCATTTTTT TATGCCTGGT TTTGCCCTT TAAACCAGCC	240

GTGGNAGCCA GCAGTTATCG AGGNTCTCAN AGTGGCCGGN AACTTNACCC AGCCAGGTTT 300  
TTCGAATGGC CCAGGAACAT GATGGGCTGN TCTGTGAACC CCGGG 345

(2) INFORMATION FOR SEQ ID NO:859:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 139 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:859:

ATCCCTCTTT GTCTACAGAG TTGTNGAATG CTCCACCGGG ANGGGGTGGG CAGTTNTCCC 60  
CTTTGGGGAT GTTGNGNTTG TGGGGAAACC ACTTCCCCGT TTGCTGGACT TAGGGGCTGG 120  
TTTGGGNGAA ATTTTTTGT 139

(2) INFORMATION FOR SEQ ID NO:860:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 191 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:860:

ANAGCAAAGA GCAGGTGGCC AACTNACCTT TTTTGGAGCA ATTCCGNAAA CGGGGCTTCA 60  
AGGTGGTATA TATGAACCGN GCCCCATTGN ACGATTACTG TTTGCAGCAG CTNCAAGGGA 120  
ATTTNANTGG GGAAGAGCCT GGGNCTGCAN TTAACCAAGG AAGGGTCTGG GAGCTGGCCT 180  
GAAGGATGAG G 191

(2) INFORMATION FOR SEQ ID NO:861:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 319 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:861:

TTTAAAAACA AGAAGAGGGT CCTNCTGGGA AGAACTGGC AAGGNAGAAG CTCNCGCGGT 60  
ACTACAAGAN CATCGGTNTG GGCCTTCAAG ACACCCAAGG GGGCTATTAA GGGCACCTAC 120  
ATTGAACAAG AAATGCCCCT TCANTGGTAA TGTTTCCATT CGAGGGCCGG ATCCTCTTTG 180

GCGTGGTGAC CAAGAATGAA GATGCCAGAG GACCATTGTG AATCCGCCGA GACTNATCTG	240
CACTTACATC CGCAAGTGAC AACCGCTTCG AGAAAGGGCN CACAAGAACC NGTTTGTTAC	300
ACCTGTNCCC CCTGNTTTC	319

(2) INFORMATION FOR SEQ ID NO:862:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 484 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:862:

GGCAGAGCA GAAGTGGGTG CGGGANAGNG CCCANAGCAC CCACTTCCCC GGNTCAAGTA	60
CACACATNAC CAGCTCTTNT TCATTGCNTT TCCCCAGAAC TGGTGATCA AGCGGCGGTC	120
GCAGTCTNC TACCTGCAGG TGCTGACTGA NAAGCATGCC CCTAAGCACT ACAGGGTGCT	180
GGGCAGTNTN TCCCAGTTTA AGGAGTTTGG CCGGGCTTTC CACTGTCCCA AGGACTCACC	240
CATGAACCCT GCCACAAGT TTTCCGTGTG GTGAGCCTGG NTGCCCCGNT GCACGCCCCC	300
ACTGCCCCCG NACGANTNAC CTCCTGCTGG NTTACCGGGG NAGGNATGCA CCCGGTGCCA	360
GNCCCGTTTT GGGNACNACC TGTTTTCCAG CCCTTCCAGG ACCGGTCCCC TTGTNGCCCT	420
AATTTNAGGA GGGGCTGGAG NAGGNTNAGG TGGATTGGG GGGTTAAGG GAATATAATG	480
GGGT	484

(2) INFORMATION FOR SEQ ID NO:863:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 340 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:863:

GGCAGACCTT GANCCAGGA GTTTAAGGCT GCAGTNAGCT ATANTNATGC CACTCCACTC	60
CAGCATGGGT GAACAGANCA ANACCCCATC TTTAAACAC ACACACAGAT CATTATCAGA	120
ATGTACANTA AACTGAATG TTTTTGAAA CTCTGTTCCT TGTTTTATAT TGGCTGCTTC	180
TGGCATATTC ACTATTTTCC CATGAGNATC CAGTATTGAT GAACTNTAT TTTTGGTAAG	240
TGAGATGAAC GATGTNAAGA TTGTGCCATA GAGGCGGGGC ATGGCGGCTC TGGCACTTG	300
GGAAGGCTGA GCGGGGTGAN CTGCCTGNCG NCTGANTTCG	340

(2) INFORMATION FOR SEQ ID NO:864:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 291 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:864:

AATNACCGCG GACGATCAAC AGCAGGTCGT NATGCAGAAG TCCGGTGAGT GTAANAAGTT	60
GCTCATTGAT CGCCGCATTC GGTCCGTTTT TTGGTAACAA CNGCAATAGC GTTTNTGGAC	120
TGGCAAACAG ACTCATAGCC TGGNATAACG AAAAGATCGC ATTCCAGTNA GTNTTGGGAT	180
NAATGGAAAA AGTGTGGTGT TCTTCGAATC CTTGTGCCCG CAGTTACCTG NACGGAACAG	240
CGTCCTGNTT NNTTCCTGGC AATAACAGAG GNTCGTTTAC CAAGTAAAAA G	291

(2) INFORMATION FOR SEQ ID NO:865:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 197 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:865:

GCTGATGGAA GTAAATGGGA ATACAGCCAN TTNTTGTACG GNCGCACCTA CGATGTAATG	60
GTGTTCCGGTG CGGCAGGGAT TATTTNCCTG GTCGTTAACG GCCTGCTGAC GCTAANGATN	120
CGTNTGAANC GACCGCAAAG NTGGACATTC GAACGGCGAA ATTAATGTGG CTGCGTACAT	180
TCGCCGGGGG GTTTTGT	197

(2) INFORMATION FOR SEQ ID NO:866:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 367 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:866:

GGCAGAGNCT GAAATAAAG ACAAGAAAGC CAGGTCTACT TTAAATAGT CTTAAGCCAC	60
TATTATTATA TTTTNAAAAT TTAGCCAATA ACTTCTAACT AGAAGCAAAA ATAATAACAC	120
ACGATCTAAT AAAAATACTT GGGAAAACAA AAAGATGAAA TACTTGAAAA CGGACAAACA	180



GAATTGTGCT TCATATGCAA AAAAATCTAA GTCACTTCCC CATACTGGAA AATCTTAATA	240
GGAACAAAGG AACAGCACCA NGCATTCTACT AAGGCCATAC CACGTGGGCA TTAACAATGG	300
AGGCCGTTTA TTGNTTGACC GTTTGNTTGA CTGAGNTGGN GTCTCGNTCT GTTCACACGG	360
TTGGGGT	367

(2) INFORMATION FOR SEQ ID NO:867:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:867:

TGGNAGGCCA AGGCGGGCGG ATCTCCTGGG GTTGGNAGTT CACGACCAGC CTNACCAACA	60
TGGNAGAAAT CCCGTCTCTA CTAAAAAAAAA AAAAAAAAAA AAANCNCGGG GGGGGCCCCC	120
T	121

(2) INFORMATION FOR SEQ ID NO:868:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:868:

TGGA AAAACT GTATCAGGCG CAGNGCTNTA GCCAACAAGA AAGNCACCAN CTGTTTTNAG	60
GNTGNTGCGT GGCAGCTGA AGCCGGAACA ACTGGCGGCG GCGCTGGTGA AGCATGAAAA	120
TTCGCGGTGA GCACCCGANC GAAATCGCCG GGGCAGCAAC CGCGCTACTG GGAAAACGCA	180
ACGCCGTTCC CGCGCCCGGT TTATCTGTTT GCTGATATCG TCGGTACTGG CCGTGNAGGC	240
AGCAANCAGT ATCAATATTT TTNACCGCCA TGCCTTTTTC GCCGCGGCCT GTGGGCTTGA	300
ANTGGGCGAA ACACGGCAAC CGTAGCGTTT TCCATAAATT TGGTTCNTTC CGTTCTGCTG	360
GCGGCGTTCG GTATTAATCT TTGATNTTGA ACGNCNNTTA ATCGGGCCAG G	411

(2) INFORMATION FOR SEQ ID NO:869:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:869:

CACTACCGGT ATCCAGCACC TTAAGCNTGA CGTGTTCCTG ATCCACTTCG GCGCTTAGGT	60
GNATGCAACC GCTCTCGGGG GTAAATCGA TGGCGTTATC CAGTAAATTT CCCAGCGCCT	120
GCTCCAGTGA ACGCCGGTTC AGCAGCAACG TTAACCTCGG TGGGCGTAAC ATGCAGAGTG	180
ATTTTTTTTT CTGCCAACTG CACGGTGCGC GCTTCGCTGA CGCGGCGGGA ATNAATGCCG	240
CCACATNCAA CAGCAGTNCA GAACGACTTC CTGGACGATT CTCCAGTNTT GCCTGGNGTA	300
GTAACGTTTC TACCAATGCC TGCAAACGNG CATTTTGNGT CAAAAGTTGT TCATGAAANG	360
GGCCACCATT TTCGGTGGNG GACCTTCGGG TAAAATTTNC GNCGTTCAG AATTCGCCGC	420
CATGGGGTTT TTTAGCTCCT GAGTTAATGC GTAAACATT C	461

(2) INFORMATION FOR SEQ ID NO:870:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:870:

TTGGCACGGA CTTTACCGTT AACCTGCACC ACGACCAGCG TGNAGTCTTN CACCATCGCT	60
TTTTCGTCAG CAACCGGCCA CGGCGCGTTG TCGATATCGC CTTGCGCTTT NAGTTCCTGC	120
CACAGCGTGA AGCAGATGTN CGGGGTGAAC GGGTTAAGCA TACGGACAAC GGCCAGCAGT	180
GCTTCCTNGC ATCAAAGCGC GATCCTGCTC GCCATCGGTT GGTGCTTTCG CCAGTTTGTT	240
CATCAGCTNN NNNNNCGNCG CAATTGCGGT GGTGTGAAAG GTCTGACGAC GGCCGATATC	300
ATCGGTCACT TTAGCGGNTC GTTTTATGCA CATCGGAGGG GGGGGCCCGG TNACCCANTN	360
CGNCCTTAT	369

(2) INFORMATION FOR SEQ ID NO:871:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:871:

TTTTTTNTGC CATTAAC TTC GGTATGCCTG CNGGACTGGC TTCGCTGGTG TTACAGGCAC	60
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AGGCGTTTTT AACTATCATG CTTGGCGCGT TTACTTTTCGG GGAGCGACTG CATGGCAAAC	120
AATTGGCGGG GATCGCTTAG CGATTTTGG CGTACTGGTG TTAATCGAAG ATAGTNTGAA	180
CGGTCAGCAT GTGGCGATGC TCGGCTTTAT GTTGACCCTG GCGGCACATT TAGTTGGGCG	240
TGTGGCAACA TCTTCAATAA AAAGAATCAT GTCGCACTCA ACGCGTCCGG CGGTGATGTC	300
GCTGGTAAAT CTGGAGCGCT TTTAATCCCA ATCATTCCCT TCTTTGGTNG CCTCGCTGNN	360
TCNTCGGATG GGTTCGCAA CCAGGNTTCA CA	392

(2) INFORMATION FOR SEQ ID NO:872:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 496 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:872:

TTCCGGTCTN ATCCAACAAG CCTGCATTCC GCTGCGAATT GCCCCACCCA CGTNAGTGNA	60
GAATCGTCCC CAACATGTAA GATCTCGCCG ATCGGCACGT TGAGTTTTTC CGCAGCCAAA	120
AAGTACATAT CGCTGAACGG TTTTAAGCGC CCGTGCGGGC CAGCGCGCAN ACAAACTCA	180
AAATAATCCC CCAAACAAA CAGCTCCGGC TGGGNCGTTA CCGTTGGTGG ATCGCCACCA	240
GCGGCCATTT CTTCGCCAGC TGTTTTAAGG TGTCGTGAGT TTGCTGCGGG ACGTTCGAAT	300
TCGGCTGCGN CATTTGGCAA AAGTTGGATT CATTGGCTGC GTGTGGCNCC TTGNATGGGG	360
CTTTCTTTTCG GGGCANTCAG CCCGNNNGNN GNGCAATNG TTTGGTTTCA ATTCGGAACG	420
TAAAACGGCC AACGCGGTTT AAGTCGTGA TNAAATTTTG GGGGTTTCCC GTTTTCCNNT	480
AACCGGCTGG NGGCAG	496

(2) INFORMATION FOR SEQ ID NO:873:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 329 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:873:

ATGGTCTCGC CGATAGTCAG GTTAAAGTAC TCTTTGAACA GCCAGAAGCC CGGTTCGTTC	60
ACATGAGAGA AAATCACACT ACCGGAACCA ACCGCAATAA CCATCAGCTC CGGGNTAACA	120
CCCGTGTTTG CCAATCAGCG GTGCCGCGAT ACCACCCGCA GTGAATTNCC GCAACGNTTG	180

CGGGAACCCA GCGCGATACG CATACGGNCA GCAATCGACC AGGCCATCAG CAGCGGGGGA	240
AATGTTGGTT TTCGTGGCAT CCATGGANGC AATGTTATTT TTTCCACGC CGTTNTNTN	300
CCCAGCAACC TGTTTGAAG CGGNACCCG	329

(2) INFORMATION FOR SEQ ID NO:874:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:874:

CTTNATGCAC AACGGCTTTT TCCTGTNCCG GCTTAACTCC TACAGTNAGA TCTTTTCCAG	60
TNAAGTCTCC GGCGTGGCGT TAAACGCTT CTTTAACTTT TNNATCCCGG CGAATGCTGG	120
TGGTCTACTT TCTGNGCCCA GGGACAGCAA AGNTNGGCTG TTATTTCCCTC GTNAGCACGG	180
TCGCCTTTGG CTGCGCTGAC TTANATGAAT TGTGNGGCGN GCACTNCGNC CCAATATCAT	240
CATCGCATTC GCTAATCTTC CTGTTTATTG GGCATTATTC GCGGGCTGGG ATTTCTGTTGT	300
GGGATGCNNG GNCNGCGGGC GGGCGTGCNT GGGGGATTTT TTGGGCA	347

(2) INFORMATION FOR SEQ ID NO:875:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 457 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:875:

CGTTNTCGCG CAGGTTTTNA ACGCGCTTAA NTAAATNAT GACCAGCTAT GTGGTTGGGC	60
AGGCGCTTAA GGCGGATAAG ATTAACTCA CCGATATGGT GACGGTCGGT AAAGATGCCT	120
GGGCGACGGG AAATCCGGCA CTGCNTGNTT TCATCGGTAA TGTTCCTCAA ACCGGGCGAT	180
CAGGTTTCGG TGGCAGACTT GAACAAAGGT GTGATTATCC AGTCCGGTNA ATGAACGCCT	240
GTATTGCGCC TGGCTGATTA CNTTGCCGGG NAGCCAGGAG TNCATTTTAT TGGTCTGATG	300
AATGGTTATG CCCAAAACT GGGTCTGNAC CAACATTACC TTCCAAACGG TGGCACGGGC	360
CTGGTTTGCG CCCGGGGCAT TTCAGNACCC GGCGGGAATT TTGGCATTNC TGGGTAAAAG	420
CNTTTTTCCC CGGTTTNCCC GNAGAGTACG CCTTTTT	457

(2) INFORMATION FOR SEQ ID NO:876:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 309 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:876:

ACTGGNTCTC GGCTGCCCTN TTGAAGANTT TAACGCATTT TGN NATGCCC ATCCCGATCG	60
GACTGTCGTC GTCTACGCCA ACACTTCTGC TGCGGTAAAA GCGCGCGCAT ATTGGNTGGN	120
AACTTCAAGC ATTGCCGTCG AACTTATTGA TCATCTTGAT AGTTTGGGNN GAAAAANCA	180
NCTGGGCACC CGACAAACAN CTGGGGCGTT ACGGGCAAAA ACAGACGGGT GGGAGACANT	240
CTATGCTNGT CAGGGTGCCT GTTTTNGTGN CATGGATGAA TTTAAAGTCT TCAGGCGTTG	300
AACCCNCTT	309

(2) INFORMATION FOR SEQ ID NO:877:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 399 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:877:

TATTTTGGCC GCATGCAAAG GTTTCATTAC ACTATTA ACT AACGGTGTGC TATCCGTTTC	60
TGGGAAAGTA AGAAATATTG TCAACATGAA GCCGGCGCAC CCATGGNAAG CTGAAGAATA	120
TTTGTGAACT GCCTGTACAT CAGTGAAAAG CCTGTTGAAG AAAAACTTA AGCAAGAGCA	180
AACGAACATT CTCACAGATT CTTT TAGATG CAAGAATGCA GCACGCAAAA AATTTGGTTA	240
CGCGTGGAAG GTTCCAGTNC AATAAAATTG CCGAACAAATG TGGTTATGCC ATACATCTTA	300
TTTATTTTAT GCGTTCCGCA AACATTTCCG NAACATTC CG AGGGGNTTC TNAGGGGTTA	360
CCNTTGTTCA AGGTCCCCCG GTTTGN TTA CGGGGCAAC	399

(2) INFORMATION FOR SEQ ID NO:878:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 338 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:878:

CATTGGCAAA GAAGAAGCCA ATCGGTGCGC CCAGCTGCGG AAAGGAGCCA TACAGTGCAC	60
GTTTGCCCGG TGGGGCGTTT TCAGTCGCCA GCAGCGCCGC GCCGCCCCAT TCACCGCCTA	120
AGCCCAGACC CTGACCAAAT CGAGCCAGCG CCACAGCAGC GGGGCGAAAA TACCAATCGT	180
GGCATAGCCC GGNCAGCAGA CCAATCACCA CGGTGAAAT CCCCATCGTT AGCAACGAGG	240
CGACCAGCGT CCCCATACG AACGGNTGTT CCCTCGTGNG GACGTTTTTC AANGACCGTT	300
GGNCNTGAAA TTGTGGGTTC AGCAAAAACG GCAGTTTG	338

(2) INFORMATION FOR SEQ ID NO:879:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 390 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:879:

TCCTGGCAGA TGTCCGCGGA TATCCGCNAG CCCCAACANT TCGAAGAAAC TTTNCTAATG	60
CAGGCTCATT TTTTTNGCNC TGAGATAAGC CGGANTGCTT TCTCCGGCAT AGGTTCGCAG	120
CGTTCCAGGT TCCAGCCCGT AGTCAATNCG CATCGAGAAT CAACANATGG CTGGNGCTTT	180
CAANATACCC CAGCAAGTTC AGTCCCTNAN TACCGCCATC GACAATNTCC ACATACTCGG	240
GCCAGTGGTA ATGGGCATAC AGCCGTTCCG NCACCCGNAC GNCGAAGCCT TCATCGGCCC	300
ACAGCAGGTT GCCCAGCCCC ATGACCACCA CGGTTTTNNT CGNTTCATGA AACGGTTCCT	360
TGTTAAATTT ATTTTNNCCA AATTTTGGG	390

(2) INFORMATION FOR SEQ ID NO:880:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 394 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:880:

CGTNAGCAGC CTGTNGCTTT ATACCGGGG GATTCTGGAA GCCAACCTGC TGCCACCGCC	60
GGAGCCGAAA GANAGCTGGC GTCGCATTAT GGATGAACTG TCAGTNATNN NCTGCNATGT	120
CTACCGCGGC TACGTACGTN AAAACAAAGA TTTTNTGCCT TACTTCGCT CCGCTACGCC	180
GGAACAAGAA CTGGGCAAAC TTGCCGTTGG GTTCACGTCC GGCAGAAACG TCGCCCAACC	240
GGCGGCGTCG NAGTCACTTA CGGCGGCATT TCCGTGGNTT CTTTCGGCTG GGACGGCAAA	300

AACCGTCTTG AANTGNTCCC CGNCTGGGNT TGGGGTGGCA GGTACGGGC GGNTTGCAAA 360  
AAGTGGGTTC GAAGACGGGG CAAAACAGAG CGAG 394

(2) INFORMATION FOR SEQ ID NO:881:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 489 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:881:

TCGAGTTTTT TTTTTTTTTT TTTAATTGA TGGGATGTTC CTAAACTTCA TCTGCTAATA 60  
AATATTTGCC AAATTAAAAT GAGCCTAACT AAATTGAAGA CTAAAATTAT TCAGTGGAGG 120  
ACCAGACCAT TTGCTTTATT TTCAGGGTGA AGAAGACCTG GNTTGCTCTA TTCAGGTCTC 180  
TTAGAAAAAC AGGCATACAC ATGAGTTTCT AGTATCCTCA GCAACACACT ACATCATACC 240  
TTACCCTGGG TAATCCTTCA GAGCACTGTC AGCAATCACC TCAAAATCCC TTCCCTAAAG 300  
NCACATACAC TTGGGGGTTT ACTCTTATTC ACCTACTCCT CCCTACTCTT TAACATGGAA 360  
TGMNCTCAAG GCTTTTGGGG GGGGNAAAAT TAAAGNATCT ATCCTTTTTT TTTTAAGGTT 420  
CCNTTTCAAA AATTGCTTTG GGGGCCCCGT GGNCAGNAGG GGAAACAGGC ACTGTTNAAT 480  
AGGTTCCCC 489

(2) INFORMATION FOR SEQ ID NO:882:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:882:

GTAAATTTAG CCGCGCCCGT GAACAGACCC AGAAATNAAC GTNCGCNTTA ATCCTCATGT 60  
NATTCCTGGC ATGGTACAAG CTGAATCTAT AAGCTTTTTT ACCGGACTCA CCATGCGNTG 120  
GTTCCGCAAT GCTTTCCTGTG CCGAAGAAAA ACTGATTGCG GAACGTTTAG GCATCGANAC 180  
CTATACGCTG CTGGAAGAGA TGGCCATGGG GTGCCGCCTG GGTCTGTTGGG GCGTAAATNC 240  
NGATCTTTTT NCGACAAAAT GCGGTTTTTA AAACNGGTAT CACGTTGGNG 290

(2) INFORMATION FOR SEQ ID NO:883:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:883:

CACCAATGCG GCAGGCTCGC TCGTCCGGA AGTGGGGGCA GGCAGCCTGG TCGCATTGAA	60
AGANCATATC AACACCATGC CCGGTACGCC GATGGTGGGT CTTAACGATG ATCGTTTTNG	120
AGAGCNCTTC TNCTCACTGG CAAATNCCTA CNATGCGGAA TACCGCGCAC TGTTACAAAA	180
AGTGGCGAAA GAAGAGGGTT TCCCTCTGAC GGAGGGCGTG TNCGTNTCGT ATCCGGGGCC	240
GAATTTGAG ACTNCGGCGG AAATTCGCAT GGATGCAAAT TAATTGGTGG GGATGTTGTT	300
GGTATGTNTG TGGTGCCTGA NGTTATTTCA GNTCGCCATT GGGACCTTTA AAGTTCGTTN	360
GCGNTCTCT	369

(2) INFORMATION FOR SEQ ID NO:884:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:884:

ACGCATTANA CCANTAAAAG CTTGAGCNT TTACCGACCG GAANTGGCAA TATCAGCAAT	60
CTGCTGAGAA CCAACCCTGC GGTACGTTGG TTTCAACGCA AAGTACCTCG TTAAACCAGG	120
GAGATATTCG CCCTGAGAAA NTNTCTTTTC ACGGTGCGTC GCCCTACCAN ATTGCCTATT	180
TAATTGAGGG GTATTAGTGC AACTAAATAA CCCTGAACCC CAGCGAATNA NTTNCCNATG	240
CCCAT	245

(2) INFORMATION FOR SEQ ID NO:885:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:885:

GGCACAGCTA GGCTGGACGN TACTCCGGAC GNAAAGNNGT CATCGTGTA GAACAT	56
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(2) INFORMATION FOR SEQ ID NO:886:



- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 311 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:886:

GGCACGAGGA GGACAGCATT GCTGCTCCTT GCACCCCTGG NTGTGGCTAC AGGGCCAGCC	60
CTTACCCTGC GCCTGCCACG TGTGCACCAG CTCCAGCAAC TGCAAGCATT CTNTGGTCTG	120
CCCGGCCAGC TCTCGCTTCT GCAAGACCAC GAACACAGTG NNAGCCTCTG AGGGGGAATN	180
TGGTGAAGAA GGAAGTGTNCG GAGTCGTGCA CACCCAGCTA CACCCTGCAA GGCCCAGGTT	240
AGCAGNGGCA CCAGTTTCAA CCAGTGTTCG CAGGNGGACT NTGCAATTGG GAAGTTGNAC	300
AACGTTGNAA C	311

(2) INFORMATION FOR SEQ ID NO:887:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 283 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:887:

GGCANAGAAA CAGCGCTCTG ACCTCTTTAA ACACCACAGA ATCCACACTG GGGAGAAGCC	60
CTATGGATGT TCCGTCTGTG GGAAACGCTT CANTCAGAGT GCAACCCTCA TTAAACACCT	120
NAGAATTCAC ACTGGGGNAA AAGCCTTACA AATGTNTTGN AATGTGGGGA AAGATTTAGA	180
CAAAGTACAC ACCTTATCCG ACACCAANNA ATTCATCAAA ATAAAGTGCT GTCGGCTGGG	240
CGTGGTGGCT CACGNCTNAT AATCCCAGCA CTTTGGAGG NCA	283

(2) INFORMATION FOR SEQ ID NO:888:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 304 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:888:

GGCAGAGCAG GTGCGCCTNT TCCGCCCTTG GNTCAACATG GACCGGATGC TGCGCTCAGC	60
CATGCGCCTG TGCCCTGCCG AGTTTCGACA AGCTGGAGTT GCTGGAGTGC ATCCGCCGGC	120

S.n. 08/ 401, 881



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re the Application of:

**William A. HASELTINE, Craig A. ROSEN, Steven M. RUBIN, Patrick J. DILLON,  
Haodong LI, and Julie EARLE-HUGHES**

Serial No.: Unassigned

Filed: Unassigned

For: HUMAN GENES, SEQUENCES AND EXPRESSION PRODUCTS-17

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**SEQUENCE LISTING**

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TNCATCGNAN TGGGACAAGG ACTGGGTCCC CGATGCCGCC GGCACCAGCC TCTATGTGCG	180
GCCTGTGCTT CATTGGGAAC GAAGCCCTCG NTGGGTGTNA GCCAGCCCAG GNGCGCGCTC	240
CTGTTCGTNA TTCTCTGCCC AGTGGGTGCC TACTTTCCTT GGAGGCTCCG TGNACCCCGG	300
TTTG	304

(2) INFORMATION FOR SEQ ID NO:889:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 50 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:889:

AGAGAGAGAG AGAGAGAGAG AGAGAGAGAG AGAGNGGGGG NGGCCCCGAT	50
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(2) INFORMATION FOR SEQ ID NO:890:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 207 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:890:

GGCAGGAGCG GCACGAGGAG AAACCCATA TATGTGAAGN AGTGTGGTAA GGCCTTCAGT	60
CTCCCCTCAA ATNTTCGAGT CCACCTGGGT GTTCACACAG GGNNAAACT CTTTGAAATG	120
TGATAGAGTG TGGTAAAGGC TTCAGTNCAG GAGTGCACGT TTTGGNAGCC CATCAAAGGG	180
TCCACACTNG GGGAAAAGCC NTACAA	207

(2) INFORMATION FOR SEQ ID NO:891:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 358 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:891:

GAAATCCCTC AGCTTTTGTT TGTNTGGAAG TCTTTATTTT TCTTTCATGT TTGAAGGTAT	60
TTTTGCAGAA TATACTATTC TAGCATGAAA GGATTTTNCC CTCAGCACTT GCAGTATGTC	120
GTACCATTCT CTCCTGGCCT GTAAGGTTTT CACTGAAAAG TCTTCTCCCA GACATATTGG	180

AGCTTAATTG TGTGTNGTTT CTTTTCTCTT GCTGCTTTTA GGGATCCTTT CTTTNTTACA	240
GNCCAGTTTT TATCCTTGAC CTTTGGGAGT TTATTAAAAT GCTTTGAGGG TACTTTTGGT	300
TTGGGGTTCC AATCTGCTTT GCTGGCTNCT ATAAACCCTC TNGTNACTNG GGNATTGG	358

(2) INFORMATION FOR SEQ ID NO:892:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 169 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:892:

NTATNTNAAT AATGCTTTTG GCACTGATCA CAGAGCCCAA ANATACCATG GTAGGAGTCA	60
ATNTGCCACA GAAGGTTGGT GGGTTTTTAA TGACGAAGGC GCTGAACTAN CTTTNNCAAA	120
GGCCTTGAG CGCCANCAG NGACCCTTCC TGGCCATACC TGGGACGGA	169

(2) INFORMATION FOR SEQ ID NO:893:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 57 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:893:

TTTTTTTTTT TTTTTTGGG NAACCCTTT TTTTTTTTTT TTTTNAANN ANGGCCT	57
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(2) INFORMATION FOR SEQ ID NO:894:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 494 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:894:

GGCAGAGCCA CCATGATGCT GTNATCTTCC TGGCCGAGCA GCTCCCCGGA GCCCAGCGTT	60
GCCAGCACTA TAAGTTCCGT TACCACCAGC AGGGAGAGGG CCAGGAGGAG CCGCCCCCTGA	120
AATCCCCATG GGGNCTGCTC GGGCAGAGGT CTATCTCCGG AAGTGNACC TTTGAACATG	180
TTCAACTTCC TGGCCTCCCA GCCACCGGGT GCTTCCCTGA GGGGGCCACC TGTNAATGAG	240
GAAGAGGATG AGGTGCAGCT TCAGGTTCAA CCAGACGTGN CCACCAGCCT GGGAGCTGCC	300

CCATGGCCAT GCNTTTTTCG TTCACCTTTA AGGAAGNACG TTCCAAAGAA AGTTGTTGGG	360
GTGTTTTTACA AGNTTCAGCC CATTNCAAGG GGGGGAGGNC TGGTTTCTTG TTAAGCGGCN	420
AAACATTCGA AGGCGGGGGG NAGATTGGTT CATTCGAGGT TAATTCTGGG GCAATTGTTN	480
ATNCCGTTCC GGT	494

(2) INFORMATION FOR SEQ ID NO:895:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 371 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:895:

GGCANAGGGA ATGACGTGCT CCACAGGTGT TTGCCACTGA AGGGGGGTAG CCAGTGGCNC	60
CAATGAAACC AGCTTACCTG GCCCAATTCC CACTTTGAAT GATGTCAGCC CCAGAAAGGA	120
TGAGCTCTTC TACCATCTCT CCTGTTACCA CATTCCCTGC CTGAGAACAG AGCAATTGAA	180
ATACAGCATC CTTAGGGCCA GAAACAGGAG GTCATGTATT GTTACGGTAT GCATGGACCA	240
GGACTTTCCA ACATTATTAC AANGAAAGGA TAACTAGGTC CCCTCTTACT GGGGCCCTCT	300
GNAGGGGTTT TNACANTAGC CACTTTTAGA GGAACCCTGN TTCCCTNACC CATTCCAACC	360
CAACAACCAA G	371

(2) INFORMATION FOR SEQ ID NO:896:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:896:

TGCAAAAAGG GAGCCAGNAA GAAAGTGGTT GNATCCATTT TCTAAGGAAG ATTGGNATNA	60
TGTGAAAGCA CCTGCTATGG TTCAATATAN GAAATATTGG GAAAG	105

(2) INFORMATION FOR SEQ ID NO:897:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 405 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:897:

TACAGGGCTC CAAGTGTCTT ATGAGAGCAG GACTTGGGCT GACCATGTCT CTCTGCCCTC	60
ACCCATGCTC TGCTCTGAAT TTCAGATCCT AAGTGTGAAA CGAGAAAGTC CCCAGCCCTG	120
CTGCTGAGCC AGTTGCTGCC CTACATGGAG AACAGGAGGG GTGCTGTCAT CCTGGTCTCT	180
TCCATTGCAG CTTATAATCC AGTAGTGGCG CTGGGTGTCT ACAATGTNCA GCAAGACAGC	240
GCTGCTGGGG TCTACTAGA AACTGGCAT TGGAGCTGGC CCCAAGGAC ATCCGGGTGA	300
AACTGCGTGG TTCCAGGAAT TATTCAAAT GGACTTTCAC AAAGTGT TTT CNGGGGAATG	360
AAGTCTCNCT GGGAGAACT TTCAGGGACC NTCNTCAGTT GTCAN	405

(2) INFORMATION FOR SEQ ID NO:898:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:898:

NAGTNTGCGA NCCTCTACTG GNGGGGTGAA GGAAACCTCA TTCGTTACAG GCCTGGTACT	60
GTGGCGCTCC GTGAANATTA GACGTTATCA GAGGTCCACT GAANCTTCTG ATTTCGCAACT	120
TCCCTTCCAG NGTCTNGTNC GAGAT	145

(2) INFORMATION FOR SEQ ID NO:899:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:899:

GGCAGAGGTT GGATGAAGAT GTGGAGGAGA TGCTGCTGCA GATTGCTGNT GNTTTTATCG	60
AGAGTNTGGT GACAGCAGCC TGTCAGCTTG CNCGGCATCN AAGTTCTAGC ACCCTGGAGG	120
TGAAANATGT CCAGCTGCAT TTAGAGCGCC ATGNNACAT GTGGTTCCCA GGNATTTGGC	180
TCTGNAAGAA ATCCGACCCT ACAAAAAAGC TTGCACCACA GAAGCTTCAC AAACAGAGAA	240
TGGGCATTGA TCCGGAAAAC AACCAAGAAA TAACACACGG AAAGGTCCAG GGAATGGGAC	300
AGCAATGTAT TTGGGNGATA CTTGAGCTGA GGAAGTTCAG CCCATCTCAT CCTTGGNTTT	360
TTTTTTTTTAA ANGTTTTTTA CAGGGAGCNA TATTTTTTAA TTTAACATGC AGCAATTTTC	420

TTAATGNCTG GAGGTTCTNN CCAAAGGNTA AAGCCTCTTA CCCAATTTTCG GNCCCTTTTC 480  
CNGNCCTTTN AAGGG 495

(2) INFORMATION FOR SEQ ID NO:900:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 297 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:900:

GGCAGAGGTG TCTCACAATG CAGTCGAAAC TGGATACTTG AATTCAGTTT GCCAGAGTTT 60  
GTTAGACAAT CTGGATTTGC TTCCTGGCAA CACTAGAACA AAAATTGGCT TCATAACATT 120  
TGACAGTACA ATCCATTTCT ACGGTCTTCA GGAAAGTCTC TCTCAACCTC AGATGCTAAT 180  
AGTTTCAGAT ATTGAAGATG TTTTATACC TATGCCAGAG AACTTATTAG TAAACTTNAA 240  
ATGAGAAGTN AAAGAGCTCG TGCAAGGTTT ACTGAAAANT TTNGNCACAA ATGTTTG 297

(2) INFORMATION FOR SEQ ID NO:901:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 347 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:901:

GAATTCCACC CATGGNAAAT TCCATGGNAC CGTCAAGGNT GAGAAACGGG AAAGNTTGTT 60  
AATCANTGGA AATCCCATCA CCATCTTCCA GGAGCAAAAT CCCTCCAAAT TNAAGTGGGG 120  
CGATGCTGGC GCCTGNAGTG ACGTGCGTGG NAGTCCACTG GNGTTTTTCAC CACCATGGAA 180  
GGAAGGCTGG GGGCTNCATT TNCCAGGGGG GNGCCAAAAG GNTNCATCAT CTNTGCNCCC 240  
CTNCTGGTGG ATGCCCCCAN GTTCCGTAA TGGGNTGTTA AACCATGTGA AAGTTATGGA 300  
CAACAGGTCT NCAAGGTGCA TTCAGCAATG GTCTNCCTGG AACCNCC 347

(2) INFORMATION FOR SEQ ID NO:902:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 357 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:902:

AGNAGAGCTG AGATCACGCC ATTNCACTCT GGCCTGGGTG ACAGANTGGA GACCCTGTNT	60
CAAACAAAA AAAGTTTCTT TCCTTTNCTA GCTCAAAAGC CAAAANTTTC TGAAAAACGA	120
ACTTTGAAAG ATCTNTNGTN CCAATCAAGG CTTCTNCCTC CAGGTNTGAC AAGAAAGGGC	180
CAAANACCAT TGCAGAGATG AGGAAGCAGG ACCTGGCTAA AGACACGGGA CCCACTCAAG	240
NTGAAGNTCC TGGNCTGGAT TGAGGGCAAG GANGCGGAAC ATCCGGGGCC TTGCTGTTCC	300
ACGTTGNACA AANTGTTGTG GGGACGGGGA GAGGCCCTTG GACGNCCTGG GGNATGG	357

(2) INFORMATION FOR SEQ ID NO:903:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:903:

GGNACAGGGA GATCTGGTGG CCTGGNTTGT NCCAAGAAGG CCGCTCAGCT GGGAAAGGAA	60
GGTNTCCGTG GTGGACTATG TGGAACCTTC TCCCCAAGGN ACCCGGTGGG GCCTTNGCGG	120
CACCTGCTTC AACGTGGGCT GCATCCCCAA AAAGCTGATG CACCAGAGCG GCACTGCTGG	180
GAAGGTCTGA TCCAAGATGC CCCCAACTNA TGGCTGGGAA GGTGGCCCAG CCCGTGNCCG	240
NCATGANNTG GGAGGTAAG	259

(2) INFORMATION FOR SEQ ID NO:904:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:904:

GGCACGAGGN AGAAGCCGGT GTACAAGAAC TTACAGCTCT TTATGGAGAA CAAGGACCCC	60
CGGGACGACC TCTTCGACAG GCTGACCACG ACCAGCCTGA ACAAGCACCT CCAGGAGCTG	120
ATGGACGGGC TGACGGCCAA GGTGTTCCGG ACCTACAACG CCTCCATCAC TCTGCAGGAG	180
CAGCTGCGGG CCCTGACGCG CGCCGAGGAC AGCATAGCAG CTTAAGNATC TTATCCTACA	240
ACCGAGCCAA CCGAGTTCGT GGCCATTCTT TGCAACCATT CAGCGGAGCA ACCCCCAGTA	300
CGTTTCGGAG GAAGTCGATT GCAGAATTTT CCAGANGGAG GNTTCCAGGT CAAAGAAGGN	360



NGCAGGTTGG TTGAGGCCAG GGCAGAGTTG AGGNGGGNNG AGGGTTTTAG CACAAGGCCC	420
AAGGGGTTGG CAANTCCAGG AGTTTTCTGG TGAAGANGAG TTGGTTCTTG G	471

(2) INFORMATION FOR SEQ ID NO:905:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:905:

GGCACAGGTT TGCCGTGTNA GCAACCACAG TNACCTTGCA GTNAGGCTGG AATCTTGGGC	60
CACCCCAAAG TCCTTTNCTG AAGGATTTAN ACGGGGATGA AGTGCCCTCC AGCCTCAAAG	120
CTAGCCACAA AGCCCCCAGA GCTGAATTCA TTGAGTATTT GTGCCTAAGG GCTTGGGCTT	180
GTTTTGTTTT AATACCCGGN CCCCCGNCAG AAAATAGNTT TNGCTTGACA ACCCAGNCTA	240
ATTTCCCCGA TTCTTGGGGC TCCCTCTTGN ATTAATTTTT TGAAAATTTN CCAGTTGTTC	300
AGGNATCAAT GGGGGTTAAT TCCGGNA	327

(2) INFORMATION FOR SEQ ID NO:906:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:906:

GGCACGAGCC CAGCTGTACC CCGTGTTAGG TGGGTGGCAG GTGGCAATTT GCCCTGACAT	60
GGCACAGCAG GGCTCTTGCA TGGCCCGCTG ATTGCTCCTC ACAGGCACCT ACGGGCTGAG	120
CAACGCGCTG CTGGAGACTC CCTGGAGGAA GCTGTGCTTT GGAAGCAGC TCTTCCTGGA	180
GGCTGTGGAA CGGAGCCAGG CGCTGCCCAA GGATGTNCTC ATCGCCAGCC TCNTGGATGT	240
NCTCAACAAT GNAAGAGGCG TGAGTGNGGC GGGTCCTGCT TGGGTGAGCC CCAGTNTCCC	300
GCNACCAGGG NCAGAGGGAA AGGCAGGCCC TGTTGCCACG GGGANGGCC ATGGAAATTG	360
GCCAAGGTTT GGAGACCATG NCTTTTGGGA AGCCCCATTT TNAGCAAGGC CNTNGTTTTT	420
TT	422

(2) INFORMATION FOR SEQ ID NO:907:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 166 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:907:

GGCATCTGGG TACTTGGTGA GGTCGAAGGT CAGGACTTTG CTGATCACAC AGTCCNNTTG	60
CTCAGGATAG ACTCCAATNA GGCTCTCGGC CTTNGTGTAG AACTCCTNCT TGAGTGAGAT	120
GACGATGGCC TGGTAAGTTG CAAGTCGACT GNCTCCTTGG NTGTAA	166

(2) INFORMATION FOR SEQ ID NO:908:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 293 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:908:

TAATCCCGTT GATCATCCAC ATCGCCGNTA CANCCCGCTC ACCGGGCAAT GGATTCTGGT	60
TTCACCGNAC CGGCTTAAGC CCNCTGGCA GGGGGNCGN GGAAACGGCA GCCAAACAGG	120
TGTTACCTGC GNCACGATCC AAATTGCTTC CTCTGCGCAG TTAATGTGCG GGTGAACAGG	180
CGATAAAAAC CCCGATTACA CCGGGGACTT ACGTTTTCAC TGAATGAACT TTGCGGCTTT	240
GAATGTCTGG ACACGTCCAG ATGCGCCAGN AAAGTNCACG ATNCNGCTGN ATG	293

(2) INFORMATION FOR SEQ ID NO:909:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 265 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:909:

NGCCNCATGG GCCANATAGG TGGCCCAGGG GCCCTGGNAG CCCCAAGTCC CAAAGGTANA	60
TCGGAAGACT ACAAGGCCAC CCAGAAAAAT CGCCTTCTAC TGCCACANGA ACCATTCAAC	120
GTCCCCCTGC GACCGGGAAC CAGACCATCC GCTTCGNACC ACGTGAATGC ACCAGCATGA	180
AACAACAATT AATGAAGCCC CGCAGTGGTC AAGTTACACC TGTNAAGTCT CNCGGGTCTT	240
CTGACTAACT TNNACCTNAC CACGC	265

(2) INFORMATION FOR SEQ ID NO:910:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 278 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:910:

AAAAGAATTT CTACGANTTG AATATTGGGG AATATTCTGG AACACTGGAG ATTCCCTTCC	60
GGGGGAATTT NGATCCTGAA GGTGCAGTGG TGGGCTAGTC ACCAAAGAAT GAAATTCAGN	120
CACGTGGGAC AAAAATCATG AACAACATATG AAAGGGNAAC TCGCCNNAN GNAAGGATCC	180
AGTCTGGTCT GGTGGTTTAA CAGGTGTGCA CTCTGGCAAA CCTGTAATGG TGTATACTTA	240
CAGNGGGCCC CTTACACGGN TNAAAACAGN CANTGGGG	278

(2) INFORMATION FOR SEQ ID NO:911:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 119 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:911:

TGGAGAGCCT GGTNTCTCAG TACTTCCAGA CCGTGAAC TG ACTATNGCAA GGACCTGNAT	60
GGGAGNAAGG TCAAGNAGCC CAGAGCTTAC AGGCCGAGGT CAAGTTCTTA CTTTGNAAA	119

(2) INFORMATION FOR SEQ ID NO:912:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 219 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:912:

CTGTNTCAGG TTCAAGGTGA AGAACCCAG AGGNNACTTC CCTCTGTCAC GGTTCCGCTG	60
TGCCCAAAGG NTTCCAAGGN CTGATGGCTC CCACTGCTAA TGCCTTGTTT TTGTCACCAA	120
AATCCTGGGA CAGATGCAGA TCTGGNGTGC CAAAAGCGGG CCTGCTGGGA AACCTGGGTG	180
TGCTGGTGCT NCANTGGGGG TGNAGGGGTT CCNTGCGTG	219

(2) INFORMATION FOR SEQ ID NO:913:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:913:

GGCAGAGGTT TACTTCAAGG GCCTGTGGAA GTNAAAGTTC AGCCCTGAGA AACACAAGGN	60
AAGGAACTTG TCCTACAAGG CTGATGGAGA GTCGTGTTCA GCATCTATGA ATGTACCAGG	120
NAAGGCAAGT TCCCGTTAAT CGGCGNCGTG GCTGAAGGCA CCCAGGTGCT TGAATTTGCC	180
CTTCAAAGGT GATGACATCA CATGGTCCTC ATNTTGCCCA AGCCTGAGAA AGAGCCTGGC	240
CAAGGTGGGA GGAAGGAACT TCACCCCAGA GGTGCTTGCA GGAGTGGTTG GATGGAATTG	300
GGAGGAGATG GTGCTTGGTG GTNCCACATG NNCCGGTTTT CCGCANTN	348

(2) INFORMATION FOR SEQ ID NO:914:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:914:

GGCAGAGGTT TTATAGTGCA AGGNATTGGG GTACAACTTT ATNATTTTCC TTGTGGATAT	60
CCATTGTCTG AGCAACATTT GTTGAAAAGA GTGTTNTTTT TCCATTGAAT TGTCTTGGTG	120
TCCTTTCTGA AAATCAACTG ACCATAAATT CAATGGTTTA TTCTTGACTC TCACTTTCAT	180
CTCATTTTTG TATATGTCTG TCGTTATGCC AGTACTACAC ATTTAATTAC TATAGCTTTG	240
TAATAAGTTT TATTTATTTA NTTATTTNAT TTTTGAGATG GAGTCTCGGT CTGTCGGCCA	300
GTTTGGAGTG CAATGGTGNC CATTTNGGTT CAATGCAGGN	340

(2) INFORMATION FOR SEQ ID NO:915:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:915:

GGCANNGCGA CAGTGAAATC CCATCTNTAC TAAAAATACA NAAAATAGTT AGCTGGGTGT	60
GGTGGTACGC ATANTNTAAT CCCAGCTACT CGGCCTCCCA AAGTCCTGGG NATTACAGTC	120

ATGGACCCAC GGNGCCTGGC CCTGAANCAG TTCTTTAAGG GGATGAGAAC TTGGCCCTCA	180
AGATCTGGGT TTCCATTACC CCTGCCATCG TCAAGGGTAA AGTNCCTGA ACCTCTGAGA	240
AAGGGGTCTC CCAACCAGG GGGATCACAG GATCTCCCAA CCAGGGNGGN TGCCCCGGA	300
GAGTGTGGTC AGGGTTTCAT GAATGTTTAC ACATTTTNA AGTTCTTTTG CAAGCTATTA	360
GTGAATAATT TCCAGNAAA TGAANTGGGA TTATTAAATN TCTGTAAAA TT	412

(2) INFORMATION FOR SEQ ID NO:916:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 378 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:916:

TTTGGCTCTG GGGACAGTTG GCATGCNAGG CCTGANTGCC TACTTTGGCC TACTTAAAT	60
CTGTGGTGTG AAAGGGTGA GAAACAGTGA ATGGTTAATG CAGCAGCTGG AGCTGTGGGA	120
CTCAGTCGTG GGGCAGATTG CAAAGCTCAA GGGCTGCAAA GTTGTGGAG CAGTAGGGTC	180
TGATGAAAAG GTTGCCTACC TTCAAAGCT TGGTTTTGAA TGTCGTCTTT AACTACAAGA	240
CGGTAGAGTC TTTGGTAAGA AACCTGAAG AAAGCGTCTC CTGATGGTTA TGATTGTAA	300
TTTTGATAAT GTAGGTNGGA GAGTTTTTCA AACACTGGTT AATCGGCCCA GTTGNANGAA	360
ATTTGGNAGG GTTTGNCC	378

(2) INFORMATION FOR SEQ ID NO:917:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 270 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:917:

GGCAGAGACG GGTAGGAGCC CTGAGTGAGT NTCCATTCCA AGGGGACGAG TCCATCCACA	60
GTGCAGGTAA CACAGAGACT TGTTTGCTGA CATTGGACCA CGGGATCCTG TGGNGTTTGG	120
TGACTCCTGT GTTCTTGNAT CTCCCTCTCC CTAAAACCC ATTCCTTTGG CTCACCTGTT	180
CCTAGGGTTT CTAACCTGTT ATTCCAAATC TGTCACCTGN ACTCCACAAT CTTNCANTAC	240
ACCCATCCGA GAAAAAAGT NGNTCTAAGG	270

(2) INFORMATION FOR SEQ ID NO:918:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 136 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:918:

CTGTCTAGCT TNNCAAAGTT CACCAATACT TTAATGTAGA GCTTATCCAG CCTNGNAGCA	60
GTCAAGGTTC TACGCCTATT ACACCCTNGA GGCAAAGCTG TACCCGTTTT CTACCATCCG	120
GAAAANGNTA GGATGG	136

(2) INFORMATION FOR SEQ ID NO:919:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 539 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:919:

TTCGGCACGA GGTCAGAAAC ACCANGNGT GGAGGTCAGN GTGTCACTTT TNTGTTTTCT	60
NTTTGAAAGA TCATTGAGA AACACGTCAC TGATCTCCCC TGCAACCATG TNTTCCATTA	120
AGATTGAGTG TGTTTTNCCA GAGAACTGCC GGTGTGGTGA GTCTCCAGTA TGGGAGGTAA	180
GTNTCCAAC CTNTGCTCTN NGTAGACATT CCTGTCAAAA AAGGTTTNCC GGTGGGATTC	240
ATTCACCAAG CAAGTTACAG CGAGTGNACC ATGGGATGCC CCAGTCAGCT CCGTGGGCTC	300
TTCGCCAGTG CGGGGAGGCT CATGTTGCCA CCATTGGGAA CAAAGTTCTG TGCTTTNAAC	360
TGGGAAAGAA CAATCAGCCA TTGTTCTTGG CCACGGTGGG TTAACGACAA GAAAAACANT	420
CGCTTTCAAT GATGGGGAAG GTGGNTCCC CCCGAGGTN ANTTGCTGGC CAACCGCAAA	480
AGTGTTTTAC AAGNTAGGAA AAGGANGAAC AATTCCCANT TGGGANTTGG TATTGATGC	539

(2) INFORMATION FOR SEQ ID NO:920:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 493 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:920:

GGTCANCAGC GGCTGCAATA TGGTTGTACC TGGGTCAATA CCCATTTTCAT GCTGGTAAGT	60
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GAAATGCCGC ACGGTGGGCA GAAACTTTCT GGTACGGCA AGGATATGTC ACTTTATGGG	120
CTGGAGGATT ACACCGTCGT CCGCCACGTC ATGGTTAAAC ATTAAGGATA ATATTGCAGA	180
TCGTAAGAGT ATGAGATGAT CTTTCNTACT GTCAGAGCAC TGATTTCTCT GACAGTAGTG	240
CTGCGTGCAA AATCCACTAC ATCAAATAAA CCAGCCAAAT CTGCATAGNG GTNAAGAGTG	300
AAACAAACCA ACAGCAGCAA GAATTTNTNC ATANTACATT CTNANGGGAA ACNTNCTTTT	360
TGCCACCTTT NTNCNTGCCC NNTGTGTGTN AGTACGGGTT NAGGAAATTC CGCATNATNA	420
NTCNTCNGAG NTGGGTNAGG GCAGTNGCTG TTTGATGTTT TTNTTTCAAA NGGTGNAAAA	480
ANTGNTGGCA CGT	493

(2) INFORMATION FOR SEQ ID NO:921:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:921:

AACTGGTCTT TCATTCACTG TCCAGCTTGC CAATGCAACG GCCACAGTAA ATGCATCANT	60
CAGAGCATCT NTAAGAAGTG TGAGAACCTG ACCACAGGCA AGCACTGCAA GACCTGCATA	120
TCTGGCTTCT ACGGTGATCC CACCAATGGA GGGAAATGTC AGCCATGCAA GTGCAATGGG	180
CACGCGTCTC TNTGCAACAC CAACACGGGC AAGTGCTTCT GCACCACCAA GGGCGTCAAG	240
GGGGACGAGT GCCAGCTATG TGAGGTAGAA AATCGATACC AAGGGAAACC NTNTCAGAGG	300
GAACATGTTN TTATNANTCT TCCTTATTGG ANTATNCATT CCACNTTtag TNTNTTCCCA	360
GGAAGTTGNT TCGTNATTTA CACAGTTATN CATTTTGTGG GTTATTCTTG GAGGAACAAA	420
ACAGGGGTTT GGGACNGTTN CNTCATGGCN TCCAGGATTT TCAACCTCAA CNTCACNGGG	480
GTGCCATTTT TC	492

(2) INFORMATION FOR SEQ ID NO:922:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:922:

GGCACGAGCT TGAACAAACC TGGACTGAAA TATAAACCAG TGAATAACCA GGTTGAGTGT	60
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CACCCATACC TCACGCAGGA GAAACTGATC CAGTACTGCC ACTCCAAGGG CATCACCGTT	120
ACGGCCTACA GCCCCCTGGG CTCTCCGGAT AGACCTTGGG CCAAGCCAGA AGACCCTTCC	180
CTGCTGGAGG ATCCCAAGAT TAAGGAGATT GCTGCAAANA CAAAAAACC GCAGCCCAGG	240
TTCTGATCCG TTTCCATATC CAGAGGAATG TGATTGTCAT CCCCAGTTC TGTGNACACC	300
AGCACGGCAT TGTGAGGAA CNTNCAGGTG TTTGGAATTT GAATTGAGTG NTGAGGAGAT	360
GGCAACCTNA TTCAGNTTTC AACAGAAATG GAGGGNCNGT GAACGTGTTG CATNCNNTNC	420
NTTGGGAGGA TTTTCCTTCG GTGCAGATNT TGAGGTTGAT CTCNGGTGNG TTNTACAGAG	480
TTCTNTTNTT CGTTGAGTGT GATTACTN	508

(2) INFORMATION FOR SEQ ID NO:923:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:923:

GGCACGAGAA GAAAACTAAG CAAGNGGCAC CAGTACCACA TCCGTGCCTA TGAATCCCAA	60
GGGAGGCCTG GGACAAATGCC CGACGTCTAA CTGGNNTTCC ATGAAACCTN CAACATNAAC	120
GAACTTTTCT NCTGGTGTAG CCAATACGTA GCGCCANATC ACGCCATTCC CCGGACTGTT	180
GGCCAGGAGA NGAAGGGTTA CTTTGAAAGA TCGTNGCCCC TCTGCCAACT GNGAACCCCT	240
TTTCGGTGNN CAGANGCCCT NCATNCGCAC GTNTTCTTAT TNAATGGNAA CCGGGGGATT	300
GAGGCCTTTA NCAGTGACAA AAATTAAGTG GGACTTAGAA CTTGCCAGCT TGTTTGNGGC	360
CNCTAGGCTT NGTTTCTTTT GAAAACCNGA TT	392

(2) INFORMATION FOR SEQ ID NO:924:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:924:

GGCACGAGTA GACATTNCCA GAGCTCTATG AGTTAGTGAA CAACTATCAG CCTGAGGTTC	60
TGTGGTCGGA TGGTGACGGA GGAGCACCGG AATCAATACT GGAACNTCAC AGGCTTCTTG	120
GCCTGGTTAT ATAATGTAAA GCCCAGTTCG GGGCACAGTA GTCACCAATG NATCGTTGGG	180



GAGCTGTGTA GCATCTGTNA GACATGGTGG NCTTCTATAC CTGGCAGTGA ATCGTTATNA	240
ACCCAGGGCA TCTTTTNTGC ACATNAAATG GGGAAACTTG GATGNCAATA GACAAACTTT	300
TCCT	304

(2) INFORMATION FOR SEQ ID NO:925:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:925:

GGCAGAGCCA GGGTGGCAGC CGGTGCCTTC CAGGGCCTGC GGCAGCTGGG AGATGCTGGA	60
NCTCTCCAAT AACTCACTGG CCAGCGTGCC CGAGGGGCTC TGGGNATCCC TAGGGCAGCC	120
AAACTGGGTA CATGCGGGAT GGCTTCGACA TCTCCGGTAA CCCCTGGATC TGTGAACCAG	180
AACCTGAAGC GAACCTCTAT CGTTGGCTTC AGGCCCAAAA AGACAAGATG TTTTCCCAGA	240
ATGAACACGC GCTGTGCTGG GGCCTGAAGC CGTGAAAGGG CCAAACGGTC CTGGCAGTGG	300
CCAAGTCCCA GTGAAGACCA GGGGCTTNGG TTNAGGGTGG GGGGTCTNGT TAGGAACANT	360
GCAACCCNTT TTAACAATGA TTCCTGGCTT TTGNNCNGGT GCGGGGGTTC AGGCTTAAAT	420
NCCAGCATTT TGGGAGGGCC AGTGGGGGGG ATCACGGGTT	460

(2) INFORMATION FOR SEQ ID NO:926:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:926:

CCACCTGCAC ACGTTTGTA GNTCCCAGCC GGCAGCCTGG GACTTCCAGT GCTCAGAGGG	60
CGGGGAGAAT CTCAGCGTGG GNCAGAGGCA GCTCGTGTGC CTGGCCCGAN CCCTGCTCCG	120
NAAGACCCGC ATCCTGGTTT TAGACGAGGC CACAGCTGCC ATCGACCTGG AGACTGACAA	180
CCTCATNCAG GCTACCATCC GNACCCATTT GATACCTGCA TGTCCTGACC ATCGNACAAC	240
GGGTAAACAT ATCAGGGTAC AACAGGGNNG GTCCTGGACA AGGGTAGTNG TGANTTGATC	300
TCCA	304

(2) INFORMATION FOR SEQ ID NO:927:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 346 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:927:

TATATTATCT	CCCCCGATTA	CCGTCATCGG	AGGAGATATA	ACTNTNAGGC	AAATATCGTC	60
ATCAAATAGG	CGGCAAACAG	TGCCAGATGC	GCTGCGCCAT	TGAGCACGTT	ATACGTNCGG	120
TGGAGAAGGA	GATATGGCAC	AGCACTAAAG	AGGCCACCAT	CACCACCATT	TCTGGCGCAC	180
CAAGTGCAAA	CTNCAATTCT	TTACCCGTCA	TAAAGGCAAT	TAGCGTNACG	ACAGTACGGT	240
AAGCGNAATG	GTTGCTAACA	NGGACCAAAG	NACAGATTCA	TCGCGCGTNG	TACCTGGTTG	300
TTCAACATGG	TTTTAATGCA	CNTAACCTTN	CGGGGACAGA	TCAACA		346

(2) INFORMATION FOR SEQ ID NO:928:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 355 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:928:

CCACCTGCAC	ACGTTTGTA	GNTCCCAGCC	GGCAGCCTGG	GACTTCCAGT	GCTCAGAGGG	60
CGGGGAGAAT	CTCAGCGTGG	GNCAGAGGCA	GCTCGTGTGC	CTGGCCCGAG	CCCTGCTCCG	120
CAAGAGCCGC	ATCCTGGTTT	TAGACGAGGC	CACAGCTGCC	ATCGACCTGG	AGACTGACAA	180
CCTCATCCAG	GCTACCATCC	GCACCCAGTT	TGATACCTGC	ACTGTCCTGA	CCATCGCACA	240
CCGGCTTAAC	ACTATCATGG	ANTACAACAG	GGTCCTGGTN	CTGGACAAAG	GANTAGTTGN	300
TGAGTTTGAT	TTTCCAGCCA	ACTCATTGCA	GTAGAGGCNT	TTTTACGGGT	TGCCA	355

(2) INFORMATION FOR SEQ ID NO:929:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 332 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:929:

GGCAGAGTTG	TGGCCCACTT	TCTTTNAGAG	ACCCCTTGTA	AGGAAAGCCT	TTAAGAAGAC	60
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CCTCAAGGAC CTGAAGCTGA GCTATCTGGA CGTCTATCTT ATTCACTGGC CACAGGAATT	120
CAAGTCTGGG GATGACCTTT TCCCCAAAGA TGATAAAGGT AATGNCATCG GTGGAAAAGC	180
AACGTTCTTG GATGCCTNGG AAGGCGATGG AGGAGNGGTG GATGAGGGGC TGGTGAAAGC	240
CTTGGGTCTG CATTTTCAGCA TTNCAGNCGA GAAGTCTTGA CAACTGGCTG AATATAACCA	300
TGANTACCAG TGGTGTCACC TACTNAGNAG GG	332

(2) INFORMATION FOR SEQ ID NO:930:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 430 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:930:

GGCAGAGCAA CACTCATTTT GGGAGGAGGA GGCTATAACC TTGCCAACAC GGCTCGATGC	60
TGGACATACT TGACCGGGGT CATCCTAGGG AAAACACTAT CCTCTGAGAT CCCAGATCAT	120
GAGTTTTTCA CAGCATATGG TCCTGAATTA TGTGCCTGGG AAATNACGCC AAGCTGCCGG	180
CCAGACCGCA ATGAGCCCNA CCGAATCCAA CAAATCCTCA ACTACATCAA AGGGAATCTG	240
AAAGCATGTG GTCTAGTTGA CAGAAAGAGG TCCAGGTTTC CAGAGCTGAG GAGTGGTGCC	300
TATTAATGGA AGACAGCGTG TTTTATGCAA GCAGTTTGTT GGGATTTGTG GACTNCAGGA	360
AAATTTGGAA GGAAATTTAN TCCCGNAAAT TTCCAGGGGC ATCAGTGGGC ANTGGNTTCC	420
CGGGGTTAAG	430

(2) INFORMATION FOR SEQ ID NO:931:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 122 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:931:

ACGGTTNCGC TGTCCCAAAG GTTCCAAGGG CTATGGCTCC CACTGCCTAT GCCTTGTTTT	60
TGTGNANCAA AATCCTNGGA CAGATGCAGA TNTGGAGTAG CCANAAGCGG GCCCTATGGT	120
AA	122

(2) INFORMATION FOR SEQ ID NO:932:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:932:

GGCANAGAGA AGATAAACGA GGGGCTGGAA CACCTCGCCA AAGCAGAGAA ATACCTGAAA	60
ACTGGTTTTT TAAAATGGAA GCCAGATTAT GACAGTCCCG CTTCTGNAAT ATGGAAAAGC	120
AGCTGTTGCT TTTGAAAAAT GCCAAACAGT TTGAGCAAGC AAAAGATGCC TGCCTGAGGG	180
AAGCTGTTGC CCATGNAAAA TAATTAGGGC TCTTTTTCAT GCTGCCAAAG CTTATGGAGC	240
AAGCTGGGAA TGAATGTTGA AGGAGATGCC AGAACTTAC CAGAGGCCGT TCCAGCTTAA	300
TTGGGGAAGG CCAGCATGAT GTGATCTTAG GAAAACGGGC ACCCCAGACA CAGGCAGCCC	360
TGGGTTTTGG GGCGAGCNTG GGAAAGTTTT TGGGAAAATN TTGATCCCGN GAAGGCTGTT	420
ACATTTTTTT CACCGNCAG TTAATGTGTT TTGAAATNGA NGGACCGTTT ACGGCCAGG	479

(2) INFORMATION FOR SEQ ID NO:933:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:933:

GGGCCTGAAG GANTTGGGAA GAGCACATTT TAAGGATGAT TGTTTAGNTT TAAAAGTTAA	60
CAAATANTTT ANTGTAGAGC TTATNCAGCT TGGAGCAGTA AAGGT	105

(2) INFORMATION FOR SEQ ID NO:934:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:934:

AGTAAAAGGC TCACTATGGA GGNTTCACTG TNCAGAATGA AGNCAAACAA ATACCAGATC	60
TCAGTGAACA AATACAGAGG NAACAGNCGG TAATGCCCTC	100

(2) INFORMATION FOR SEQ ID NO:935:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:935:

TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTNCCCCC CNNAANG 58

(2) INFORMATION FOR SEQ ID NO:936:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 383 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:936:

GGCACGAGGT GACAACTGCC GGNAGGTGCA CCTCGANAAG CGGCGAGGGG AGGGCCTGGG 60  
CGTGGCCCTG GTGGAGTCGG GCTGGGGCTC CCTGCTGCCC ACAGCCGTNA TCGCCAACCT 120  
GCTGCACGGG GGGCCTGCTG AGCGCTCGNG GGCCCTCAGC ATCGGGNACC GCCTGACCGC 180  
NATCAACGGG ACCAGCCTGG TGGGGCTGCC CCTGGCTGCN TGCNAGGCCG CTGTACGCAA 240  
AAACGGAATC GCCAGACGTN CGGGTGAACA CTTNAGCATT CGTCCACTTG CCCTTCCCGT 300  
TAACCACCGN CATCATTTCCA CCGGGCCCCC AAGGCCCGNA AAGCAAGTTG GGGTTTTTGC 360  
GNTNGGAGGA CGGGATTNAT TTT 383

(2) INFORMATION FOR SEQ ID NO:937:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 481 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:937:

CGCGTGGTCG CATGAAAGAT CTGAAAGCCA GCTATGTNCT GAACAGCAGT GAATTGCATG 60  
CGCCGCTGCA AAAGANTCAG GTCGTCGGAA CTATCAACTT CCAGCTTGAT GGCAAAACGA 120  
TCGAGCAACG CCCGCTGGTT GTNTTGCAAG AAATCCCGGA AGGTAAGTTC TTCGGCAAAA 180  
TCATTGATTA CATTAATAA AATGTTCCAT CACTGGTTTG GTTAAAAATT AAACACTTGA 240  
AAGTGTAATT TCCGTCCCCA TATACTAAGC ATCAGTAAAA AAACCTCCGC CTTCTGGGGG 300  
TTGGCCTTNA TTTNAATTAC GTTAACGCCG GAGCTGACAT GGAAAACCAA ACTTAACGGA 360

CTGCTTGATT TNCCNTACTC CTTTTACTTA CAAAGTTTTG GGGGCAGGCG TTACCGNGGN 420  
TGGTTGATCA GNGGGTTGAA GTGGTACAGN GCCTGGCCAG GTGGCTACAC CCCACGGTNA 480  
A 481

(2) INFORMATION FOR SEQ ID NO:938:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:938:

GGCAGAGTGA ATCATCAGAG AATTCACACA GGGGAGAAAC CCTTTNANTG TAATAAATGT 60  
GGGAAACTT TTGGCCAGAA ATCAAACCTC AGANTACATC AAAGGACTCA CAGTGGGGAG 120  
AAATCTTATG AATTGCAATG ANTATGGGGA AATTATGTAA GAGAGTCTAC CCTAAGCTTT 180  
ATACCAGAAA ATTCAGGGN GAGGGGGGAA TCCCTATTGA TGTATTAAC NGGAAATNCC 240  
TTTTGACCAA AGGGATTNCC CCNTTTGAT 269

(2) INFORMATION FOR SEQ ID NO:939:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:939:

CCCAAAATAA CCAGCTAGGG TGGCTGTGGG GCCANANCCG TGCCCTCTAT CCNAGCATCT 60  
ACATGCCCCG NGTGCTGGAG GGCACAGGA AGTNACAGAT GTATGTNCAA CACCGTGTGG 120  
GCCGAGNGCA TTCCGTGTGN GCTGTGGGCT GCTGGTGAAC CCCAATNTTG CCGGTNGTTG 180  
CCCTATTGTC CCAGATTTTN CTTATGNACA CGGACAAACC ATTTTTTTTG CCCCCTGGGA 240  
TTGAGCTTGG GAGCAAAGNC TTGGGGGGAG AGTNNGGGCC CAGGGGGG 288

(2) INFORMATION FOR SEQ ID NO:940:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:940:

TGGGGACCTC AAGGCCCGCG GGCTGACCCT NCAGTGGGTG TACTCGGCGC GGGGGGACTA	60
NATCCGGGCG GCGGAAAANC TGCGGCAGGA GATCTACAGC TCGGAGGAGA GAGACGAGCG	120
ACTNANACGC ATGTACAACG TGCGCATAAT GCGGGTGGAG TTCTACTTCC TTTCCCAGTA	180
CGTTTCGCCA GCCGACTCCC CGTTCCGCCA CATCTTCATG GGCCGTGGAG ACCACANGCT	240
NGGCGCCCTN CTGGACCACC TGCGGGCTGC TTGCGCTTCC CAACAGTTCC GGGNACCCCC	300
GGGGGNCCAA CTTTCTTNCA ATTGGGTTTT CCAAGGAAAA GCNTTTTNCC GGGTTCAAT	359

(2) INFORMATION FOR SEQ ID NO:941:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:941:

TGCAGGATTN CGGCAGAGGG AAAANTTGTT TNNTTAGGTT TGGTTAATGC AGGCAAAACC	60
ACTTTCTTCC ACATGCNCAA AGATGACAGA TTGGGCCCAA CATGTNCCAA CANTACATCC	120
GACATCAGAA GAGCCTAACA TTTGCTGGGA ATGAACCTTT ACAACTTTTN NACCTTGGTG	180
GGCAGGAGCA AGCACGTCGC GTTTGGTAAA AATNATCTCC CAGCAATTNA ATGGGGATTT	240
TTNTNNTTGG TGGGACTGTG CCAGATCATT CTCGNCCTCG TGGGAATCCA AAGTTGTAGC	300
TTGAATGGCT TTANATGGAT TGGATGGAAA ACAATTATCC CAAATGNTGC CCAATCCCCT	360
NATTTTGGG GGAANCAAAN AT	382

(2) INFORMATION FOR SEQ ID NO:942:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:942:

GGCACGAGCC AGGATTGGTG CCTTCTCTNA TGGCTCTGGT TTAGCAGCAA GTTCTTTTC	60
ATTTTCGAGTA TCCCAGGATG CTGCTCCAGG CTCTCCCCTG GACAAGTTGG TGTCCAGCAC	120
ATCANACCTG CCAAACGCC TAGCCTCCCG AAAGTGTGTG TCTCCTGAGG AGTTCACAGA	180
AATAATGAAC CAAAGAGGAG CAATTCTACC ATAAGGTGAA TTTNTCCCCA CCTGGTGACA	240

CAAACAGCCT TTTCCCAGGT ACTTTGGTAC CTGGGAGGCG AAGTGGGACG GAGCCAGCAT	300
NGCCGGAANG TATTGCCCCG GGGGTCCCNG TTTTNAAGG TGTTTTTTNG AAGTTCCATG	360
GGAAAGTTTC CTGGGGAAAC GTTTTTTTTG GCAGGGTTTT TTCCCCGNGA AATCANTNTT	420
TTTNAAGGG TCCCCANTTT TTAGGTTGGG AAAA	454

(2) INFORMATION FOR SEQ ID NO:943:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 376 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:943:

GGCAGGAGCG GCACGAGCAC CAAGCAGGCA GTGAGCATGT TTCTNGGAGC AGTGAAGAA	60
GCAAAGAAAG AAGGTGGCAC AGTGGTCTAT GGGGGCAAGG TTATGGATCG CCCTGGAAAT	120
TATGTAGAAC CGACAATTGT GACAGGTCTT GGCCACGATG CGTNCATTGC ANANANAGAG	180
ACTTTTNCTC CGATTCTCTA TGTCTTTAAA TTCAAGAATG AAGAAGAGGT CTTTNCATGG	240
AATAATGAAG TAAACAGGG ACTTTCAAGT AGCATCTTTT ACCAAAGATC TTGGGCAGAA	300
TCTTTCCGCT GGCTTTNGAC CTAAAGGATC CGACTGTGGG CNTTGTAAN GTNCAACATT	360
NCCAACAAGT GGGGCT	376

(2) INFORMATION FOR SEQ ID NO:944:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 351 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:944:

GGCAGGAGCC TGTATCAAAA AAAGGAGACC TGAGGAGGGC CTTGAGCAGA TACATCTCCT	60
CTCTCATCCA CTCAGGTGGC CACTAACACG GACACCAGCC GAAATGCCGG AAATGCGGTC	120
CTGTTTGAGA CAGTACTCAC CATCATGGAT ATCCGCTCTG CAGCTGGCCT ACGGGTTCTA	180
GCTGTCAACA TTCTTGGTCG CTTCTACTC AACAGTGACA GGAACATTAG GTATGTAGCC	240
CTGACATCAC TGCTTTGAC TGGTGCAGTT TTGATTCACA GTGCTTGTTG CAGCGGGNAT	300
TCGGGCCCCA CTNTGGGTGG GNAATGTTCT AAGGGGGAAA CTNGANTGCC T	351

(2) INFORMATION FOR SEQ ID NO:945:



(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:945:

GGCACGAGGT GTTAACTTCC AGATAAGGGA ATATNATTNA ATAATTNATN ATTTTNAAAA	60
TACTGTATTA TGAAGCCATG TTCATAAAGG TAAGAAAGGC AGATTCTACA ACTAGTCAGA	120
CAACTTAACA TTCATACTAA TGACAGCTTC ATTGAAATCA CTTTACTACT CCCCTAGTAA	180
TGGAGTCATT GCATTTATAT TATACATTAT TCTCTTTNCA GTTTTGCTAG CCACCCTAAT	240
TATCCATATT CAGATGAATA TTTAACATGG AGGAGCTTTG CCTGAGGTCT ACCCAGNAAG	300
CCCTGTGTGT GGGTGGTGAC GNCGAGGACG GTCTCTTTTG CCGGTGGACT GGACANATNA	360
CNC	363

(2) INFORMATION FOR SEQ ID NO:946:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:946:

GGCAGAGTTG AGCGGCGCAG GGACCGATAC TTGTAATCAG GGATCGCNAC CTCANANAGT	60
GCCAAGCCCC CGACGCACAA ATATGTCCGG GGAGAGAATG GCCCTGGGGG CTTCATCGTG	120
CTCAAGTCGG CCAGTTAACC CCCGTNTTTG NACCTTTNTN TGGGNTCTTA ATACAGGTCT	180
	180

(2) INFORMATION FOR SEQ ID NO:947:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:947:

GGCAGAGCGG ATCACTGGAG CAAAACCTG TCCCAGTTTT TCCCTGAGGC CATTTCTTTC	60
ATAGATGAAG CCCGGGGCAA GAACTGTGGT GTCTTGGTAC ATTGCTTGGC TGGNCATTAG	120

CCGCTGCAGT CACTGTGAAC TGTGGCTTAC CTTATGCNGA AGCTCAATCT GTCGATGNAA	180
CGATGCCTAT GAACATTGTC AAAATGGAAA AAATCCAACA TATCCCCTGA ACTTCAACTT	240
CATGGGTNCA GCTGCTGGAC TTCGAGAGGA CGCTGGGGAC TTCAGCAGCC CATGTGAACA	300
ACAGGGGTTT CCAGCACAGC AGCTGTATTT TTACCACCCT TTCCAACCAG AATGTGTTAC	360
CAGGTGGGAC TTTTGTCAAT CTAGGGNAAA GACCCACAC CCTCNTGNTG GGATGTTGTN	420
NGGCCTTCAG CAATTTTTTTT GGCAGC	446

(2) INFORMATION FOR SEQ ID NO:948:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 318 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:948:

GGCAGGAGCC ATCATTCCCC AAGANCTTCA AAGATTTTAA AGGCCACCAT TTCCATGCAC	60
ATGTTTCTTG GCGTTGCTGC TGTTTACACT ATGTGGAAAG CTGGACACTC AGCCTGTTTC	120
GGGGGGACCC AGGCTAAAGG TTNTGCCCTA GGTGTGGTAA GTATCTATTG ATGCGTAGTG	180
TGGCTTGCAG GGAACACAG GGGCCACACA CCAACCATTA AGCACCAGGC CTAAGGCAGN	240
AAGCAGAGAG AAACCAACTT CAAGGTCAGA GGAGCCGCTG GGNAGGGAGA AAGGTGTNTN	300
GGTGGAGGNC TAACCAGA	318

(2) INFORMATION FOR SEQ ID NO:949:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 146 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:949:

ATGCCAAAGT NTTGATGAA TTTAANCCTC TTGTGGAAGA GCCCTTCAAA ATTTAAATTC	60
AAACAAAATT GTGAAGNTTT TTGAAGNCAG NTTGGAGGAG TTACAAATTN CCAGTAATGA	120
GCCTATTAGT TCGTTAACAC CANGTA	146

(2) INFORMATION FOR SEQ ID NO:950:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 376 base pairs
  - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:950:

AACCCATAAN TCCAAAAAGA AGATCAGAGA ATATTATAGA CTGCTGANCG TGGAGGAAGG	60
ATGCCCTGCA GATGAAAGTC AGGGNAATCT TTTCATAAGC TTGCCAAGCA ATATCATCCT	120
GAACAGTGGC TCTNAATACT GCTGATTCTG CCAACATTTA TAAAGGNTTG AAAAAGCTTA	180
TAGNAAAGGT GCTCTCCCAT GTGAATAGAN CAAACAAATG CCAGTCAAGN GTNAAAGGTG	240
AAGNAGGANG NAGATGTAGG AAAANTTCAA ATATNAAAAC ACCCCAACAC CGGCNTTATT	300
TAAGTTTTTG AAGGGTTNTT GGTTTTGGGG NCTCCAAATT CAAGGGGGGA AGGCTTTTTG	360
GGGNCANTTT TGGGGG	376

(2) INFORMATION FOR SEQ ID NO:951:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 462 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:951:

TATTTAGGTT TCTTTAATTT TATTCAACAA TATTTTGTA TTTTCAGCAT ATAAGTCTAT	60
CACTGCATTG GTTAAATTTA TTCCTAAGTA TTTTACTGTT TTTAATGCTA TTCTAAATGG	120
ATTCTTTTTTA AAATTTCCCT TTCATATAGT TCATTGCTAA CCTATAGAAA TACAACTGAA	180
TTTCATCATG GGCAGTTTTT TTTCTACATC TTAAGGAAAT TAGTTTATTA GCTCTAAATG	240
GGGTTTTATT TGTGGATTCT TTAAAGGTTT TCTTCCATAT TAAGATCCAT GTCCATCTCT	300
AAAATAGGGG ATTAGTTTTA ATNTTTTCCA TTFNCCCATT TGGGCTGCCC TNAAANTTNC	360
NTTTCCTGCC CNAATGTTCC CGACCNGAAC TTCCGCAGGT ATTGGATAGA GTGGTGAAGC	420
AGGGANCTTG GCCCGTTTTT TAACCTAAGG GNAAAGGTTN CG	462

(2) INFORMATION FOR SEQ ID NO:952:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 505 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:952:

GGCACGAGGT TTTCTCATGC TTTTNAAATC ACTCCATCCG TAGCCAAGAA GATTGCTGCT	60
GTACTIONACGG ATTCATTTCC ATTGAAAGTT CGTGGCATCC ATTTGATAAA TGAACCAGTA	120
ATTTTCCATG CTGTCTTTTC CATGGATCAA ACCATTCTCTG GACTGAAAAA NTTAAGGAAC	180
GGACAGGGCC TCACTTTGTG NCAGTGGGCA CGATCTTGGG CTCACTGCAA CCTCCACCTC	240
CTGGGGCTTC AAGCAATCCT CCTGCCTTCA GCCCACCAAG TTATCTGGGG ACTTACAGTN	300
CCTGCACCAC CANGGCTGTN AAATCCCCGC ACNTTTGGGA GGGCCCNNGC GGGCGGGTTC	360
ACGGGGTTCA GGGGNTCGGG ACCCTTCCGG GTTAAAANGG TGGNAACCCG TTTTTTANTT	420
AAAATTCCAA AAAATTTGGC CGGGNGTATT TGCGGGGGGC TTTTAGTNCC CATTATTTGG	480
NGGTTTNGGC AGGGATGGGG GTTAN	505

(2) INFORMATION FOR SEQ ID NO:953:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:953:

GGCACGNGCG CATCATAAGG GGCCGCTGG CGAAGGCTGG AAGTGGGGCG GCTGCAGCNA	60
GGACGCTGAC TTCGGCGTGT TAGTGTCAG GGAGTTCGCG GATGCNCGCN AGAACAGGCC	120
NGACGCGCGC TCGGCCATGA ACAAGCACAA CAACGAGGCG GGCCGCACGA CTATCCTGGA	180
CCACATGCAC CTCAAATNCA AGTNCCACGG GNTGTCTGGC AGCTTTNAGG TTGAAGACCT	240
GNTTGGTNGG GCGCAACTTG ANTTTCCGTT GCCATCGGTG ACTTTCTCAA GGACAAGTTA	300
TGACAGCGNC TTTGGGAGAT TGGTTAGTAG AAGAAGNAAC CCTTNNTT	348

(2) INFORMATION FOR SEQ ID NO:954:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:954:

TTTCCTTTAA TCTTCCCGCC CTGTAAGTGT TTCCATGCTT TATGAGCAAC AGCCTGACGG	60
ACCGCGACAT AGACATGCGC CGGATGCACG GGTATTTTGC CAATATCTGC GCCATCAAGC	120
CCGATATCTC CTGTCAGTGC ACCTAATACA TTACCCGGGC GCATTTTGGC TTTTTCCTCCG	180

NCATCGATAC ACAACGTTGC CATTTCTGCT TCCAGCGTCG CAATGTGAAC TATTTAGCTG	240
GCGGCGTTTT GNCAGTNAAA GTTTTTATCT TGCAACATGT NCAGAAATGG ATATTGGGCC	300
CGCTGGTGGT TTNTTCCGG AGNCACAGT	329

(2) INFORMATION FOR SEQ ID NO:955:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:955:

GGNAGAGCCA TGGNGGNGCT GGTGGATNAG GGNCTGGTGA AAGCCCTTNG GGTCTCCAAT	60
TTCAGGCACT TNCAGATCGA GAAGCTCTTG AACAAACCTN GACTGAATNN TAAACCACTA	120
ACTNNCCAGG TTGCAGTGTC ACCCATACCT CACGCANGAG AAACNTATC CAGTACTGCC	180
ACTCCAAGGG CATCACCGTT ACGGCCTACA GNCCCCTGGG TTCTTCCGGA TAGACCTTGG	240
GCCAAGCCAG AAGANCCTTC CCTGCTGGAG GTTNCNAAGC TTAAGGTAGA TTNTTGCAA	299

(2) INFORMATION FOR SEQ ID NO:956:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:956:

ATCACTTTTG ACCTCAGTTT TAACAACCTGA GGAGGAGGAG CTCATCATGT ATCTGTTTAT	60
TCATTTACCA TATATTTATT AAGCACCCAC TCTATTCTGG GAAATAGTNT ACAGTAGTGA	120
ATACTAAAAT GCCGGGCTAA TATCTCTACC TTCATATAGC TCACATTCTA GTGGCAGGAA	180
GAGATAATAA GTAAGATAAN ATGAAGTACA ATATATAATA TGTTAGATAA ATGCTCCAGT	240
GGGAAAAAAT AAAGCGGGGA AGGAATACAG GGAATGCCTG CAGAGTTGAA TGGTTAAGGT	300
AGCTTGGGGA AATCCCTCAC TGGGGNNTCC GNGGAACTCC AACAAAGGGN CCCCCTGAGG	360
CTTGTCTGGG GGNCCAGAAA GCTCTGTCTG GGGGCCTGGG	400

(2) INFORMATION FOR SEQ ID NO:957:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:957:

AGAAGAGCTA ACANTTGCTG GAATNACCTT TACAACCTTTT ANTCTTGGTG GGCACGAGCA	60
AGCACGTCGC GTTTGGAAAA ATTATCTCCC AGCAATTAAT GGGAATTNTT TTTNTGGTGG	120
ACTGTGCCAG ATCATTCTCG CCTCGTGGNA ATCCAAAGTT GAAGCTTAAT GCTTTAATGA	180
ACTGATGAAA CAATATCCAA TGTGCCCAAT CCTTATCTTG GGTAACAAAA TTGAACAGAN	240
CAGATGCAAT CAGTGAAGA AAAACTCCGT GAGAATAATT TGGGCTTTAT GGGACAGACC	300
ACAGGTAAAG GGGGANTGTG AACCTGAAA GGAGCTGAAT GCTCGGCCCN GGAAGTNTTN	360
CAGTGCCATG TGGTTCAAGA GGCAAGTTAC GGCGAGGTTT NC	402

(2) INFORMATION FOR SEQ ID NO:958:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 409 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:958:

CAGNAGGGAA ATNNTATTTT TAANTCCAGC ACGGGGTAC TGTTTTTTTA TCTCAAAGCC	60
AAAAGCCACA GGCATGGCCA CAGTTACTGT NCATCTCAGG GAATGTGAAA AGANTCAAGA	120
TCCAAGCAGC CACAGACTCA AAGGNACATC AGTGAAGTGC NTGGCCAAAG CATACCCACA	180
GTACTACAGA AAGCCGTNCA GTGGTCAAGC GGATGCCGGC CATGCTCACT GGACTCTNTC	240
AAGGTCTGTG GCACTCGGNC AGGTGGTGTT TACTAGTGNT CCTCATAAAA NTTAACCTCC	300
CTGGTGCGAA TTTCCAGTTC ACCTGGTGAT TCGGACTGG GAATTCTTGA GNTTTTGNTT	360
AAGAGCTGTT GCTGTTGGCT GNAGTATGGG TTGTGTTATG TNNAAGGTG	409

(2) INFORMATION FOR SEQ ID NO:959:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 278 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:959:

TAAAGCTAAC CAGCAATTTT AAGTCTACTG TAAAATCAAT GGGTCTGGAA ATGGATGGNC	60
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TGTTTTTNA AAGAGAACTT GNATGGCAGT TTAGATTTCA AGAAAACTG GTTTCATTAT	120
GAAAGNAAGG NTTTGGANCA TCTTTTTCCT NACTGGGCAC AACAAATTTT TGGCTGGGAA	180
AATGAGAAAG GTTCATTTGA ATAAAGGCNC ACAGTCTGCC ATCCCATATG CTTTNAGAGN	240
TGGGACTGGG AAGGACTGGG ATGGGCAGAN CCCNTACT	278

(2) INFORMATION FOR SEQ ID NO:960:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 188 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:960:

CGCGTCGTTT TNACCTGTNA CGTTCACGCC CATTGCAGCG GCACAGTCAC GCAGACGTGC	60
AGCGGCGACT TTCCTGTTGA ATACCTGAAC GTGCGGCANA AAACGGCGTT ACATACACCG	120
TGTGGCAGGT TGTAAGAAACC GCCCAGCTGG TGCGCCATCG CATGAACATA ACCCAGAGAA	180
GCATTATT	188

(2) INFORMATION FOR SEQ ID NO:961:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 159 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:961:

TTAACCAAAA TCCTGGACAA ATGCAGATNT GGCCTGCAAA ANGCGGCCCT NTGGAAACCT	60
GGTGTNTGTC CTCATTGGGG CTTAAGGGNT CCTTCCGTTT CCTCCCTGGT TGAANAGCAT	120
TGGTTAACAN CTACTTCATA ACGTTTGGTT TGGGNCTCC	159

(2) INFORMATION FOR SEQ ID NO:962:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 307 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:962:

CCGCCTCAAG GACCCTCAGG TNTGGATGGA TGCGGGCACC CANNTCTNNT TCTCCTTTGC	60
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CATCTGCCAG GGGTGCCTGA AAGCCCTGGG CAGCTACAAC AAGTNTCACA ACAACTGCTA	120
CAAGGANTGC TTCGCCCTAT GCTTCCTGAA CAGTGCCACC AGCTTTTTTGG CTGGGTTTTTT	180
NGTCTAGATT TGGGACATAT CTCCTGGAAG GAGCTATTAG CCATGACCCA CAAAGGTCAG	240
AGATTAGGGT TGCTGGTATT TTGGTTTTGG CTGNTTAAAG AGGCCCTTAG GGACCANAAT	300
TTTTCCN	307

(2) INFORMATION FOR SEQ ID NO:963:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 423 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:963:

CGTGGTGGNT CATGCCTGTA ATCCCAGCAC TTTGGGAGGC CAAGGCGGGT GGNTCACGAG	60
GTCAGGNGTT CAAGACCAGC CTGGCCAAGA TGGTGAAACC CCATCTCTAC TAAAAATACA	120
AAAATTAGCC AGGCGTGGTG GCAGGTGCCT GTAATTCCAG CTACTCGGGA GGCTGAGGCA	180
GAGAATTGCT TGAACCTGGG AGGCGGAGGT TGCAGTGAGC CGGGATCACG CCACTGCACT	240
TCAGCCTGGG CAACAGAGTG AGACTCCATC TCAAAAACCA AAACAAAACA AAAAAAATT	300
CTTGCTCATT CTGCGCTAAC NATGCTTTCC CTGTTACCGT CANAGTAAAT ATATCTTACT	360
GGGGCTGGNA TTATAATTTA CANAACATTT TTNACATATT TGAGTNTTTC CTCTTGAAAA	420
AAT	423

(2) INFORMATION FOR SEQ ID NO:964:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 422 basepairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:964:

CGAAGNCCAT ACCTGATGGA GTCTCTGCCA AAATATTTTT GTCATCATCA GAACTCAAAA	60
GCCACAGCAC CTGAGACAGA AGGAGAAATT CTAGAGTTGA ATGNCANTTC TGAAGCCCTC	120
AAGCAAGAGA CTTTCCCCC GACATTACGA CACTGTATAG AGCGGCTTTA CTCCACCATG	180
TAAAAAATA CCTCTTTAAC CGGNTCGACA TTCCACCATA TGAGTCCTAT GAGAAGCTCT	240
ACGAGAAGCT GCTGACAGCC GTGGAGGAGA CCTGCGGGTT TGCTGTGGAG TGAAAAGCAA	300



CCAAAGGCAA CAGAGTCTTA GTCATGGCC ACCAGACCAA AAGCATCCAG TTCTGTTGCA	360
CCTCCTGGAA AGCTNGCAGA GGCCCTGGAN TTTCCAGNTC ANCTNAGGGG AAAGGGTTGT	420
TT	422

(2) INFORMATION FOR SEQ ID NO:965:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 410 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:965:

CGAAGNCCAT ACCTGATGGA GTCTCTGCCA AAATATTTTT NTCATCATCA GAACTCAAAA	60
GCCACAGCAC CTGAGACAGA AGGAGAAATT CTAGAGTTGA ATGACAATTC TGAAGCCCTC	120
AAGCAAGAGA CTTTCCCCC GACATTACGA CACTGTATAG AGCGGCTTTA CTNCACCATG	180
TAAAAAATA CCTCTTTAAC CGGNTCGACA TTCCACCATA TGAGTCCTAT GAGAAGCTCT	240
ACGAGAAGCT GCTGACAGCC GTGGAGGAGA CCTGCGGGTT TGCTGTGGAG TGAAAAGCAA	300
CCAAAGGCAA CAGAGTCTTA GCTTCATGGC CACCAGACCA AAAGCATCCA GNTTCTGTGC	360
ACTTNCCTGGA AAGCTGGCAG AGGTCCTGGA TTNCCANTTC TACCTNGGGG	410

(2) INFORMATION FOR SEQ ID NO:966:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 374 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:966:

GGCACGAGCA AACTATAAAA AATGGTACCC ATGGTTAGGA CATAGCTACA CAAGCATTTG	60
TAGTTTAGAA TATATAATTC ATAAAAATTT GAAGTGAGAG GAATAGTTAA TATGTAATAG	120
AAGAAAAAGT ACTTGCTCAG GTAGTTGTAA CTCTTAATAA AACCAATGAC TAGAATACAA	180
GTGGAAGTAA AAAGGTGGAG ATAGATTAAT AGCCTAAATA ACGAGAGAAC CTTATGCCTT	240
TTTTAAAACA AAACAAAACC ATTGAGACAT TTTACTTAGT CCTAAAATCT AGCCTGGGNT	300
TTATGCTATA AATGGATATT CTATTTTTC TGTAAATTG TACATTACNC AGAAATNATN	360
AATATTNTTA CTTT	374

(2) INFORMATION FOR SEQ ID NO:967:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:967:

CGAAGACCAT ACCTGATGGA GTCTCTGCCA AAATATTTTT NTCATCATCA GAACTCAAAA	60
GCCACAGCAC CTGAGACAGA AGGNGAAATT CTAGAGTTGA ATGACANTTC TGAAGCCCTC	120
AAGCAAGAGA CTTTCCCCC GACATTACGA CACTGTATAG AGCGGCTTTA CTNCNCCATG	180
TAAAAAATA CCTCTTTAAC CGGATCGACA TTCCACCATA TGAGTCCTAT GAGAAGCTCT	240
ACGAGAAGCT GCTGACAGCC GTGGAGGAGA CCTGCGGGTT TAGCTGTGGC AGTNGNAAAG	300
CANCCAAAGG TCAACAGTGT TTTNGNTTCA TGGCCACCAG TCC	343

(2) INFORMATION FOR SEQ ID NO:968:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:968:

GGCANAGCCA TNATGCTTTC ACCAAGGCAA TCCAAGAAGC TCGGCAAATG AAGGAGCAAC	60
TCCGACGGNA ACAACANGTN CTTTANGGGT AAGGTGGCTT TTGTGAATAG TCTGGGTCTC	120
AATAACTGGC CGAACAGAAA AAAAAAAAAA AAAANCTT	158

(2) INFORMATION FOR SEQ ID NO:969:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:969:

TTTTTCTCTG AACTATTTGT TNATATCACT TTGCCCATTT TAAAAATTGG GTTTCCGCCC	60
CTCTTAATGA GCAGGAGTAG CCTTCTGTGT ATTGAGTTTA ACTTTGTGAT ATAAGTTGCA	120
GATTCTTTTT CTCAGGTTTT CATTTCTATT TTTCTGTAG TTTGTACCTT TTCCATTTTT	180
ATGGATATCT AACTCAACC TTAAGTGCA GAACTTCACT GATACTTTTG TTAGGTAAAC	240

ACACATCTGT CCCAGGATA ATTTAACACA ACGACAGAGA AGGGAGGTAG NAAAANNAGT 300  
TNGTAGAGAG CTCAGNAAGG GGCTGG 326

(2) INFORMATION FOR SEQ ID NO:970:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:970:

GGCAGGAGCT AATATATAGA ATACACTTTT ATAATATATT NTAATATATA GAATACACTT 60  
TTATAATATA TTNTAATATA TAGAATACAC TTTTATAATA TATTCTAATA TACATAATAT 120  
ATTCTAATAC ATGTAGACAC ACCCAATTTA ATGCTTTGCA TGGGCATAGT TATGCAAAGC 180  
CTAGTTCTTA AGTGCGGTGG TCTCAATGTG TCCCCCAGAA TTCATATGAT TGANGCTTAA 240  
TCCCCAGTGG CAACAGTGTT GAGNAGCTGG GGCCTAATGG GAAGTGTTTA GTTTNTGAAG 300  
GCCTCTGCCC TGCATGAANN AGGTTNAATG TTGTTGTGGA AAAGGGTGTG GA 352

(2) INFORMATION FOR SEQ ID NO:971:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:971:

CTTATCTAAT TCCNCTGGCT AGANCCTCAA GTATAAGGTT AAATACAAGT GGCAAGANTG 60  
AATATCCTCG TCCTGTTTCT GAGCTTAGAG GAAAAGCCCT ATCTTTCACC ATTAAATTTG 120  
CATGGTGGTC GTCAGTTTAA CATAGCTGTT CTTTATCAGG TTGAAGGTGT TCCATTCTAT 180  
TTTTNAGTTT ATTGAGTGGT TTTACTATAA AAAAGCATGT TGNAATTTTG TNAAAATATA 240  
TATGCCTTTT TCCTATTGGG NATACTTAGT GGGATTTTGG TCCCTTTAAT TCCCGNTNTA 300  
TANGGTTTTT TAACANTTAA TTTGGATTTT CAG 333

(2) INFORMATION FOR SEQ ID NO:972:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:972:

GGCANAGTCG CATTGCCCC GCGGCAGCCC CACCCCGCT CCCTTCCCCA GGCACCGCGG	60
CGGGANGCCC TGCCCTGCCG CTGAACCCCC TGTGTCCTGC TCCGGCCCTC TCGCCAGGNA	120
CTCCTGGCCT AGCCTTGCAC CCCGACCCTT TCCCGGGGAA GCCGGGGGA CCTTACGCTG	180
GGGGCTTGGT GCCGCCCGAA GTNATGACCC CGCGTGGGAA GAAGCAGGGT TAGGGGGTNG	240
GGAGTCCTTG GTAAGATCCC TGGACGTCAG NACAGTAGAG GCGGGTGGTA GANGGGTNGG	300
	300

(2) INFORMATION FOR SEQ ID NO:973:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:973:

GGCAGGAGCG GGAGCAAGAG TCCGCTGAGC TGCAGTGTCT GGTGAGAGT ACCCGTGGGA	60
CGGTGCNCNC GGGGAGGCAG CCGTCCCGGG TTAGGTGGCG TGGCCGACCG GACCCCCAAC	120
TGGCGCCTCT CCCCCTGAGG GGTCCCNAGC TAGGAGATGG GAGGCACAGC TNCGTGGGCC	180
TNGGCGGAAA GNAATGCGGG GTCCGCTTN	209

(2) INFORMATION FOR SEQ ID NO:974:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:974:

GGCAGAGCGG GGACATAGTG AACACTTGTT CGGGGACATG NTAGACACTT ACAACTAAGG	60
CATAAGAACC CGTTTATGGA GTCGCTTATG CCCTGGGAAT GCNAGAAATA CCATGTCATT	120
ACGTACTGAG TTTGTTTNGT TCGCCTCGCA GGNACGGGGC GACATCCGTT CCCTCTGCCG	180
TCGCTTCGGC ATTTNACCTG CCACCGGTTA CAAGTGGCTC CAGCGCTGGG CTCAGGAAGG	240
TGCCGCCGGT CTTCAGGACC CCCCCGNGCC ATTCCGCACC ATTCCCCGAA CCGTTCATCT	300
GAACGACATC ACGGCCCTGC TGCCTATGGN CCCATGAACC GTAAGNAACG TTGGGGAGCC	360

CGNAAGTTTA AGCGTTGGTT CNAGGGGGGG CCCGTACCAT TGGCCTTTAA TNAGTCGATT 420  
A 421

(2) INFORMATION FOR SEQ ID NO:975:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:975:

GGCACGANAA GCGTACTGCA ATTAAGGCCT TCAATNAGAC TATCAAGATC TTTNAAGAGC 60  
AGGGCCAGAC TCAAGAGAAA TGCAGCAAGG AATACCTGGA GCNCTTCCGG CGTGAGGGCA 120  
ACGAGAAAGA GATGCAAAGG ATCCTNCTGA ACTCCGAGCG GCTCAAGTCC CGCNTTGCCG 180  
AGATCCATGA GAGCCGCACG ANGCTGGAGC AGCAGCTGCG GGCCCAGGCC TCGGACAACA 240  
GAGAGATCGA CAAGCGCATG ANCAGCCTCA AGCCGGACCT CATGCAGCTG CGCAAGATCC 300  
GAGGACCAGT ACCTCGTGTG GGTTCACCCA GAAAGGCGCC CGGCAGAAGG AAATTCAANG 360  
NTGGTTGGGG GTTTAAAAATG NGATNNGTGG TAT 393

(2) INFORMATION FOR SEQ ID NO:976:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:976:

GGCAGAGAAA CAGCTGTNTG AATTATGTCT GCACTAAGTC TCTGGCAGAG GAAGCCCAGA 60  
GGCCGTGAAC AGCATATCTA AAAGCCCCGA CATGTCTTGA AAAGGTCAGG GANACGTCTG 120  
TAAATAAGGA CTGACGTTTG GGAAGGAGGC CTGAAGGATT AAGTAGACCT TNCCCCAGTG 180  
GGGNCGAAGG AATGGGGAGA GAAGTCCCTG GTAGAGGGGA ACCCCATTTA NCAGAGCTTC 240  
CGGAACGTGG GNAAGGAAGC TTGAACTCTG CCGAAGGNAA CTGGNAGGAA AGACCTGTGT 300  
TACTGCCAGG GTCCAAGAGC TTGGGAAGAG GGTAGGTTGG GGGCCAGATG GTGCCCCGGT 360  
TTTGGTTGGN CGGTGAGGAG GAGNCTGGGG ATTTGGAACA CCTGCCTTTT TGGAGCTGTT 420  
NGAAAGGATC CAATGAGTTC ATCCTTCTTN TTACCAATNC TGGNTTCCCA TT 472

(2) INFORMATION FOR SEQ ID NO:977:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 410 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:977:

GGCACGAGTG GCCACAATAG AGGCCATTAT GCAACCTTGA AAAGTTATTG TGATAATGAC	60
CACATAGCAA TGTGAAGAAA TAGGCATGAC ATGTATCTAA GTGAAAAAGA TGACATAAAA	120
NCTCTGCACC CAAGTAAAAC TATGCAAAAAG GTAAATATGC AAAAAGGAAA TAATGCAAAA	180
NGAAAAGGGT TGTATATGGTG ATAAAATTAT GGCCATGTTT TTATTCTTTA TTTCATAAAC	240
TCTGTAATAT GTTATTATTT TCATAATTAA AAATTATACT TTTAAGAAAG GAATGCCAC	300
TNGGAATTGA GCTCATTTAG GCATTGAGTG AAATTACTGC TTTCAAAGNN ACAGCNTTAT	360
GAAGGATTNA CAAATGTGTT TAGAAGCCCN TTTTGTGTTT TTGTAACATT	410

(2) INFORMATION FOR SEQ ID NO:978:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 358 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:978:

GGCACGAGNA TAAACAGCTC AATGAAATTA CTAAAAAGGA AAACACTGGC ATAAACGGTC	60
CCCAGATCAA GATATAGAAT GTNACTAGCA CTTGTAAGGC CCTCTTGTTT CCACCTTTTCT	120
AATTCTGTTC CATGGAGAAC CACTATCCTG AACTTCTGAA TACCATAAAT NAATGCTTAT	180
TTGGGGGTTT AATTTTGAAA GGGATTAGGA AATACATAGT GTTCTGGGTC TGGTTTTATC	240
CATGCCATTG AATTATGCTT GTGGTTCATT NCATTCTCAT TGCTGNCATA TTAATTCCTT	300
TTGAAATTNT TNTGAGCACA ATTTAATTTT AANTGTTGAT GGGACATTTT TCCCTGCA	358

(2) INFORMATION FOR SEQ ID NO:979:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 100 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:979:

AAACATGGTG CTGTTTACTG NGGACCCGAN CANCGTCCAG GAAGCATGGG GTCCGGTCGG	60
AGCGAAAGAT GGCGNGTTTG GTNAGGAGGC ACTGGCGAGG	100

(2) INFORMATION FOR SEQ ID NO:980:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 237 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:980:

GGCACGAGCG GCACGAGGGA ATGGAGTNAA ATGGAATGGA ATAGACTCGA ATGTAATGGA	60
CCAAAATNAA ATGGACTCGA AGGGAATGAN CTCGAATGCA ATGGAAGCGA ACGGAAAGGA	120
ATGGAATAGA CTCGAATGGA ATGGACTGGA ATGGTATGTN AATGGNAATG GNAATGGAAA	180
CGAATGGTAA TGAATTCAA TGGGAATCGA ATGGGAATCA AATGGNAATG GNAATGG	237

(2) INFORMATION FOR SEQ ID NO:981:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 415 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:981:

GGCAGAGGNC ATGGCTGGCT AGTTGTCTGG AGTGTGGATC AAGAGAGACA GGATTATATT	60
ACATGCTCTG GTATATTACA TTAAGCTGGG TCCTGATTCA GGGCCAATAT TTAAGTTCAC	120
TGAATGCTTG TTGCCTCGGA ATNTCTCTCT GGCTGAATGG CTGAATTTAT CTCCCTGAAA	180
GAAACATGGT GGTAAAGTCT CATGAAGCAG TCCATAGACT TATGAAACAA AATGCTGCAG	240
CACTTTTCTG TCTCAGGGAT AGAGACATGT AGGGAAAATG AGCACTGGGC TGAGAGTCAC	300
ATGTACTATA TTCTAGACCT GACACTGCCG TCAAGCAGGT GTTTTCACTC AGGGGCAATT	360
CTGTTGTATT TCCGAAAAA CTCNNTTCT NAATCTATAA ACTNNGGNGA AAATG	415

(2) INFORMATION FOR SEQ ID NO:982:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 220 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:982:

GGCACGAGCC CTGCACTCGG GTTGATTCCA ATCCATTCCA TTCCATTCCA TTCGATTCCA	60
TTCCAATACA ATTNITTCCA TTCCATTCTA TTCCGTACCA TGCCATTCCA TTCCACACAA	120
TTCCATTNCA TTCCATTCCA GTCCGTNCCG TTCCGTTCGG TTCCATTCCA TTCCATTNN	180
ATGCTATTCG AGGTTAATTC CATTCCATNC CATTGATTG	220

(2) INFORMATION FOR SEQ ID NO:983:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:983:

GGCACGAGCT GGGTCGCCAC CCCTTCCCTC TCCACCTCCT CCAGCCCAAG CCCTAAGGCG	60
TAGNAAGGTG GCCCTGAGGC CCCGCTTGGC GTNGGANNCG GGGGTCTTTT TGCCTTAAGG	120
AACCCGCCGC CGCATTCCTA GGGTTTTTAA AGATCCTCTC CCCCCGCTCC TCCAGCTCCT	180
CGTTGAGCCG GAGGAAGGCC TC	202

(2) INFORMATION FOR SEQ ID NO:984:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:984:

CTGCTTCCTA GAGGGCAGCA AGGTCTCCCG GGTNACCCTG CACAACGAGA GCTACATAGA	60
GGAGTTGGAC ATCCGCATCG GGGACTGGTT TTTGGTGCAC AAGGCGGGCG GGGTCATCCC	120
CAAGGTCCTC CGGGTTNCTC AAGGATTNCT GCACGGGGGA GGAAAGGCC ATTCGCTGGC	180
CCGAAACCTG CCCCATTNCT GNCACCGTT TCCTTCAAGG TAGGGGNAAG GTTNCACCGC	240
TGGCCCCCAA CCCCTTTTNT CCCC	265

(2) INFORMATION FOR SEQ ID NO:985:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:985:

CTTGGCCAGN AATGTGGTTT TAATTTGTAT TCCCCTGATA ACTAATGAAG TAGAACTCTT	60
TTTCATATAT TTACTATTCA TTTGGAGTGN TAAAAAATT TTATGANCAC TTGCATTTTA	120
AANTATTAAA CTTTCCTATG TTAAGAAGGG CTGTTGTAAA TTAGTTATGT NCTAAAACAT	180
TTGGGCATAN TCATTGCAGT CTATCTCTGT GATTTGCNTA AGTTGTGNAT TCTTTGGAAA	240
TATTTTTTTC CNT	253

(2) INFORMATION FOR SEQ ID NO:986:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:986:

GGCAGAGNCA CCTGCGGTCT CCTGCATTAT CAGGAAGATC AAGGNAGCTG GTGGAATCAT	60
TCTAACAGCC AGCCACTGCC CTGGAGGACC AGGGGAGAGT TTGGAGTGAA GTTTAATGTT	120
GTCTCAGACA AAATCTACCA AATCAGCAAA ACGATTGAGG AATATGCTAT ATGTCCTGAT	180
CTCCAAATCG ACCTATCTNC GACTAGGGAA GACAAGAATT TGAACCTAGA GAACAAATTC	240
AAACCATTCA GAGTAGAGAT AGTGGGACCC ATGGGATTAT CTATCTTNAA CCTCCTTTTCG	300
GGACCATCTT TTGGACTTTN CATGCCCTTC AAGGAGTTTG GCTTGGNACT NGGGGGCCCC	360
AGGCCCAAAC TNGGAAAGGA TTTTCGGCGG TTTGGTAN	398

(2) INFORMATION FOR SEQ ID NO:987:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:987:

GGCAGAGGTA ATTCTNCGTT AATTCGGCAC CANAGGATTC AACTGGAGA GAGACCCTAT	60
CACTGTAAGG AGTGTGGGCG AGCCTTTAAT GATAATGCAA ATCTGAATCA GGCATCAAAN	120
AATCCACAGT GGGGNACAGA CCCTATTACT GTACAGAAAC ACGTGAATGT GGGAAAAGCA	180
CCAGGACATC CCCACAGTGG AAAAATATCC AAGGAAAGGT TCCAAGGAAT CCCCTGTGCC	240

AAGGGAAACC TTTGCATATG TGAAGGTAGT GTGGGGAAAT CCTTTCAGCT TACTTTTCCT	300
TACTNTTGCT TAGGNCACCA GTGTNTTCC AACTGGGGG NGGAAACCNT ATGGNGTGTA	360
ATTGAGTTTG GGCAAAGCTT TTGGNAAGGN CTTTCCCTTT TAGGCCANCA NCAGCGTTTT	420
TCNCACAGGG GGGAAAGGCN TTATTCTTGT AAAGTATTGT GGGCCAGNCT TTCAATTTTT	480
CCTTCCAAAC TTA	493

(2) INFORMATION FOR SEQ ID NO:988:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:988:

GGCACGAGGG CTAAGTGAGA GGGGGCAGTG CTTCAGGCTT GCTTCAGGTC ATCCAATAGA	60
CAGCAAATCC TGCCACCTTG TCCATCAGAG AAGCCATTCG TCCTCCCACT AAGAGAAGTG	120
AATTAGGGTA CAGAGGAAGG AAAAACCAGA AGTAATACCC CCAAATGCA CCCCTCCTGG	180
GGGCTAAGGC AGGAATCCCC TCATCAAAAC AAGACTGAAT TAAGAAGTGC TTGACCTTAT	240
GAGTACTAAG CCCATGTCTC TGTCATTGAG TTCCTGTGCT ATCCTTTGGC ACTATGGATG	300
AGGACTTCGA AGGGAATGAT GATGTCCTTA TTCTTTCACA ACATCACTAT CCAAGCTTGA	360
AGGAAGGAAN TATGGGCACA CCCGAATTAA NTGCAATATT TTAGGAAAAC TGTAGTGGA	420
GTTTTNAAAT TGTGGTACNT GCCCAGTATT GGATGGGGGT AAAAAGGAAG GTTCCAAAA	480
GNGNTNAAAA ATT	493

(2) INFORMATION FOR SEQ ID NO:989:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:989:

GGCACGAGCA CATCCTCACT AGTATGCCAT TATTTCTTCA TGTACTTTTT CAGTCCA	60
GTCCCATTTG GCAGTTCTGA TACCACCAGA GAAGGCTGAC GGAGGGAGTC CTATTAATGC	120
TGGTTAGGGG TGGAAGTCCA GATAATCCAG GCAATCTCCA CTGCCACTGT GTGGTGGGAG	180
CTTGTTATNA CCTACTGGAG TAGAAGGTTT TGGGGTCCCT AAACAGTCAG CCACCTCTNA	240

CGTTACCCCA ATGTGGGTTT GAGTGCTTCG TTACTGCCTG ATGGTGGTGA AAGTCTAGTA	300
TCTCCAATTG ACCTTACTCG TGTGGGTGGG GATTAGGTCA CAGTTTTTTTGT GTGTGGGGGG	360
CAGAGGGGGT TGCTNNTTGA CAGCAGGGTA GTGGTTATTG TTTAAAAGTT TTCTGTTCTT	420
AAATAGGGTG ACCTTTTCCT GGTCTTTTGG CTAGAGAGAG CAAGTTTTTTG TTGGAGTTCT	480
TTCTGTCTGT CCNGTTGGTA T	501

(2) INFORMATION FOR SEQ ID NO:990:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:990:

GGNGGAGATG GCCTTCTCCA CGGTGNCTGC GGATGTCCCA CGNGTCTCCG NCACCCACTG	60
GACATCTGTG CTCGCAATTA TAGATGCCCT TTAGCTCCTC ATTTTGAGCA AGAGGAGCTC	120
GAGTTCTCCT TTGGCTCGTG NATGGAATCN ACAGCAGGTC AGGAGAGATT CAACAGCATT	180
ACCTCAGCTT ATTACAGAAG TGCCAAGGGG ATCATATTAG TATATGAATA TCACTAAGGA	240
NGAAGTTAGA AATCCTTNAT GAAGGTACC ANCAACAGCA NGTGN	285

(2) INFORMATION FOR SEQ ID NO:991:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:991:

GGCAGAGCCA CAATGTAAGC ACCAAACTTC AGCACTTGGT CGTACATATC TATGGAGAAT	60
GNGACAAATT AGAAATCAAG AAATTTCTCT TCCTCAAAGC AGTACTTTTA AACACTGTTC	120
AGGACCTCTG GCCACGNAGA AGCCTCCTTT NACTATGCCT CCTGTTTGGC CACCCTATAG	180
ACTAAAGGGA GTATCGACCT GTATCCCATT CAAGACTCCA GAGGATCTTC AAAAGCACAA	240
GACAGCAACA GAGAGATGCA CTGTCTTTCA CAAGATACAG TGTGTAAGTC TTNCCAGATT	300
GNCCTTTCCC ATTTTATATC CNCTCNGNAT TTCTGTACTC ACGGTTTTCA CCNCCNTTAA	360
TTTCACATTT GGTCTTACA AAGGTTGGGG TATTTTCCA AG	402

(2) INFORMATION FOR SEQ ID NO:992:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:992:

GGCACGAGGT CCTTTTTATT CCAGTCCACT GCATTCTGGT CCATTCCATT TGATTCCATT	60
CCATTCTATT CCATTCCATA CAGTTGCATT GCTTTGGATT CCATTCTATA TCTATAANTT	120
CAATTCGAGA CCATTGCTTT TGAGTGCATT CTATATGATT CCATTCCATT CAAGTCCATT	180
ACATTTGGTT CCATTCCATT CCATTCCATT CCCTTCCATT CCATTCCATT TGATATCAAT	240
CCATTCGATT CCATTCCATT CGAGCACATT CCATTCGAGT CCATTCCATT CGNATGCCAT	300
TCCATTTGAA TTCTATTCCA TTAGTCTCCA TTCAATTCCA TTAAANTTCC ATTCCATTCC	360
ATNCTATNCC AACTGN	376

(2) INFORMATION FOR SEQ ID NO:993:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:993:

GGCAGAGNAA AAAGTGCTN CTTTGACCA GATTTATCA CTGTCACAAA GGAAAATNAA	60
GAATTAGACT GGAATTTACT GAAACCAGAT ATTTATGCAA CAATCATGGA CTTCTTTGCC	120
ATCTGGCTTA CCCCTGGTTA CTGAGGAAAC ACCTTCAGGA GAAGCAGGAT CTGAAGAAGA	180
TGATGAAGTT GTGGCAATGA TTAAGGAATT GTTAGATACT AGAATACGGC CAACTGTGCC	240
AGGAAGATGG AGGGGATGTA ATCATTACTN CTGAAAAATG GAATTCCAGA ACATGCTGCC	300
AGTTTTATAT TCCGGAGGTA GAAGGCGTAG AACAGGTTAT GGATGATGAA TCAGTTGAAA	360
AAGGANGCAA ACTCACCTTA AATNATCTNG GNTTTTTTTN GGCNTAACA TCCGANTGTT	420
GATATATATT CCAGTTTTTA TTATTAAANG CTGGGGACTN NAGGTTATNA AATTGCCTTC	480
CGGGATGTTT TTAANTG	497

(2) INFORMATION FOR SEQ ID NO:994:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:994:

GGCANAGCCA GCACTTTGGG AGGCCGAGGG GTGGATCACG AGGTCAGGAG TTCAAGACCA	60
GCCTGGCCAA GATGGTGAAC CCCATCTCTA CTAAAACTA CAAAAATTAG CTGGGCATGG	120
TGGCAGGCTC CTGTAATCCC AACTACTTGG GAGGCTGAGG CAGGAGAATC TCTTGAACCT	180
GGGTGGCAGA AGTTGCAGTG AGCTGAGATC GCGCCACTGC ACTCCAGCCT GGGCAACAGA	240
GTGAGGACTC CGTCTCAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAANN NTGGGGGGGG	300
CCCCNANCCC	310

(2) INFORMATION FOR SEQ ID NO:995:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 431 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:995:

ATTTATTATT ATTGTTTATT TATNCTTGCA CTTGATGAAA TGTAATTAAN CGCTTTGTCT	60
TATGTGGTTT TTTAATTGTC ATTTTACTGT TTAATTTCTC CATAGAGTAT ATGTATTTTT	120
GNANCTCAGA GACTCTGCCT TTTCCCCTCA TAGTACACAG CATAATACTA AGCTGTTAGA	180
AGAGTTCAAT TGAATGTTAA TTCATCTGAG TAAACAAACT TGTATATGTA TTTCAAGTAC	240
CTCTACCAGT GGTAGTTGGA ATCTGTTCCA TCAGAAGAGN TTTCTTAAAT CTGNAATAGT	300
NAAAGTGTTT TATATTCTTT GCTCACAGAA TGAAGGGCAG GAGACCTTTN AAAATGGTAA	360
TGATGGTGGG ACCACATATT TTTAAAAGNG GTGGAGGTTG TTCCGGCNGT GGTATTGNTT	420
TAANCCATGG T	431

(2) INFORMATION FOR SEQ ID NO:996:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 326 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:996:

GCCCCACCCN GGNCCGCCCC CCCTAGANCT AGTGGTTCCC CCGGGCCTGC AGGNNTTCGG	60
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CAGAGCAGTC TTTGGCCTCC CAGTAAATTC CAATTTCAAA CAACTTTTAA CTCAAACTTC	120
ACTCTTAGAT TTTTAACAAG CTTTTCACAC ATACATCATT AATGCTTCCC CTAATCTTTC	180
ATGTTGTACT GGCTATTGGG CAGTTGTGTT AAAAAAAAAA AAAAAAAAAA AAAAAACAG	240
CACTCCCAAA GCGCTTGAAT TTATTTTNNT TTGGGGGAAT AAGAGACCTT TTNTAAATNG	300
TTTTTCGATA AAAGGTAATC CNTTTT	326

(2) INFORMATION FOR SEQ ID NO:997:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:997:

GGCACANGAT TTTNTNAGTT TTTGGGTGTC TGTAATTAA AAAGGAAAAG TAGAAATAAG	60
TAAAACTNAG GTTGAAGGAA ATATACATAA ATAAGATAAA GCTGACCTGT AGATATAGGC	120
AGGTTATAAG AGCTTAGAGT TGTCTAAGTT GGGTGCAAAT TTNCCTCTGA NCTTTCTGAT	180
GCCGAGACAA AAAAGGCAGT CCATATTTNT TACGTGATTG GGGTGGAACC CGAGAGGAGA	240
ACATGCTGTN TTCTTNTGGG ACAGGAAAGC TTGCNTGGCA CCAAGTCTGA ACCANNACT	300
TCATTGGTGA CATAGATTAT NTGCTGGAAC ATATTTTCAC ANCGGCCTGG CATAACCNCT	360
TGTTAGTGTT TGTACATTGG GAACGGTTCA TTTTCCCTTA AGCACCATGT GTTTTTGCCA	420
TGGGAATGGT CCTCNCCCT TAAGGACANT TNCCTCGNAG TTATGC	466

(2) INFORMATION FOR SEQ ID NO:998:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:998:

G TTCACAAGT NGGGGAGCCT GTAGCTTTGG GTCTCANTAG CTCCTGGGGT AGTATTTNCC	60
CTTNATTTCT GGCCCTGTAT ATCTAATTTN AATGACATCT GTNAAGGAGA CAGTGGAGGG	120
	120

(2) INFORMATION FOR SEQ ID NO:999:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:999:

CCTACCCATT TAACTTATAT GCAGAGTACA TGATAAACGC TGGGCTAGAG GAAGCATATT	60
GTCCTCGATT CCAAGCATAT TGAATCAAG ATTGCTGGGA GAAATATCAA TAACCTCAGA	120
TATGCCAGAT GAACACCACC CTTATGGCCG AAAGTGNAAG AAGAACTAAA GAGCCTCTTG	180
ATGAAAGTGN AAAATGGAGA GTGCAAAAAN TTGGCTTAAA AGCTCCAACA TTCAGAAAAC	240
TAAGGATCCA TGGCATCTGN GTCCCATCCA CTTCCATGGG CAAATAGATG GGGGAAACAT	300
GGAAAACAGT GGGCTGACTT TATTTTCCTG TGCNTCCAAA TTTACTGCAG ATGGTGGACT	360
TACAGCCCTN AAATTTAAAA GACGTTTTTAC TCCCTTGGA AGAAAGTTTT GACCCAACNT	420
GGNCCGGCTT TTAAAAAACC GGGTTTTTTA CTTTGTGTTCA CCGGGGTNCC NTTNGTTCAA	480
GGTTTGTTTT T	491

(2) INFORMATION FOR SEQ ID NO:1000:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 274 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1000:

GGCACGAGGN GAAGGACGGC AAGGCCTACT NTCGCAAGGA CTACTTCGAC ATGTTTCGCAC	60
CCAAGTTTGG CGGCTGCGCC CGGGTTCATC CTGGAGAACT ATATCTNNGC CCTCAACACG	120
CTGTGGNCAT CCTGAGTGCT TTGTGTGCCG GGAATGCTT CACGCCATTC GTGNAACGGC	180
AGCTTCTTCG AGCACGACGG GGCAGCCCTA CTNTGAAGGT GCACTACCAC GAGCGGCGCG	240
NCTCGNTGGT GNTTCTGNCG TGCCAGAGGC AGAT	274

(2) INFORMATION FOR SEQ ID NO:1001:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 352 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1001:

ATGTTTTTCAT CATGGACAGC CATGATGATA TATTATTATC TCANCTTTAA TCCTTGGTGT	60
GGTTGATTTG GGATCTGCCC CTGAANCATC TNTCGAGAAA TGCTCCAACA GAGCAGNAAT	120
CTTAACANTC ATTCACAGAA ACATTGTTAA GAAGTGCCTT GAAGCTGTTT TTTGAGGTGG	180
CAGAAGACAA GGAGAATTGC AAGAAATTCA ATGAGGCCTT ATCTAAAAAT CTAAAGCTTG	240
GGNCCAGTTG TGGGTATCTC ACCTTTGTAA TCTCAGGCAC TTTGGGGAGG GCCAAGGCCA	300
GGTGGGNTTT GNTNGGNAGC CCAGGGGTTT TTGAATACCC ANCTTGGGGT TG	352

(2) INFORMATION FOR SEQ ID NO:1002:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1002:

GGCACGAGGN AACTTTNAGT GCAATGTTCC TCTGGGCATG GAGTCTGGCC GGATTGCTAA	60
TAAACAGATC AGTGCCTNAT CTACCTACTC TAATGNGAAG GTGGACCCCT CAACAAAGCC	120
GGNTCCATGG TGATGACAAT GGCTGGACCC CCAACTTGGG ATTCCAACAA GGAGTATCTC	180
CAGGTGGNCC TGCGNTTTTT AAACCATGCT GACGGCCATC GCAACANAGG GGAGCGATTT	240
CCNGGGNAAA CACAGGAATG GCTACTAATG TGCAAATCCT ACAAGCTNGG NAAGTTCAGC	300
ACTTAATGGG TGAGGACTGG NATGGTGTTA CCGGTGATGG CCAAAAACCA CANGGTTTTT	360
TNCA	364

(2) INFORMATION FOR SEQ ID NO:1003:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1003:

CCTCTNAAAA TGTGCTTTGC TGCTAGAAAC CTAAGCATGC CGGATCTGGA AAACAGATTG	60
ATAGAGCTAC ATTCTCCTGA TAGCAGGAAC ACGTTGATCC TACGCTGCAA GNATACAGCC	120
ACAGCACACT CCTGGTTCGT AGCTATCCAC ACCAACATAA TGGCTCTCCT CCCACAGGTG	180
TTGGCTGAAC TCAACGCCAT GCTTGGGGCA ACCAGTACAG CAGGAGGCAG TTAAAGAGGT	240
GAAGCATATT GCCTGGCTGG CCAGAAACAG GCAAAACTAG NTGGTGGGAG GACAGCAATT	300



GGNGACCTGT TCCTCATGGG NTGTGAACTG NGAAAGGGAT TTGCTGGNTC TNTGGACTGT	360
TATGCCCTTG GGACCAGGGT TGCCTGGGGN TTCACCCTGG CCACAGTTAC CCANTTTTTN	420
GCCACCAGGT TTGGTTTCCT TTTTGGGTC CGGATNTTGG TTCCCCTTCC CTTTGGGT	478

(2) INFORMATION FOR SEQ ID NO:1004:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1004:

GGCAGAGGTC TTNCTTNGG AGATGGGCAG AAGCTGAAGG ACTGGCATGA CAAGGAGGCT	60
ATCCGGTAGG AACGCTCAGC GCGTAGTAAA TGGAGAACAA GGAAGACCTT ACCCATGAA	120
CCGATGCTGA GAGAGTGGAT CAGGCATACC GNGAAAATGG TTTTNAACAT CTACGTCATA	180
ATAAAATCTC CTTGAATCGC NNTCTCCCAG ATATCCGGCA CCCAAACTGC AACAGCAAGC	240
GCTACCTGGT NGACACTTNC CACACAAGC ATCATCATCC	280

(2) INFORMATION FOR SEQ ID NO:1005:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1005:

AGTATGAAAG TCTCAGCAAA TTTATTTTTA TTCAGTTAAA TATGTTTTAC TCAAAGTGAA	60
CTGAAATAAA TTTCATCAAA TTTGATATAT TATGAGTTTA TTTAGAAGAC AGACAAATGT	120
AATCCCCAAA GTTCTGAACC TTCTAACTTC AGTTCAGTTG CTCAGTTGAG TCTGACTCTT	180
TGTGACCCCA GGAACCGCAG CACGCCAGGC CTCCTTGTC ATCACCAACT CCCAGAGTCC	240
ACCCAAACCC ATGTCCATTG AGTCGGTGAT GCCATCCAAC CATCTCAGCC TCTGTTGTCC	300
CCTTCTCCNN CTGCCCTTNA ATCTTTCCCA GCATCAGGGT CTTTCAAAT GAGTCGGGTC	360
TTACATCAG GTGGNCAAGT ATTGGGNTTT CAGATTCAAC GTCAGTCCTT NCAATNGAAC	420
ACTCAGGACT GATCTCCTTA GGGTGGACTA GTTGGGTCTN CTTGCAGTCC AGGGNCTTTC	480
AGGGTCTTTT NACGG	495

(2) INFORMATION FOR SEQ ID NO:1006:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1006:

GGCACGAGCG GAGGAGAAAA GGTGGTGCTC NGACCTAATG ATGTTTCAGT ATTTACGACG	60
CTCACCATTA ATGGACGCCT NTTTGCTTGC CCGCGAGAGN AATTCGATTC ACTGACTCCC	120
NTACCAGAAC AGGAAGGCC AACTGTTGGA ACAGTGGGAA CTTTTGAACT GATGAGCTCC	180
AAAGATTTAG CATACCAGAN GACANTTTAT GATTGGGAAC TCTTCAACTG CGTGCATGAG	240
CTGGAGCTAA TCTATCACAC ATTTGGAAGG CATTAATTTT TAAAAAGACC ACAGCAAAC	300
TGGGATTTGT TCCTGAGGAG ATTTTAATTG AAATTCAGTT TTGGGTCGTG CACTGAGATC	360
TNCCTTTGTT TCTTCAGCTT CAGNAAGCGG TGGTTTCAGN TATTTAAAAA AAATTTGTTT	420
AAGNTAGCAG NCCACTGTTA AGGGGTNTAA AAAATCTGGA ATTCC	465

(2) INFORMATION FOR SEQ ID NO:1007:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1007:

CCAGGCGCGA ANATCCCTCC AAATTNANGT GGGGCGATTT TGGCGCTGAN TACGTCGTGG	60
AGTCCACTGG GGTNTTCAC CACCATGGGA GAAAGGTTGG GGGGTCATT TNGCANGGGG	120
GGGTGNCCAA AAGGGGGTNC ATCATGTTTG	150

(2) INFORMATION FOR SEQ ID NO:1008:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1008:

GCNTCGTNGC GAATATNTGG NACCCAAAAN TAGACCGATG CCATCACC GC AATATTAAAA	60
ACAGCGATCA ATAAAAAGGT GTACGCCAGC TAAATTCCTG ATTTAAATAC GTTCCCAGCG	120

GAATGCCCAG CAAATTGGCG ACTNTGNATC CCGGAAACCA TCCCCGNCAC GGCGNCGGGT	180
GAACTTTTCC GGGTTTGAAT ATTTTNGAAT AACACGATCG NTTCCGACGG CCAATAATTG	240
CGCCCTGGGG AAAGCCGGNT ACCAGCCGNC CATGGGGGN	279

(2) INFORMATION FOR SEQ ID NO:1009:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1009:

AAATCTAACA TTCGAATCAA AGGTGCCATT AAGCAGCCAG TCAAACTTA CGCCAAGAGC	60
TGACGCAATT CCTGGTAAAA AGCGTGGTCG CTTAGTTTTA CCGTTTTCAA GCTGCTCTAT	120
AGACTGCTGG GTAGTCCCCA CCTTTTAAGC AAGTTCAGCC TGGTTAAGTC CAAGCTGAAT	180
TCTTTTGCTT TTAAACCCTG GAAGAAATAC TCATAAAGCC ACCTCTGTTA ATTTACCCCC	240
AATCTTCCAC AAGAAAAACT GTATTTGAAC AAACAAGTTA CATTGTATGG AAAATTACAA	300
GAAAGTTTGT TTGATGGGAG GCGGTTTTGC AAATCCTTT NCTGAAACGG CTTCAAGAAG	360
AGGGGGATTT GCGGTAAAA TGNACGGCAA ACCGGAANTG GGCAACCAAG GCCGGTGTTT	420
AAACNGCAAT TCATTTCAANN GGTGA	446

(2) INFORMATION FOR SEQ ID NO:1010:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1010:

CCTCGCTNAA ACTNTNACAG GTCGGCGGCG CACGTNTTTC TGCNACCCTT GCGGCGCGTA	60
TTCCCGCTGA AATTGGCTGT AAGTTGCAGC AGGTGTTTGG NNATGGCGGA AGGCCTGGT	120
GAAACTNACA CCCNGCTTGA ATGGATAGCG CCGNGAAAA TTAATCCATA CCCAGGGTTT	180
ACCCAATGTN TTCCGGTTGG NCGGAA	206

(2) INFORMATION FOR SEQ ID NO:1011:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1011:

AATAAAGATG CAGGANTTTA ATATTGCGGT GGGGTAAAAC CCGGATGANA TGGCTCATCC	60
GCTANGATTA AAGNATTTAA AATNCCTGNA TTAACGCGTG CNAGGCCGTC CCTGAATNAT	120
TGCCGCTTCA CCCGTNGCCA CCAGGCAGCA AGCCATCTGG TTTTNAAGCG AATTCGGGAA	180
TCGNTTCGCT GCCAGCANGG CAACG	205

(2) INFORMATION FOR SEQ ID NO:1012:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1012:

CAAAGACGCC GCCTCGAGAA CATCAGGTTT CTGAAAGGGA TGGGCTACTC CACGCACGCG	60
GCCCAGCAGA TTCTGCTCAG CAATCCTCAG ATGTGGTGGT TAAATGATTG CAATCCTGGA	120
AACCGACAAC CGTCAAGAAA GTCCTTCCCA GGAAAACATT GACCGATTGG TGTACATGGG	180
TTTTAATGCA CTCGTGGCCG AAGCTGCGCT GAGAGTNTTC AGAGGCAACG TCCAGCTGGC	240
CGCCCAGACC CTTGCTCACA ACGGAGGAAG CCTGCCTCCC GAGCTGCCGT GTTCGCCAGA	300
AGACTCTTTG TCCCCGCCAG NCACGTNCCC TTTTGACTTC GNGGAACCTT TTAGTGNCTN	360
	360

(2) INFORMATION FOR SEQ ID NO:1013:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 347 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1013:

CCTAAAAAAA ACAAACTA AAGAATTGGT TAGAACAGCA AAATTTTCTT AAGGTATTGA	60
TTTACTCTTA ATAAATTAC AAGAGATTTT AATTTTTTTT TAGCCCAAAG TTCAACTTTT	120
ATTGCATTTT GCTGTTTTCA GCTTTCTCTC CCCTTTTAAA AGGCCTGAAA TAATAACTCT	180
CCTTCANCTG CATTTTCAGC TCCTGTGAGT TTTTCTCCCC TCAGGTCTTA ATTATTGTT	240

GTGGCCTGAT GCTTAAAAAT GTTTTATCTT AAAGGTCTAA AGGGAAATGT TTTCTTGCTT	300
AACATAGTGT CCCGTGGCTC TTGGGNTTNN AAANTGNTN CTATGGA	347

(2) INFORMATION FOR SEQ ID NO:1014:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1014:

CAAGCCCCAT AGGCAGGAGG CCCCCGGGNA GCACATCCTG TCTGCTTGTG TCTGCTGCAG	60
AGTTCTGTCC TTGCATTGGT GCGCCTNAGG CCAGGCTGCA CTGCTGGGAA GCTGGGCCAT	120
GTCTCCCCAC CCCACCGCCC TCCTGGGCCT AGTGCTCTGC CTGGCCCAGA CCATCCACAC	180
GCAGAGGATC TGCCCAGACC CTCCATCTCG GCTGAGCCAG GNACCGTGAA TCCCCCTGGG	240
GAGCCATGTG AACTGTCGTG TGCCGGGGGCC CGTTGGGGTT CAAACATTCC GCCTGGAGAG	300
GGAGATAGAT GCACATACAA TGATTATTGN AAGATGTGTC TCAAGTTAGT NCCNTNTGAG	360
TCANAGGGGC CAATTTCCGC	380

(2) INFORMATION FOR SEQ ID NO:1015:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1015:

CCGCCTTCGC TGGCATGACC AACCACCAGC TGAGCACCAC TGAGTGGTAA TGACGAGACT	60
NTCTACCAGG AGTTCAATGG CCTGANGAAG ATGAATCCCA AGCTGAAGAC CCTGTTAGCC	120
ATCGGAGGCT GGNAATTTCA GCACTCAGAA GTTCACAGAT ATGGTAGCCA CGGCCAACAA	180
CCGTCAGACC TTTGTNAACT CGGCCATCAG GTTTNTGCGG CAAATACAGC TTTGNACGGG	240
CCTTGACCTT GGACTGGGGA GTTACCCAGG GAAGCCAGGG GGAGCCCTGC CGTAGGACAA	300
GGAGCGNTTT CACAACCCTG GTTACNGAAN TTTGGCCAAT GNCTTTNCCA GCAGGAAGGC	360
CCAGACCTTT AGGGGAGGGA CGGCTTTTTT TTAGTNCAG GGGTTTTCCA ATTGGGGNAG	420
ACCTTTNTNG GGATGTTGGT ACGGGGGTTG GNCAAAATTG GCCCGAACTG GGTTTTTTTN	480
AACTTTTTTG CT	492

(2) INFORMATION FOR SEQ ID NO:1016:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1016:

CTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TNAAAANNAA AAGG 54

(2) INFORMATION FOR SEQ ID NO:1017:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 163 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1017:

CAGGGNCTNC CCGACCTCAA CCACTCCCAG GNTTATGCCG TNAAGACTGT NCTGCAAAGA 60  
CCACTGAGCC TGATCCANGG NCCGNCAGCA CGGGGTAAGA CGGTGACGCG TTCCACCATC 120  
GTCTACNCAC CTTGCCCCGC AAGGCAACGG GCGGTTNCTG GTG 163

(2) INFORMATION FOR SEQ ID NO:1018:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 291 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1018:

CCGTCCCCTT CGANAGCAAC GTGGGGNAGT ACCGGGCGGT GAACGGAGCT GGGGCGNCCT 60  
TNATGCCNAG TACTGGAACA GCCAGAAGGA CCTCCTGGAA GCAAAGGCGG GCCGCGGTGG 120  
AACACCTACT GCAGACACAA CTNACGGGGT TGGTGAAAAG CTTCANAGTG CAGCGNCGAA 180  
GTTGAAGCCT GAAGGTGACT GTNTATCCTT CAAAGAACCC AGCCCCTGGC AGCACCACAA 240  
CCTCCTGGTC TGCTCCTGTG AATGGTTTNC TATTCCAGGG CAGCATTNNA N 291

(2) INFORMATION FOR SEQ ID NO:1019:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 477 base pairs  
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1019:

CGCAACATTT TGGGAAAATA CAGTTCCATT GTACCTGCCA CCNTNNAGCT GTAGCCAGAG	60
ACCTTTATCA AAATGGGCTT GTTTCACAG AACAGCAGAA CGGTTGGGGG TTTGCATGTA	120
CAGTTAACCA GCATAAGACT CGTACTGGGN AAAATCCAGC TGGGAATGTG ACACAGCTTA	180
ACTGATAGCT TAAGGCATCA GTATTGGGAC CAAAGGCTGG TCAGATTTGT ATCATTCTGA	240
GGACCAAATG ATGGGGAACA ATAAAATTGT TCCATGNACA GTTGTTCCTC ATTTTGCTGT	300
NCCAGATGAA GACTCTTAAG ANTGACAGAA GGTGATTTTT CCTGGGTGNN TCGAGGACTT	360
CCGGGGGTAA TGACCNTGAT GGAAATGCCA GGGGACCCGG TTAGGTTTTT TTTTGGGNGA	420
NTAACCGGGG GGTGCCNCG TGGGACAAAC AGCNGTTTNC CAGGGTTTGG GTTGGTC	477

(2) INFORMATION FOR SEQ ID NO:1020:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1020:

CTTTTTTTTT TTTTTTTTTT TTTTTTANCT TTNCAANTTT TTNAAAAAAA	50
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(2) INFORMATION FOR SEQ ID NO:1021:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 489 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1021:

AGAGGTGTCT GTGTTTGAAG TCAACATTCG ATTTATTGGA GGCCTACTTG CAGCATATTA	60
CCTATCAGGA GAGGAGATAT TCAAGATTAA AGCAGTGCAG TTGGCTGAGA AACTCCTTCC	120
TGCCTTTAAC ACACCTACTG GGATTCCCTG GGCAATGGTG AATTTGNAAA AGTGGAGTAG	180
GGCGAAACTG GGGCTGGGCA TCTGCAGGTA GCAGCATTCT GGCTGATTTT GGTACACTAC	240
ATATGGNGTT CATGCACCTG CAGCTACTTG TNNAGGGGAC CTGACTTNNC TACAAAAAGG	300
TTATGGCACA TTCGGAACT TACTTTCAGA AAATGGGTTC GTGCCAANGG GTCTTTTATT	360

CCAANTANTT TGNACCCAG NACAGGGCGN TGGGGGTCAN TATTCANACA TNTGTTCGGT	420
GGNCCGGGAG ACAGTTTTTA TGGATACTTA CTGGAAGCCN GGTTCGATGT CCAGTTAAAA	480
CAGACCCTG	489

(2) INFORMATION FOR SEQ ID NO:1022:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1022:

GGGAGCCTCA GTGAAGGTGG CTGTCCGGGT AAGGCCCTTC AATTCTCGAG AGACCAGCAA	60
GGAATCCAAA TGCATCATTC AGATGCAAGG CAACTCGACC AGTGAGTACA TGTTGTTTTTC	120
TCTCAGCTGT GTATCTTACT TTCCTTTCTT CTTTCCCTGT CGTCTTGCTG TGTTTCAGAAT	180
AGATGAACAT CTGTATGTTA ACACTTTGAA CTTTGCTATT CTGAATGATC CATTGGAATG	240
TATTCCCCTC TGTGGTATTT GCTATAGTAT ATTTGAAATA TGGACTATTT ATTTTACCCT	300
GTACAATTGA GAAACCCGGA ATAACCTGAAC NATTTAGCAA GTGTTTATGC TTATTAAGTT	360
GAAATTTAAT GGTATAAAG GTTTAAACAG TGCTTTTGC CCAGTCCNAA GGGGNATTAT	420
ACCCATGGNG GNGGCAGATT CCATGTTTTN CT	452

(2) INFORMATION FOR SEQ ID NO:1023:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1023:

TTCAAAGAAC TACTTGAAAA TGCAGAGAAA TCCCTGANTG ATATGTTTGT AAAGACATAT	60
GGCCATTTAT ACATGCAAAA TTCTGAGCTA TTAAAGATC TCTTCGTAGA GTTGAAACGT	120
TACTACGTGG TGGNAAATG TGAAACCTGG AAGNAAATGC TNAAATGAAC TTCTGGGATA	180
CGCCTACCTG GAGACGGGAT GTTCCCGCCT GGTGAAACTA CCCAGTGACC ACTTTGACAG	240
ATGGAGTTTA CTGGGAATGT GTGAGCCAAA GTNTGACGGT GNCAGCTGNA AGCCCTTNCG	300
GAGATGTACC CACGACAAAT TGAAAGCNCC AGGTTTACT	339

(2) INFORMATION FOR SEQ ID NO:1024:



(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1024:

TTCAAAGAAC TACTTGAAAA TGCAGAGAAA TCCCTGANTG ATATGTTTGT NAAGACATAT	60
GGCCATTTAT ACATGCAAAA TTCTGAGCTA TTTAAAGATC TCTTCGTAGA GTTGAAACGT	120
TACTACGTGG TGGGNAATG TGNAACCTGG NAAGAAATGC TAAATGAACT TCTGGGNTCG	180
CCTCCTGGNG CGGATGTTCC CGCCTGGTGA ACTNCCCAGT ACCACTTTGA CAGATGGAGT	240
ATCTGGNAAT GTGTGAGCAA AGTATACGGN GNCAGCTGGA AGCCCTTCGG GAGATGTGCC	300
CTGCGCAAAT TNGAAGCTTC CAGGTTTACT CGTGGCTTTT GTNAGCAGCC CGTTANTTTC	360
GTTCAAGGTT AGCGGTTNCG GGGAGATGTC GTGGAGCAAA GGTCTNCCGN GGGTAAAACC	420
CCACAGNCCC AGTGTACCCC TGGCC	445

(2) INFORMATION FOR SEQ ID NO:1025:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1025:

CACGGCAGGT CAGGAGCNAT TCCAAAGCCT GAGGACACCA TTTTACAGAG GTTCTNACTG	60
CTGCCTGCTT ACTTTTAGTG TCGATGATTC ACAAAGCTTC CAGAACTTAA GTAAGTGGTA	120
GNAAAGAATT CATATATTAT GCCAGATGTG AAAAGAGCCC TGAAGAAGCT TTCCTTTTGT	180
GAATTCTGGG TAACAAGGAT TGACATTAAG CGAAACGGCA GGTGTCTTAC AGNAAGGAAG	240
CCCAAGCTTG GTGNCAGGGG ACAACGGGCG GACTTATNCC TTATTTTGAA AACAAGTGCC	300
AAAAGATTGC CACAAATGTG GCAGCCAGCC TTTGAGGGAA GCGGTTTCGAA GAGTTNTTGT	360
TACCGAGGNT AGGTTCAAGT CNTTTGATTN CGNACAGACA CGTCATTTTT CACCGGAAGG	420
CCCAGCCTAG TTCANTTGCT GTTGNTGTTA GGTTGTTGNT GCNTTTTAAC CACTTACACT	480
TTTNCCCAAT TCACCT	496

(2) INFORMATION FOR SEQ ID NO:1026:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1026:

CCTGGNGGAC CATGAAAGCC TTTAAACCT CGTNATTAAT TGGACACAGT GCCAGAGTGT	60
ATGCACTTTA CTACAAAGAT GGACTTNTCT GTACAGGGTC AGATGACTTG TCTGCCAAAG	120
CTGTGGGAAT GTGAGCACAG GGNAGTGCCT TTATGGCATC CAGACCCACA CTTGTCCAGC	180
GGTGAAGTTT GATGNAACAG TAAGCTTGTG AACAGGCTCC TTTGAACAAC ACTGTGGGCT	240
TGCTGGGNAA TGGAGTTCCC GGAGCCAGGA CCCAGCACTT TTCGGGGGGG CACACGGGGG	300
GCGGTNTTTT AGCGTGGGAC TACAATGATT GAACTGGGAT ATCTTGGTGA GCGGGTTCTN	360
CAGACTTNAN TGTGGAAATT ATGGGNTTTA TTCTGTTNGG GGACATGCCC TGAACACANT	420
NACCGGGGCA CAGGGATTGG GTTCACCCAG GTAGTTTTTT CCAGAAGTTN CAAGTCAGTT	480
TTTNT	485

(2) INFORMATION FOR SEQ ID NO:1027:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 94 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1027:

CAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	60
AAAAAAAAAA AAAAAAAAAA AAAANNAANA NAAN	94

(2) INFORMATION FOR SEQ ID NO:1028:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 294 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1028:

CCCATTAAGG AAAGAGAGAA GAGGTGGCCA TTTACTTAAT TCAGNAGGTG GAGCCAATNG	60
GCTAGTAAAA CATACTTTTT TCATTTTCCC TTTCTNTAAT TTCCTGCGTT TCCTGTTTCT	120
CACATTCAGA ATCTGAATTT AGTTCTTTAC ACTCGTCCTC ATCTGCCTCA TCTGNAATCT	180

GCCTCATCAT CTGNTTGAAA TGGCTCAAGA GTTGCTTTTA TTAGTGCCCA TATTGACCAA 240

ACCAAGACTG GGAATTTTNT GGCTCCATCT TGATATGCTT TTTTANAAAA NNCN 294

(2) INFORMATION FOR SEQ ID NO:1029:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1029:

GTCAGGACCA GCTGGATGAC TTGGTGGTGG AGTGTAGAGA TATAGTTGGC AACCNCACTG 60

AGTTAGNATC AGAGGNTATT CAAATAGAAG CCTTGCTGAT GAAGAGCCTG TNATGCCCAT 120

TAATTCAGAA CTTCTGCCAC GGTGTGNAAT GATACCAGAT TAGACTCTGG GGGACCTGNA 180

TGGNAGTGTC TGGNTACAGG NCAAAACACCA GAAGGGACAT GTAACGAGAA ATGTTGCCAT 240

CGTTGTTACC CACTTNCAGT 260

(2) INFORMATION FOR SEQ ID NO:1030:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1030:

CAACAAAAAA AGATATCCTC CGGCATATGG CCCANACGGC AAACCAAGAC CCCGCTTCAA 60

TAATGTTCAA CTGAATCTCA CAGATGAGGA GAGAGAAGAA ACGGANGAGG AAGTTTATTT 120

GTTTGAATAG CACAACCTCT TAACCTGAGG GNAGTCATCT ACTTTTTTTT CCTCCTTGTA 180

CAAAAAAAGG AAGGTNANTA TAAAANCCGG GTTTTTGTCA ACATGGTTTG CANATAAATG 240

ACTGGTGGA ATGNG 255

(2) INFORMATION FOR SEQ ID NO:1031:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1031:

CTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTGGANTNC

50

(2) INFORMATION FOR SEQ ID NO:1032:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1032:

CGGACCTGCT GAAGGACCAG AGAGGGAGCC CTGCCTACAT CAGTCCCGAC GTGCTCAGCG	60
GCCGGCCGTA CCGTGGCAAG CCCAGTGACA TGTGGGCCCT GGGCGTGGTG CTCTTCACCA	120
TGCTGTATGG CCAGTTCCCC TTCTACGACA GCATCCCGCA GGAGACTCTT CCGCAAGATC	180
AAGGCTGCCG AGTATACCAT TCCTGAGGAT GGACGGGTTT CTGAGAACAC CGTGTGTCTT	240
CATNCCGGAA GCTGCTNGGT CCTTGANCCC CCAGCNGTGN CTTGGTCCG	289

(2) INFORMATION FOR SEQ ID NO:1033:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1033:

CGGAGNCCA GAGGCCGAGT CGGTCACCCG NACGGATCAC TGGAAAAGTC GCACATCGGA	60
GGGGATNCTC NNTGAAGATT GT	82

(2) INFORMATION FOR SEQ ID NO:1034:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1034:

CCTGTGAATT ACCTAGAAGA GAAGGGTATT GAAACCTACC TCATCATTGC CTCCAAGCCA	60
GAGGTGAAGA AAACAGCCAC CCAGAATGGC CTCAATGGCT CGGCCCTGCC CAATGGAGCA	120
CCAGCTTCCT CAAAGTCCAG CTCCCCTGCC CTCATTGAGN ACCAAGGAGC CCAACGGGGA	180
GTNCCCACAG CAGTGGGTTC CACGTCGGAG AAAGCCCAG GAGCAGGATN CCCAGGNCGA	240

CAACCCCTNA TTTCCCCAAC CCACGTCGGA GTTNCGGCTT

280

(2) INFORMATION FOR SEQ ID NO:1035:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1035:

CGGCCTGGTT TCTGGTGGCC TCTATGNATA CCCTGTAGGG TGCNGACAGT ACTCGATNCC	60
TCCCTGTAAG CACGACGTCA ACGGTTCCCG GCCATGCCAC GGGGGGAGGG CGGATACCCC	120
CAAGTNTAGC AAGCTGTGAA GCCTGGCTAC AGCCCGACCA AACAGGNACA NGTACTACGG	180
ATATTCCTNA CNGTCT	196

(2) INFORMATION FOR SEQ ID NO:1036:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1036:

CTAAAAATAN TGGNTAAAAT TACCTTGCAA GCTATGTTGT ATAAGGTGNA TATAAAACAA	60
AGNAATTTNG NNGTTTAGAC TTGGGTCTAC TCCCAAGANG ACCTCATNAT ATATATACAA	120
AAATCCCCAA ATCCAAAAAC ANTTGNAAAC ACTTCTGGTC CCACACATTT TGGN	174

(2) INFORMATION FOR SEQ ID NO:1037:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1037:

CTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTNCNCGG GN	52
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(2) INFORMATION FOR SEQ ID NO:1038:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1038:

CATTTTGGGC AATAAACCTT ACAGCAAAAA GGACTACAGA TCCTAAGCCG GCCCCGCCCCG	60
CNTGCTCGGT ACAGTTTCCG TTCCCTCCTA GTCTCTGTTC GCTCGCTTAA GCTGTTTTTAA	120
AGACCAAGTG AAAGAGTGTG GTTTGCATCC AAGAGAAAAC ACCACACTGT GATGTCATCG	180
GGNAAATGAA TCTCCCAAGT CGCTGCCAGA NACCACCCAC TGNTTCGCCG GACAATGTCG	240
AAGTCCAGTT TGTNGCCGGG GGAAGGCNTG GTTTAGGGAA GGATGTTCAA ACGGTCCCAC	300
CCANGCNTGT NNAACTCTGG TTGATTCCTT NCAAGAGCCA CCCAGGTTTT TTCCCAGGNC	360
ACAGGCCAGT TTNCCAAAG TTCAAGGGNC CAAAGATTTT TCCAAGGTTT CCCCAGTNC	420
AAGGGCCAGG GNCAAGG	437

(2) INFORMATION FOR SEQ ID NO:1039:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1039:

CGGTAGGTAA GGAAGGGGCC TTAACCTNTG CTGGTGACCA GAAGCCTGCA TTTCTGCATT	60
CTGCTTAATT CCCTTTCCTT AGATTTGAAA GAAGCCAACA CTAAACCACA AATATACAAC	120
AAGGCCATTT TCTCAAACGA GAGTCAGCCT TTAACGAAAT GACCATGGTT GGACACAGAG	180
ATGCCATTCT GGCCACCAA CTTTGGGATC AGCTCCGTGG ATCTCTCCGT AATGGAAGAC	240
CACTCCCACT CTTTGNATA TCAAGCCCTT CACTACTGTT GGACTTNCTT CCAGCATTTN	300
CTNATTCAC ATTACGGAGG ACATTCCATT TCACAAGGAA CAGATTCCAT GGTGTCNCNG	360
	360

(2) INFORMATION FOR SEQ ID NO:1040:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 442 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1040:

CGGCCATGGC TTTCTGGGCG GGGGGTTCGC CCAGCGTCGT GGACTATTTT CCTAGCGAGG	60
ACTTCTACCG CTGCGGCTAC TGCAAGAACG AGTCGGGCAG CCGCTCCAAT GGCATGTGGG	120
CACATTCCAT GACAGTACAG GATTATCAGG ATCTCATAGA CCGAGGATGG CGAAGAAGTG	180
GAAAAATATGT GTACAAACCT GTCATGAATC AAACATGTTG TCCTCAGTAC ACAATAAGGT	240
GCCGACCTTT ACAATTTTCTAG CCTNCAAAAT CTCACAAGAA GGTTTTGGAA ANAAATGTTG	300
AAATTTCTGG CTAAAGGGGA GGTTCCCAA GGAAGTTNTN AAGGGTGAGC CCATGGGTTT	360
CCACAATGGG TTGATGTTGT NGCCGGGTGG ACTTTGGCAT TGATTAAATA AACTNGGTTT	420
TACCGTGNGG NTCNTTAAAC CA	442

(2) INFORMATION FOR SEQ ID NO:1041:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1041:

AAGTTTGNT TCAGGTAAAC AAACCTCGTN AGGNGNNGG GGGGTNTNT TCNGACTCAC	60
ACTTCCATCT CCGTGTGTAG GTGTCCATCA GCGGAGAATG GTCTCCGTGG CAGGCCAAGG	120
TGCCTCAAAT TGAAGTGGAG ACGCACAAGG TGGCAGCCCC TAATGTCGTC GTGCCAACCC	180
TGGGACACAG TCCGCCACGA AGCCCTCTTG TACACTTGGC TGGCCGAACA CAAGCCCCTG	240
GTCTTGNTG GCCCTCCTGG GTCTGGCAAG ACCATGTACA ATTTTNNANN GNCTTCCGGC	300
CTT	303

(2) INFORMATION FOR SEQ ID NO:1042:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1042:

CNCGTNTGCA CGCGGGCTGC CCAGCTCTNT CCTGCCGCCC TGGCCGCTGT NCTCTCCTGC	60
NTCCAGCACA GCCGGGAGCA ACAAACACTC CAGGTGCTG TGGCCACCGG AGCCGAGTNT	120
NTAANNGGCA CCCCAGGTTT TGCAGCGTCC TGCAGGGACA NTAATGCTCC TGGGCCCCGA	180
ATGCAATGTC TCNTAATCCC CTCTGTGGAT GGTGGTGGCC GGGGAGTGGC GATGGTGACT	240

GCCNTGGCTN NCCGTTTGGT TGCCACCGGG GCTGTNGAGG AGACCCTGGN CCCATTTCGGT 300  
T 301

(2) INFORMATION FOR SEQ ID NO:1043:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 107 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1043:

ANAAGGTCCC CCCCTNNGGC CGTTTTGGGC CATGCTTTTT TCCCATTGAC TTAAAAANCAA 60  
TCGGGAGGGG GNGGGGCCTG CCCCCTTTNA CCCTTTTCCC CCTTNCA 107

(2) INFORMATION FOR SEQ ID NO:1044:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 365 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1044:

CAACTTTATT CATGGCAAAG AGAAAGAAAA GTAAAGACAG AATTTTCCCT TCATGATGGA 60  
CCTCCTTATG CAAACGGTGA CCCTCATGTT GGACATGCTT TAAATAAGAT TTTGAAAAGA 120  
CNNAGCCAAT CGATTCCATA TGAATGAATG GCTCCAAAAT ACATTTNGTG CCCC GGCTGG 180  
GAATTGTNAA TGGGTTGCCC ATTGAAATAA AAGTATTATC CAGANCTTGG TAGAGAAGCT 240  
NCAGAATCTT TGCAGCTATG GGAATTAGAA GGAAAGCTAG NTCCTTTGCT NAAGGCAGCC 300  
CTTGNGGAAC CNGGATCCAG CATTTTTTTCG TTGGGGGGAT TAATGGGCNG TTTGGAATAA 360  
TGGCT 365

(2) INFORMATION FOR SEQ ID NO:1045:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 251 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1045:

ACCCTGATTC CGGAGGCACC AATGGCACTN AGGAGCGGAT GTCCGTGAAT CTGGGACAAG 60



GCTGTGGTCA CTGGGAAAGA TGGATGAGAA CCAGTTTGTG GCTGTGAACC ANCACCAATG	120
ACAGCCAAAG TNTTCAAGGT TTACGNGNGG GAAAGGCCGC ATTGCTGTGG GATCCGATGC	180
CGACCTGGTC ATCTGGGAAC CGNGACAGCN TTAAAACCAT CTNTGGCNGG GACACANAAC	240
AGCTCTTTTC G	251

(2) INFORMATION FOR SEQ ID NO:1046:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 56 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1046:

CTTTTTTTTT TTTTTTTTTT TTTTTTTTTT AAAAAANNNN TTNTTTTCCC CAAAAA	56
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(2) INFORMATION FOR SEQ ID NO:1047:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 387 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1047:

CGGGTCTCCC CGACCGAGGC TCGANTCCAG GTCGAAGGGT NGCCGGAGNN ATGGTTGGAG	60
AATGTGGAAG GAGCTGGAGG ACACCCGANT ATTCTTAAAG CAATCCCCAT GGCCAGATGT	120
CATCAGCAGC TGAACAGCAT CTCCAGAAAC CAGCTGCAAA GACAGAAGCA GAACAACTGG	180
TTTGGTGGAG AGATCTGATA ACAAAAAGTT GGGAAACAGG TAAAATAATA ACTTGGGGTA	240
GAAGTTATGC TTGTTTTTCT CCAGGCCAAA ATCAACAGCT GATCTGGATA CCATCAAGAC	300
ACCTGAAATT TTATCATGAG CCAATGCTGA GGGAAGAGAN TCCGGGNGTT TCCNCAGGAC	360
GCCCCATTTN CAGCCCTGTT TGAGANT	387

(2) INFORMATION FOR SEQ ID NO:1048:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 370 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1048:

CCCCAAAGTC CTGGGATTAT AGGTGTAAAC CTCCATGCCC GGCCGGTTTT AACATTTTNA	60
AATGGTTAAA AAAATAGTAT TTTNTGAATA CATGANCATT ATATGTAATT NCCNTTTCAN	120
CATCTATAAA TAAAGTGTTT TTTTGGAACA CAGCCATGCT AATTCATTTN CATATTGTNT	180
GTGGCCACTT TTCCTATTAA AATGGTGATT TCGAGTAGTT ATGACAGGGA CTGCATGGCC	240
CACAATGCCT AAAATATATA CTATTTGGCC CTTTACAGAA AAAGTTTAGG CTGGGTGCAT	300
GGGCTTACGC NGTAATCTCN GCNNTTGGGA GGTCGAGGCG GGTGGGTCCT CTGNGGTCCG	360
GGGTTCGGGG	370

(2) INFORMATION FOR SEQ ID NO:1049:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1049:

CCCACTGTG AGNTGCCCAA TTACCTGCCC TCGGTGNGCT CNNCCATCGN GAGGNAGGTG	60
CNCCAGCGCT ACGTGTGGCG TTTCTGCATC GGCCTGCACT CGGCGCCTCG NTTCTTGGTG	120
GCCTTCGCCT ACTGGAACCA CTACCTCAGC TGCACCTCCC CGTGTTCCTG CTATCGCCCCG	180
CTCTGCCGCC TCAACTTCGG CCTCAATGTC GTGGAGAACC TCGCGTTGCT AGTGCTCACT	240
TATGTTTCCT CCTCCGAGGA CTTTCAACAT CCACGGNAAA GGCTTTCATT NGTGTTTATT	300
GNCTTCATCC CTTNGGGGCA CATGGTNCCT TCACCTGGCA TTCTCTGGGC GGTGGAACCA	360
AGAAGCACAC AGTTAAGTTC AGGNGGGNTC GCAA	394

(2) INFORMATION FOR SEQ ID NO:1050:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1050:

CCTGTAGGAG TGCAATTGGA ACCTAAGCGC TTGGTCAANA TCCTAGAGGT GCTTCGGGAA	60
CTCCCTGTCC CAAACTACAG GACCCTGGAG TTCCTCATGA GGCACCTGGT ACACATGGCC	120
TCATTCAAGTG CCCAGACCAA CATGCATGCN CGNAACCTGG CCATCGTGTG GGCTCCCAAC	180
CTGCTGAGGT CTAAGGACAT AGAGGCCTCA GGCTTCAATG GGACAGCGGC CTTCATGGAG	240

GTGCGGGTAC AATCCATCGT CGTGGATTCA TCCTCACACA CGTGGACCAG CTCTTTGGGG	300
GTGCTGCCCT CTCTGGTGGT GAGGTGGAGA GTGGGTGGCG NTCGTTTCCA GGACCCGGGG	360
CNTCAGGCAG CCCCAGGAC NTATGCCCAG GCCATGNNTT GTTCACNGNN NGAGCTGATG	420
CAGTTGGCGT TGGACCCCCA CAATGGGGNC TACCTNATTT TCNTCGGGTT TGCCAGAGCA	480
CAAGAGGAAG GGGTTTTTTA AANGTTCAGN AAT	513

(2) INFORMATION FOR SEQ ID NO:1051:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1051:

CTTAAGCGCT AACGTCTTTN TNTNTCCCCG CGGTGGTGAT GACGGTAAAA ACTAAGGCTG	60
CTAAGGGCAC CCTNACTTAC TCCAGGATGA GGGGCATGGT GGCAATTCTA ATCGCTTTNA	120
TGAAAGCAGA GGAGGATGGG TCTGAAACGA ACTTTATTCA GAAGATTGCC AATNAACTCC	180
TAATGNCATG CAAACACCCT GAAAGTTCCA GTCCATCTTG AAAGATCTCC CAACCTCCAG	240
GNAGCCTGAA GCTTATGAAA TGCCAACCCT TCTTCCTCCA CCAAGTCCTT TCTTNAGGCA	300
AATCAACCTT GGGCCCGTGC GTCCCAATCC TGCATGGGTT AAACCCTNCT GAAGCTTTTA	360
AATTTTTTTG GAAAGTGNAT TCGGGAAAGG GGNCNTTTTT TTGGGNAAGG GTTTTTTCTT	420
	420

(2) INFORMATION FOR SEQ ID NO:1052:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1052:

CCCGAGAAAC ACTTATCAGT TGCCATGGG GAAACAAGCC ATGGGTACTA TAGGATACAA	60
CCAGCGAAAC AGAATTGATA CTCTCATGTA TCTACTAGCA TATCCACAAA AACCCATGGT	120
TAAGAACAAA AACCATTGAN TTGATAGATT TTGNAAACT GCCAGCTGGA CAGAATGCAA	180
CANTTGCTGT GNATGAGCTA TAGTGGCTAT GNTATTGAAG ATGCTCTTGT TTAAACAAG	240
GCCTCTTTAG ACAGAGGCTT TGGGCGTTGC CTTGTATATN AAAANTGCTA AATGTACGTT	300

GAAACGATAC ACCANTCAGA CTTTTGATNA AGTGCTGGGG CCCTGTTGGA TGCTGCTACA	360
GGAAACNTAT TNGGGGACNG GAATNNTAGN TGCAGATGGT ATTTGTTTCNA CCAGGTGAGN	420
AGTTGGAAAA CANACAAGTG GTTGTTAATN AAGTNCCNGC CCACAGTGAC TCCGATTCCT	480
TGGAAGGNAG TTATG	495

(2) INFORMATION FOR SEQ ID NO:1053:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1053:

CGANTCAAAA AGGCTGACCT CCCTTTACTC ACCAGCACTT NCCTTGGCAG CCACATGTNC	60
TCCTGCTGCC CCGAAGGACG ACAACTGGAC ATAAAGAAGT CAAGCTACAA AAAGCTCTCT	120
AAGTNCTGC AGCAAATGCA GCAGGAGCAG ATTATACAGG TGAAGGAGCT GAGCAAAGGG	180
GTGGNGAGCA TTNTGGCTGT GGA CTGGAAA CACCCGAGGA TTACATCTTT NGTCATACCC	240
GAGCCCTCCC CGACCTCCCA GACTATCCAG GNAGGGTNGC AGGGGACAGC CCTNATTNAC	300
CCTTCCAG	308

(2) INFORMATION FOR SEQ ID NO:1054:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1054:

CCCCCGGCCT CATNAGTACC TNTCCCCAGC GGATCTGCCC AAAAGCTGGN ACTGGCGCAA	60
TGTGGATGGT GTCAACTATG CCAGCNTCAC CCGGAACCAG CACATCCCCC ANTACTGCGG	120
CTCCTNCTGG GCCCACGCCA GNACCAGCGC TATGGCGGNT CGNNTCAACA TCAAGAGGAA	180
GGGAGCNTGG CCCTCCACCC TCCTTTCCGT GCAGAACGTN ATCGACTGCG GTAACGCTGG	240
CTCCTNTGAA AGGGGGTAAT NACCTGTCCG TTTGGGACTA CGCCCACCAG NACGGAATCC	300
TTNAA	305

(2) INFORMATION FOR SEQ ID NO:1055:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1055:

ATGGTCCAGT AANTNNTGAG CTGTTCTGGN TGTTAACNAG ATGGAGCCGT TTTTGTCCCTG	60
CATTTGGAAT TGTATGAGTG TGGGACAGGG AAGGTCTGTT GNTTTNANNA CAAGTTTtag	120
TTAGGAGTTT TTGGGTCGTT ANGtagGT	148

(2) INFORMATION FOR SEQ ID NO:1056:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1056:

CAGGACTGCT GGGACCCCCT GCACCTCCTG GCCACGGAGA GATCCTGCTC CCAGGGACCA	60
GCGTCTGGNT GGGACACAGT TCACTCCTCT NTCCACTTCA TGTTCCTTTT CTCAGCAGA	120
TGGCTCAAGT TCCTTGTTTT TNTCCTTGCT TTCTGACAGC NGTAGCTTCT GAAACCTGCC	180
ATTTTTGGTC TCCTGATGCC TGATTTCTTA ATTGTCCTGA CTGTGTCTTC TAGGAAGCAT	240
TAAGTCTGAA CTGACTTATT AGGGAACCTT AGAAAGTTAA ACACACAAAA CCCTTTCTTT	300
GACTCCTATC TTNAAGGACA TGGAGATACA GTTNACATAT ATTTATACAC AAGGNTATTT	360
CATATGGCAA AAACGGGGAG AAGGCACAAT TTTAAGAGCC CAATGGGGAC TGGGGTTGTG	420
TATGCATCTN TACAATGACA TGTTATGAAG TCATTCTGTT TTTAATAAAA CTTTTTAGTG	480
GNCATGGGGN AAATACAAA	499

(2) INFORMATION FOR SEQ ID NO:1057:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1057:

TACTTATCCC CCCACTATGG ATTCTGGGTN ANAAGGCTGA GGAAGGGAAA TAAGTACCGA	60
NCAGGCACCG ATNAGTACCC AATCCTNTCC TTNCGGGTCC CTCCTCGCNG GGTGGNAATN	120

TNCGTGGATT ATAAGGCCCA TNANATTNNT TTNTACAATN TNACTAANTG TGGCTCCCAC	180
ATCTNCACTT TCCCCCGCNA TCCCTTCCCT GGGCGCCTCC TGCCCTATTT AAGTCCTTGC	240
TACAGCATTG GAACCAACAA CACTGCTCCT NTGGCCATCT GCTCCCTGGA TGGGGAGGAC	300
TTAAGAAAGC TNACCACCCT AACCACAGAG GCTTTGGAAT TGGGNCTGGC CCCCATGGGG	360
CTTGGAGGAC CGANCCACTT GAAAGGTATC CCCTGAAAAC TTAAGNTTGA GCCCAGTATT	420
CCAAGGATTC CTCTGTTNTN ATCCTTTGGT CTTTGCTACC AGGGNTGAAG	470

(2) INFORMATION FOR SEQ ID NO:1058:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 498 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1058:

CGGTCTACTT ATCCCCCAC TATGGATTCT GGGTNANAAG GCTGAGGAAG GGAAATAAGT	60
ACCGAGCAGG CACCGATNAG TACCCAATCC TNTCCTTGCN GGTCCCTCCT CGCNGGGTGG	120
AAATNTTCGT GGATTATAAG GCCCATAAAA TTTTTTTNTA CAATNTAACT NANTGTGGCT	180
CCCACATCTT CACTTTCCCC CGCNATCCCT TCCCTGGGCG CCTCCTGCCC TATTTAAGTC	240
CTTGCNACAG CATTGGAACC AACAACACTG CTCCTTTGGC CATCTGCTCC CTGGATGGGG	300
AGGACTAAAG AAAGCTTACC ACCCTAACCA CAGAGGCTTG GGAATTGGGC CTGGCCCCCA	360
TGGGGGTTTG GNGGACCGAG CCACTGGACA GGTATCCCCT GAAACTAAGC TGAGCCCAANT	420
ATCCAAGGAT TCCTCTGTTT TGATCCTTTG GGTCTTTTGT TACCAGGGTT GAAANTTTTA	480
AATGGAAACC ATTTTNTT	498

(2) INFORMATION FOR SEQ ID NO:1059:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 342 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1059:

TCANCCCCC AAANTGGATT CTGGGCAGTN TTTTTTTGGT ATGGGAAAAA AATATTGGGC	60
TCTNACCTCC CCAATAACTG CCGTACCCCT GCGGACCCCG CTCCANGATG AGGGATTTTT	120
TTGGACTATA ATGCTGGTAA GGTCTCCTTC TACAACGTGA ACAAGAAGGT GTCACACCTT	180

GCACTTTCTC TGNATGGTAA CCTTTTGTNG GCCTNTCCCG GCCCTNACTT GNAGTNTGAN	240
NTAACTTCGG GAAGGGGAAA AGTGCCAGTT CCTCTGAATC CATCTGCCCC CATGANTGGG	300
NATAGATGGG TTTTGTGGN CCATGTTTGG GGNATTCATG GN	342

(2) INFORMATION FOR SEQ ID NO:1060:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1060:

AGGGTGCCCA GTTACCCAG GNTGAGGTCG CTGCTTCTGN CAATCCTGAN TGCNCCACCT	60
GGTTGAGGNG CTGGGAGGTA CCCCTTTCCA AAGCCGTGTG GTCCAGGNAG GNGCCCGNCC	120
ACCTCATGAG CNTGTTTGGT GGAAGCCCT GATCCTNTAC AGGGCGGCAC CTCCCGGAGG	180
GAG	183

(2) INFORMATION FOR SEQ ID NO:1061:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1061:

CGCTTCCTTC NTGNGGTGGT GGAGCCAGTT TTTGGCCAAC TCAGCCGACC GCAAGAGGNN	60
GCTTCTGGGG GCTGNGAGTC ACTTCCGCAG GTGGAGGACC TTTCTTGACC TTCGCCCANT	120
GGTCTGCNT TCAAC	135

(2) INFORMATION FOR SEQ ID NO:1062:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1062:

CCTATNAAAT GCGACGCTGG AACGAGGCCT TGGTCACCAA CATGTTGCCT GAGCACGTGG	60
CACGCCATTT CCTGGGGTCC AAGAAGAGAG ATGAGGAGCT GTATAGCCAG ACGTATGATG	120

AGATTGGAGT CATGTTTGCT TCCCTGCCCC ACTTTCCTGA CTTCTACACA GAGGAGAGCA	180
TCAACAATGG TGGTGTGAG TGTNTGCTTT TCCTCAATGA AATCATCTCG GNATTTTGAA	240
CTCTNTCCTG GGACAATCCC AAGTTCCTGG GTGGATCACC AAGATCAAAA CCATTGGCAG	300
CACGTTATTT GCGGGCTTCA GGAAGTCACC CCCGATGTNC AACACCATGG GNTTTGNCAA	360
TTCNCAACAA GNAAGACAA	379

(2) INFORMATION FOR SEQ ID NO:1063:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1063:

CCTATNANAT GCGACGCTGG NAACGAGGCC TTGGTCACCA ACATGTTGCC TGAGCACGTG	60
GCACGCCATT TCCTGGGGTC CAAGAAGAGA GATGAGGAGC TGTATAGCCA GACGTATGAT	120
GAGATTGGAG TCATGTTTGC CTCCCTGCCC AACTTTGCCT GACTTCTACA CAGAGGAGAG	180
CATCAACAAT GGTGGTGTG AGTGTCTGCN TTTCTCAAT GAAATCATCT CGGNATTTTG	240
AACTCTCTCC TGGGACAATC CCAAGTNCCG GGTGGTTCAC CAAGATCAAA ACCATTGGCA	300
GCACGTATTA TGGCGGGTTC AGGAGTTCAC CCCCAGGTN CAACACCAAT GGGTTTGN	360
AGCTCCCAAC AAGGNAGGNC AAGTTCCNAG AG	392

(2) INFORMATION FOR SEQ ID NO:1064:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1064:

CTTNTNCTCT TCCCTGGAGA CCTGAGAAAC CAATCTGAAC CGACAGNNAG CTGGCAGAGG	60
NAATACCTGT ACCGCTATGG TTACACTCGG GTGGGCAGAA ATGCGTGGTA GAGTCTAAAT	120
CTCTGGGGCC TCGNTNGCT GCTTCTCCAG AAGCAACTNT NCCCTGANCC G	171

(2) INFORMATION FOR SEQ ID NO:1065:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
- (B) TYPE: nucleic acid



(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1065:

TAAACGGAGG AGCTGTTCCA AAGGCTGCCC NGAGGATGCC GCAANTCCCC CNTAGGCNTC	60
TGTTTTACCC CNTACCCGGA GCCTTCAAAG TGCTCCTGGA AGAACCCCGA GGCAGAAGCN	120
GCCCTTAANC TGGCGTTAAG ATCACGGAGN NGTGCCTTCC TGGGGCCGAT TAAANCTTAC	180
CGGTTCGGGC TGATGTTTCC GG	202

(2) INFORMATION FOR SEQ ID NO:1066:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 110 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1066:

CAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	60
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA ANAANAANAN AANAANAAAA	110

(2) INFORMATION FOR SEQ ID NO:1067:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 513 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1067:

CCCCAGAACC TGGATTTTNT NAACCTTATG GCCTACGACT TCCATGGCTC TTGGGAGAAG	60
GTCACGGGAC ATAACAGCCC CCTCTACAAG AGGCAAGAAG AGAGTGGTGC AGCAGCCAGC	120
CTCAACGTGG ATGCTGCTGT GCAACATGGG CTGCAGAAGG GGACCCCTGC CAGCAAGCTG	180
ATCCTTGCCA TGCCTACCTA CGGACGCTCC TTCACACTGG CCTCCTCATC AGACACCAGA	240
GTGGGGGGCCC CAGCCACAGG GTCTGGCANT CCAGGCCCTT TCACCAAGGA AGGAGGGATG	300
CTGGCTTACT ATGAAATCTG CTCCTGGAAG GGGGCCACCA AACAGAGATT CCAGGATCAG	360
AAGGTGCCTT ACNTTTTCCG GGGACAACCA TGGGTGGGGT TTGATGNTGT GGAGAGTTTC	420
AAAACCAGGT TCAGTATTTG AAGCAGAAGG GATTGGNNGG GCCNNGTNTT GGGCATGGGA	480
TTAGATGATT TGCCGGTTTT CTGCAACCAG GCC	513

(2) INFORMATION FOR SEQ ID NO:1068:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 198 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1068:

TCACGGATCA TATGCTGACG GTGGAGTGGT CCACAGAGTT TNGATGGGNG AACCTCATA	60
TCAAGCCTCT TNAGAACCTG TTATTGCACC CNNGACTTCA TCAGCTTTGC ACTANGCANT	120
GGNATTATTT GAAGGATTGA AGGCATTTTCG AGGAGTTAGA GAATAAATTC GACTGNTTCA	180
GCCAANCCTC AACATGGA	198

(2) INFORMATION FOR SEQ ID NO:1069:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 465 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1069:

CCCGGAGGTG TACCCGACCC CCCAGGCTTG GAGGCAGCCA AAGAGGTGAT GGTGAAGGCC	60
ACTGGNCCTC TAGAGGACAC CCCAGCAATG GAACCCAACC CTTCAGCAGT GGAGGTAGAC	120
CCCATCAGAA AGCCTGAGGT CCCACAGGA GACGTAGAAG AGGAGAGACC TCCCAGGGAC	180
GTGCACTCAG AAAGGGCTGC TGGAGAGCCA GAGGTGGCAG CGGACTTATN TGNAAGTTCT	240
CCAAGGAGAA GTACATCCTG GACTTCATCG CCAGAGAAAC TCCACAAGGA ATTGGGAGGA	300
GGAGCTTCAA ACTCAGCAGC ACGGATTTTC CGCAGCCATG CCTGGTTACC ATGGTCCGNA	360
TTCCCCCGAG AGGTCTTCGG AGACCTTNGT TACAAACGGC AAACGGNGAC TTTCTCATN	420
CCGGGANTCA ATTCAACCAG TCTTGGGGGA TTATGTGGNT CAAGT	465

(2) INFORMATION FOR SEQ ID NO:1070:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 69 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1070:

GGNCTCCGTA GCCGCACAAA CCAGGGCTCN NCATGGAAGC CAGGATTCAN TCCCCGTGGG 60  
GGTGGCTTT 69

(2) INFORMATION FOR SEQ ID NO:1071:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 367 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1071:

GGCAGAGTNT AGGGCCTGTN CACAATGAGC TTGCATTCCA GCCTCCCATT TCCAATCATC 60  
CTGCTCCTGA GTATTGGTGT TCCATTGCTT ACTTTGAAAT GGATGTNCAG GTAGGAGAGA 120  
CATTTAAGGT TCCTTCAAGC TGCCCTATTG TTA CTGTTGA TGGATACGTG GACCCTTCTG 180  
GAGGAGATCG CTTTTGTTTG GGTCAACTCT CCAATGTCCA CAGGACAGAA AGCCATTGAG 240  
AGAGCAAGGT ATTGATTGTA TAGTCAGATA GTTACTTTTA AAAAATTGGN GCATAGTACA 300  
TTGTCTTTTA ATTCAAGGTT NAAGTTTTTC CCCTGTTACA TNATATGTNG TTCCTTAAAT 360  
TNTAATT 367

(2) INFORMATION FOR SEQ ID NO:1072:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 317 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1072:

GGCAGGAGCA GCAGTGGAGA AATTTGTTTA TTCCTGTNCA GGCTACTGTN TGGNANCCTT 60  
TGTCTTGGA ATAGGCGACA ANCACAATGA CAATATTATA ATCACCGNGA CAGGAAACCT 120  
ATTTAATATT GACTTCGGGC ACATTCTTGG GAAATTACAA AAGTTTCCTG GGCATTAATA 180  
AAGNGAGAGT GCCCTTTGTG CTANCCCN TG ACTTCTCTT TGTGAATGGG NAACTTCTGG 240  
GAAAGAAGGC AAGCCGACAC TTTCTGAAA TTTCAGGACA TNTGTGTTGA GGCTNATCTA 300  
GNCCTTCGTC CTCNCAC 317

(2) INFORMATION FOR SEQ ID NO:1073:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 320 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1073:

TCCTTCCTCG CGGCACCNNC CTCCCCCGCG GCCTTCCTCC GCCGCCGGGN NCTCCGGCAG	60
CTTTATCGCC AAATTCCCTG AAACNTTCGC TTTCTTTTAA ATCCCCTGCA TCGGAATCAC	120
CGGCNTGCCC CACCATGTNA AAACGCAGCC GTANACACCA GCTCCNAAAT CACCACCAAG	180
GAACTTAAAG GAGAAGAAAG GAAGTTTTGG AAGAGGCAGA AAATGGAAGA GACGCCCTG	240
CNTAACGGGA AATGCTAATN AGGGAAAATG GGGGGAGCCA GAGGCTGACA ATGANGGTTA	300
GNACGGAGGA AGAGGGAAGN	320

(2) INFORMATION FOR SEQ ID NO:1074:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 296 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1074:

GGCAGGAGGA CCAGGTGACG GCGGGCGCCA TGCAGCGACT GGGGGCNGGG GGCCTNACGN	60
TGGACAGNAT CCTGCAGACA GATGATGCCA CGNTGGGAAA GCTCATNTAC CCCGTGGGTT	120
TCTGGAGGAG CAAGGTGAAA TACATCAAGC AGACCAGNGC CATCCTGAAN NAACACTACG	180
GTGGGGACAT CCCAGCCTTT TTGGCCGANT TGGTGGCGCT TCCGGGTTTT TGGGCCCAAA	240
TTGGCACACC TGGGTTTATG GNTTTGNNCC TGGGGGANAA TTTTTTTCGG GNTTTT	296

(2) INFORMATION FOR SEQ ID NO:1075:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 198 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1075:

CAGATGATGC AGAGGNAGCN ANCTGAGCNC NTCCAGGAAG AAAGTTAAGG GAGAAAGGCG	60
GGCCCCGGGAA ACAGGCTGAG GCTGAGGTGG CCTCCTTGAA ACCGTAGGAT TCCACCTGGT	120
TGAAGAAGAG CTGGACCGTG CTCAGGAGCG CTTTGGCCAN TGNCCTGNA AACTTGGANG	180
AAGTTGAAAA AGCTGNTG	198

(2) INFORMATION FOR SEQ ID NO:1076:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1076:

GGCACGAGCG TCGCGNCGCC TTCTGAGTGG TCGGGTCGAG GCTTCTCGGN CTAGCAGTGC	60
CCTCGCTGCG CGATCTCAGG CGGGTTCTCC TCGGCTCCGC GCAGCCGNGN CGCGNTGGGG	120
GACCCGGCGC ANGGTCACCT GCTGCCGAGG GACCCCGNGG CCCGCCCGG TGCTCGTGAT	180
GGNGCTGATC TNCGCCAAAC TGTGGAGCCT CNNCTGTAAC CAAGAACACA AAGTAATTAT	240
AGTGGGACTG GATAATGCAG GGAAAACCAC CATTCTTTAC CAATTCTTAA TGGAATGAAG	300
TGGTTCATAC TTNTTCCAAC CATTAGGAAG CAATGTTGAA GAAATTAGTT TGTGAAGAAC	360
ACTTCATTTT TCTTTATGTG GGGATTATTG GGTGTTGTTCA GGAGTTCTCT GCGGATCATT	420
NNTGGGGAAN CACATTATTT ACNTCAAATT ACAAGAGNTT CATTC	465

(2) INFORMATION FOR SEQ ID NO:1077:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1077:

GGCACGAGCG ATAATGCACA GTCCTGGTCT GTGGACCCTG CCACATTCCA CGGACTGGGN	60
CGCCTACACA CGCTGCACCT GGACCGCTGC GGCCTGCAGG AGCTNNGCCC GGGGCTGTTC	120
CGNGGCCTNG CTGCCCTGAA GNACCTNTAC CTGNAGGACA ACGTGCTGCA GNAACTGCCT	180
GGATGNCANC TTNCGTGACC TGGGCAACCT TACANACCTC TTNCTGTACG GCAACCGCAT	240
CTCCAGCGTG NCCGAGCGNG GNTTCCGTGG GCTGCACAGN TCGACCGTTT CCTACTNCAC	300
CAGAACCGCG TGGGCCCATG GTGNAACCGG ATGNTTTTCC GTGANCTTGG CCGTCTCATG	360
ACANTTTTAN TCTGNTTTC CAACAATCTA TTCAGCGGTT NCCANTTTA GGGCCCTNNG	420
CCCCCCTNNG NTTGCCTGGA AGTAACCTGA GGGTCAAAGG GCAAACCCTT GGGTGTTTTG	480
AATTTCCGGG GAAGGTCAAT TTTGGGGG	508

(2) INFORMATION FOR SEQ ID NO:1078:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1078:

GGCANAGGNA GTAAACAGAT AACAGGTGGT GGTACCTGGT TGGGGGAGGG GGGCGTGCAC	60
TGCCATGTCT TTTTTTTTTT TTTTTTTTTT TTCCCNANT	99

(2) INFORMATION FOR SEQ ID NO:1079:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1079:

GGCAGAGCCT TGGTACTAAG TCATCCTCAG GTTTNATAAC TAATGGTGCC TTCTTTNATC	60
CATCAAAGTT ATGACTGANT GTGGCACCGG GGACAGTTAG TTGCTGTCCT AGAGTTAATT	120
TCCTAGCTTC TTGTGTTACA NATNGGTGGC AGCTAATGCC TTAAAGGCAA AGGGGCCATC	180
TTAACACCAC GGGGTCTAGT TGTTGGGNAT AAATATGGCC ACTGGGGTGA CGGCCATGAT	240
NCCTATAAGT TGGGGTCAGA GCCCCCTATG GGCCATTGTT TTTTNGGGTN CAGGAACATT	300
NTGGGGAAGG CNTTAGTTAA TGT	323

(2) INFORMATION FOR SEQ ID NO:1080:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1080:

GGCACGAGGG ACAAATATAC AGCTGTTGTA AAGATGATTG ATTCTGGAGA CAAGCTGAAA	60
CTTGACCAGA CTCATTTAGA GACAGTAGTT CCAGCACCAG GAAAAAGAAT TCTAGTTTTA	120
AATGGAGGCT ACAGAGGAAA TGAAAGGTAC CCTAGGAATC CATCANTGNA GNAAGACTTT	180
TTNCAGCTAC TATCGTGCAT TGGNAACTGG GCCCTTTGAA AAGGGACGCA GAGTTGGAAG	240
GGAATTCAAT GATGGAAGGA CATTTCTAAA CTTGNCCTGA GTTTTGGAAG ATTTGTTAAA	300

CANTGACATT GAAAATCTTG AAAGCATNCA AATTGGGTGT TCCGNCCAAG GGCATTNATG 360  
AAGGACTCNG ACTGTGGTTT AGGGGT 386

(2) INFORMATION FOR SEQ ID NO:1081:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 71 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1081:

GACCGAGGNC NNCCTGAACC CCCAAGGACA ACCGAGAGTN GATGACCCAA ATCATGTTTG 60  
AGACCTTCAA C 71

(2) INFORMATION FOR SEQ ID NO:1082:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 266 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1082:

GGCAGGAGGT GAAACTCATC ATGGCAAATA TGCTTATNTG NATATATCCT TTGCCATACA 60  
TGNCCTGCAA ACTGTAATGA AATGTTATTT ATAAGACTCG TAAGGCATGT NTNATTAGAC 120  
TGGGACACAC AAAAGCCNT GAATTATCTA GGCAAGCAAT CCTCTAGGGT CCAGATGTAG 180  
TTTGTAATG TGGGTGTTCA GTGATCACTG NTAATTGCAT TGANTGGATT TTNAATTTGC 240  
TATGCCTGTG TTGAANTAGT NATTAG 266

(2) INFORMATION FOR SEQ ID NO:1083:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 256 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1083:

GGCAGGAGGT TAAACANCCG ANNCTNNGCN GCAGGTGCC CNCNTTGGGG CTGCTGGCTG 60  
CTGCNTTTC GGCAGGAGGT GGTGGCCGCG GTCCCACGAG AGGGGGTATT TTNCGTCAGC 120  
CAAGATGGGT TCCAAAAGGA GAAATTTGAG CTGTAGTGAA AGGCATCAGA AATTAGTAGA 180

TGAAAACTAC TGCAAAAAAT TACATGTCCC AAGCTCTAAA AAANCGTCCA ACAGTCCAAT 240  
TNNGGGTNTA NAATTG 256

(2) INFORMATION FOR SEQ ID NO:1084:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 322 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1084:

TAAGTAACAC GNGGTGAGGG TTGCAGATGC AGTTNCCTGT TTTAATCGTA TAGACAGGGC 60  
AGCTCTACTG CGGAGATGGT CAATGTCCCT AAAAGCCAAA GAACCTTGTN TTAAGAGGTG 120  
TGGTAAGCAT CACCCTTACA AAANTAACAC AGTATGAGAA AGGGCAAGGT TTCCCTGTTA 180  
TGCCCAGGGA AAGAGGTGCT ATGAATTGGA AAGCAGAGTG GCTGTGGTGG GCAGACAAAG 240  
TCAGTTTTCC AAAAGAAGGC TGGTGCGGTT TGGNCTGTNT CCCCACCCAG NTTTGCCTCT 300  
TGATTTTCCC ACATGTTNNT GG 322

(2) INFORMATION FOR SEQ ID NO:1085:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 396 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1085:

CTACATCCAG TCCCTNCCAC AAACCCCAGG AAGGATTTC A CTCAGCTGTT CCCACGGGCC 60  
ANCCCCCAGG GTNAGTNTNA AAGCCCGCTC CCCAGGGGCC TCTNAGCGTA TCCCAAAGGG 120  
CGGGCTCTCC CAGCCCCTGG TGTNAGGCTC TTGGCTCTNC CCCTGCAGCT GCGGACCTGC 180  
TGGAGAAGAT GCTGGAGCTA GACGTGGACA AGCGCCTNAN GGCCGCGCAG GCCCTCACCC 240  
ATCCCTTCTT TNAACCCTTC CGGGACCCTG AGGAAGAGAC GGAGGCCAG CAGCCGTTTT 300  
AATGATTCCCT TAGNACACGG AGAAACTTNA CAGTGGGATG AATGGGAAGC NTTAAGANCT 360  
GGGGGCCTCG GGGTTCCTCG CCTTCGNCTG CAGGCT 396

(2) INFORMATION FOR SEQ ID NO:1086:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 451 base pairs  
(B) TYPE: nucleic acid



(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1086:

GGAGCTCTCA GCATACCGTG CAACAGTTCT GGGAAATGCC AGTNCAAAGT GGGTGTNATT	60
GGCTCTATAT GTNACCGATG CCAAGATGGA TATTATGGCT TTAGTAAGAA TGGCTGCTTG	120
CCCTGCCAAT GCAATAATCG GTCTGCCAGT TGCATGCNC TCACAGGTGC TTGTTTAAAC	180
TGCCAGGAAA ATAGCAAAGG TGATCACTGT GAAAGAATGT AAAAGAAAGG NTTTTATCAG	240
AGTCCTGATG CCACTAAAGA ATGTCTTCGC TGCCCTTGTT CCAGCAGTGG ACATCTACAG	300
GCAGCTGCTC CTATTAAAAT TCGAGTGGAA TTGGGNGCCT GGAATGTGGA ACCAGTGGTN	360
AAAGANGGGT TACATAGGGC CCGAACTGGC ATTAAATNTG GNAAATGGGT TATTTACAAT	420
TTTNGACCAG CATCTGTTGG AAAGTGCCCA T	451

(2) INFORMATION FOR SEQ ID NO:1087:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 288 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1087:

GGCANAGGAA GACCTACATC GCCAGCCAGN GNTGTTCTGG AGGCCACGGG TCAATGACTT	60
CTGGCAGATG GCGTGGCAGG NGAACAGCCG TGTNCATCGT CATGACCACC CGAGAAGGTG	120
TAGAAAGGGC CGNAACAAAT GCNTCCCATT ACTGGGCCCG TAGGTGGGCA TGNCAGCGTG	180
NCTTGATGGG CCCTACTACT GTNAACCAAN TTTCGGGGGA GCATGTACAC AACCGATTNA	240
CAAACTNCC GTACCTTACA GGTCTGCCCC GTTTTGGACA ATTCNCCG	288

(2) INFORMATION FOR SEQ ID NO:1088:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 282 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1088:

CGTCGAGATC ACTTTAAAGA AGCCATGCCC TTTGCGCGNG TTNTGTAAGT AACAAATAACA	60
TTCGGAAGTN TGAAATGTTT GCCCAGACCC TTNAGCAGAG TCGGGGCTTT GGCNAGCTTN	120

AAATTCCCTT NNAGGGAAAC CAGGGTGGAA GCTGGCCCCA GTNAAGGGCA GTGGAAGGCG	180
GGCACAGGTG GCCAGTNTAT ACACAGNAAG ACAATGAATG GTGAACCTGT NTGGTTNAAG	240
TGGTGGTGGC CAGCGTGCCA GTGAAGCTGG ACCTGNCCTG GT	282

(2) INFORMATION FOR SEQ ID NO:1089:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 152 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1089:

ATCAAGACGG GCAACAGGGT ATCTTGGGAA GTACTTTNCT GACATCATCA AGGAGGTTAT	60
GTCAGACCTG GGAGGANAGC ANNTACCAGA NTGCAAGAGC TTGCGGCTCT GCCATTTACT	120
GGGCGCTCGA NGGGTGGATT GGGGACAAAG CT	152

(2) INFORMATION FOR SEQ ID NO:1090:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 134 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1090:

GGCANAGACT GGACTGGTTC AAGCGGCCCCG ACGGCTTCCT GCTGGTGCTG GAGCGGCCCCG	60
AGCCGCGCAG GACCTCTNCA ACTTTATNAC GGAGCGCGGC GCCCTGGAAC GANCCGCTGG	120
GCGNCCGTTT NCTT	134

(2) INFORMATION FOR SEQ ID NO:1091:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 505 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1091:

GAAAATACGA GGTAGAAAC TTAACCATTG AAGAGGAGTA AGGCTACTTA AAGCGTTAAA	60
AACTAATTGG GTAAGGTATG GTTGACCCAG CTACTTCATT TGCCTTACGA TGTATATTCA	120
TTAANCTAAG TCACTCACCT TCTCTGTGNA TGTGTATGGT TTGGTACAGT AAACATGAGA	180

TATGATTAA	GGTGATT	CAG	GGATAGAT	CA	AGTGTCT	GCC	TAAGTAA	ATC	TGTGTTTT	TCA	240	
TTTTTTTT	TTTC	TAGTACC	ATA	ACAGCTT	GGG	GGAAAGAC	CA	TGAAAA	AGAT	GCTTTT	GNAA	300
CATATTGT	GTA	ACACAGT	TTTT	CCATCAT	GCC	CTGTTNCT	TGT	GGGTCCAN	CG	NTAGCTAT	GG	360
ACCATTTT	TN	AATGCGT	GTG	GAGNAA	ATTN	NGGGGGT	GAA	GGTTNCA	AGA	CATTTNAT	TTA	420
GTTTCCGG	GGA	AGTACNC	CNG	GCNCCN	NNTAT	TATTCAG	ACC	NGTTTT	CGGG	AACCCNCT	NG	480
NCACNTGT	TAA	AAGGTTT	G	GGT								505

(2) INFORMATION FOR SEQ ID NO:1092:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 363 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1092:

GGCAGAGGGC	ACTGGGGAAA	ACAGAGGAGG	AGGCACTGAA	GCACTTCCAA	GTAAAGTTTA	60
ACGANNCCCT	CCGTGAAGAC	CTGGCAAAC	CAAAGTAAAC	TGGCTGGCCC	ACAACGTGTC	120
CAAAGACAAC	AGGCAGTAGT	GGCTCCTCCC	AGCTCTGGGC	CCAAAAGGAG	GCGGCTNCGG	180
GTCGTGGGGA	CCAAGCACAT	TGGTNCTAAA	GGGGCTGAAG	AGCCTGAACT	GCACCTTAAC	240
GGGCAAAGAA	ACCGACATGG	CTGCCTTTTG	TTTACACTGG	TTATTTGATT	TCATGANCTT	300
TGAAATAGTT	TANGGTGGCT	AAACAGCCAT	AAACGGAAAC	GGCTNCTTTT	ATGCANCGGN	360
GGT						363

(2) INFORMATION FOR SEQ ID NO:1093:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 407 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1093:

GGCAGAGGNA	GCAGCTCACC	CCCTGGGGGN	CCCCCNAAGC	CCGGGGGCCA	GCTGGACAGC	60
ATGCTGGGGA	AGCCTGCAGT	NTGACCTGAA	TCAAGCTGGG	GGTCGCCACA	NTCGCCAAAG	120
GAAGTCTGCG	GGGCCTGCAA	GAAGCCCATC	GCCGGGCAGG	TTGTGAACCG	CCATGGGGAA	180
GACGTGGCAC	CCCGAGCACT	TCGTCTGCAC	CCACTGCCAG	GAGGAGATCG	GATCCCCGAA	240
CTTCTTCGAG	CGGGATGGAC	AGCCCTACTG	TGAAAAAGGA	CTACCACAAC	CTTTTTTTCC	300

CGGGCTTGTT ATTATTGNAA AGGGCCCCCA TCCTGGGTNA AATGGGTGAA CAGCCTTTTA 360  
ACCGGACGTG GGAACCTGAA AAATTTTTTTT TGTNGNAANA TTTTGGG 407

(2) INFORMATION FOR SEQ ID NO:1094:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1094:

ACTTTNTTGG CCCCAAACCT AGGNCCTGGG GGATCCCCTG ANCCCACTGG AGAGTNTNCA 60  
GGGCTGGCCC CTGTCCCCAA AATCCCAGGC TCCCATTITT TCCCAGGTGT CCTGCTTTTT 120  
AATCTCATCT TCATGTTGAG GCCGTTTTAT TTGACCCTCA AAGAGGAAGA CCAGCTTCTA 180  
GGGCTGTCCC CGCCCCAGGA CCAANAGTCC TGCAGGGCTA AAGTNTCCCA CTGTGCCATG 240  
TTAACACACT GCACAATTAA CTCCAGGGGG TGCCGCTCAT NNTTGAAAAT TNACAGTCAA 300  
TGCTTGAAGT CACGACATTT TTTCCAGAAG ATGGGCNTTA AGGNTCTCGA AGAAGGGGGC 360  
ATTTCTTAAT CCCTTACAAA NTNGTTTTGG GGTNTNGGT GGAGGTCGNT CTGGTNTCAG 420  
NAGCCCTAAT TTTCTCCCC GGACCTGTCA AGAATT 456

(2) INFORMATION FOR SEQ ID NO:1095:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1095:

TAAATAAATA AATAAATAAT AAAATGAATG AGGAGCCAGG TGCAGTGGCT CGTGCCCTGT 60  
GAATCTCAAC ACTTTGGGAA GGCCAAGGGT GGAGAATCAC TTGAAGCCAG GAGTTCTAAA 120  
CCAGATTGGG CCAACAAGTG AAGAACCTCA TCTTTACAAA AAGTTAAATT AGCCAGGCGC 180  
GNTAGAGTGT ATCTGCCAGT NCCAAGTAC TTGGGAAGGC TAAGGCAGGA GGATTCACTT 240  
GAGCCCCAGG AGGCTGAGGC TATAGTGAAG CTNTTGACCG TGNCCATTGN ATTNCCAGCC 300  
TGGGGNAACA 310

(2) INFORMATION FOR SEQ ID NO:1096:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1096:

CAGGTTATAA GTTGAGAAAA CCACTAAGGG AAACGCCTGA TGACGCCCAT TCTGAATCAC	60
TATTTTCCCC GTATTAACGT GTCGGGAAGC TGCTGCGNTC AATATTGATA CGCTTNGTGC	120
ATTGCNCTGA AAACACAATT GCACCATTCG GTTTGAAAAC CTCGACGTTT TGCTGCCGAG	180
GGAAATACAG CTTGATAATC AATCGCCGGA AGAGAACTG GTGATAGCCC GTCGTGGCGG	240
TTACTGTTTT GAAGCAGAAT GCGGTGTTN AGCGGGTGTT ACGCGAGCTT GGGTTTAACG	300
TTTCGCAGTT GTTAGGGCGC GTAATGTTTA TTCAAATTCC GNCCAGNTTA NCNGCNGGGA	360
ACCCATCGTT TGCTGTTTGG TGGGACTGGA GGAGGAAAAA TGGGTTGCTG A	411

(2) INFORMATION FOR SEQ ID NO:1097:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1097:

GGCANAGGGT ATTTACCTAC TGTAACAGC TAATAAGATG TGTGTATGGA AGACTGAAGA	60
CAGTCTGAGA GATGCATCTC AACAAGGCCT AAGTCTCCCT TCCTCTGGGA ACTGTCCGGT	120
AGTGNCTAGT TCACTGGGGT CCTTGCTCTG AGGCTGGTGG GAACTGGAT TTCAGGGACA	180
CAGGCTGACC ACACAGGGNG CTGTACCGNA CCCCTTCCAA CTGGGAACTC CCCTCGGTTT	240
CTCACACTGT GGNCACTTAG TGGGTTTGGG NAGGCTCTAG GCAAGGGGGA TGGGTAGTAG	300
GGTGGTTGAG GATNGGTGGT TGANTATGGA CAAAGGTACG NGTTATGGGT TTTCACCCCA	360
GAAATCCCAC NANA	374

(2) INFORMATION FOR SEQ ID NO:1098:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1098:

GGCANAGTGA TTAACAGATG CAGGCCTATT CAAATTTNCT ATTTNATGTC AGTCTTGGA	60
AATTGTAATT TTNAAGATAT TTGTCCATTT NATCTAATTT TCCTAATTTT TTGGCATGAA	120
GTTGTTTCGTA TTTNAATCCT TTTNACGCCT CTAGGATCTG TAGTGAATGT CTTTGCCTCA	180
TGTTGCTCAA AGAACCAACT CTTTGGCTT TGTGAAGTN ATCTGNTTGT TTTNATGGAT	240
TCTGATTCCN TAAGAATTTT CNTGCTTGCA TTTAGT	276

(2) INFORMATION FOR SEQ ID NO:1099:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1099:

GGNANAGTGC ACGTTGGCGC TACCGGACGG AATGCTGTAT CCCCCAAAAA GCCCGTCGTG	60
GCAGCGCAAG AGCTGGACGG CCTCTAAAGC TTCCNGNACG ACTTCTCCAA NAACCAANGC	120
CGGGGNTTCA	130

(2) INFORMATION FOR SEQ ID NO:1100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1100:

TGTATAAATC CTTATTTTAT TAACAGNATA CTATCATAAA TAGTATTATA ATGCTGNNAT	60
TTCAGGTAAG NAAATAGCTA AACTNCAGTA CACTCTACAG TAGCAACTCA GGACAGCTGG	120
TTACAAGCTG GTTGTNNTAG GACATTGGTT ACACGGATTC TTAGACACTT TAATGGCTGC	180
GATAACTGTN ACTCTCCATG ATCCATGTTT CTTTTATGCG CATATNATTT GACGCACACT	240
CATTGAGAGT CCTCCGAGAG GGGCACCCAT ACACGGCAGA NGTGTTTCATC TCCAACATGA	300
AAGTGACCAG CTCTCATCCT CGTCTCCCCA ACACCATAAC GTCCTCATCC CGCCTCCAAC	360
CCACACCAGG NCGAAGCCCT TCANAGGGTG TTTTCATCCA GGAACCACT CTCGAACCTG	420
AAGGTTTNAC TTTAGCGTTT AGCNAACCCA GGGCGGGTGT GTGTGTTTCC CGTTTTGTTT	480
TTCTG	485

(2) INFORMATION FOR SEQ ID NO:1101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1101:

GGCAGGAGGG NCCCCTGTGC AGAGACTGCT TATNTNCTGG GGAACATAA GACGGAGCCT	60
TGCAAGAAGC CCCC GCGGCT GTNCCGNCAA GGCTATGCCT GTCCCTACTA CCACAACAGC	120
AAGGNCCGGC GCGGAGCCN CGGAAGCACA AATACAGGTC CTTAGGCCCC AGGAGGCCAG	180
CCACGGGAGG GAGGAGTGGC AGGGAAGGGG TCAGGCAGAG GCTGCTCCCA CTGGCTCTCC	240
GGGAGGTGNG GNGGTTGGTT CTGGGGATTA CAGGATCGCA AAGCCCAAGG GCCCAAGGGG	300
AGGGCATTAG TTNAGGATTA GTTGGACAAT TAAGGAGNCC CAGTTTTAAA CTTNCTTNCA	360
ATTAATTTNG GGG	373

(2) INFORMATION FOR SEQ ID NO:1102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1102:

GGGNTACACG CAGGCGCCAA CCAAAGTGGC CAGGTCTTCG GCCTGGGCCC GGNAGATATA	60
TAACCCCAAG TACTGCCCCA ANGGAACAGT GGCCGATGGG GTTCCCTCGG GNNACNGGGA	120
ACTGNCCGGG NCCCGGGGGA AGGTCCCTGA ANTATCCCCC TTNATNACCA GGAGGAGGCC	180
GGCTNACTGA GNGCTCCCAG CAGGTTTTCT CCCCAAATGC GTNTTCCCCA TCTGGGATTT	240
TGGGGNTTTT CATGTGTTTT AAANTTTTTT TTTTTTTTTT T	281

(2) INFORMATION FOR SEQ ID NO:1103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1103:

GGCAGAGGGA CCTCTGGCAA GTNTNTTCCT TTCTTGGGGC CTCACCTGTT TCATNCGCAA	60
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ATGGGGATGT NCCACCTGAA CCCCACCCAC ATCTNCAGGT GGTGAGAGCA GATGGAATGG	120
CACTTTGCAA ATCCCCACCA GCTGGTAAAG GTGAATAGCC TCACTCTTCT GCTTAAAGCC	180
GTCAGTGNGC TGCTNCATCA CACTAGANTA AAATGGAAAC TCCTCACCAT AGGGATCCAG	240
NCTTGCNCC AACTTTTTGA ACAGCATCTT CCCTGGGATT TTTCCANCNC AAAATTGG	298

(2) INFORMATION FOR SEQ ID NO:1104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1104:

TGGNTTAANC GANTTANAGC TGCTAGCCAG GAACATGGAC TGANGTATCC AGCGCTCATT	60
GGGAATTTAG TTAAGTCCCA GGTGGAGCTC AACAGGAAAG TCCTAGCGGG ATCTGGGCCA	120
TCTTNCGGAG CCAAAGANTT TNAAATCTTT TGGGCTTGCC TTTGGCCCAG TAGGGAGGGC	180
NGTCACGGAG GGNTTTTCCT TG	202

(2) INFORMATION FOR SEQ ID NO:1105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1105:

GGCANAGTTT CTCCACAAA ATATAATTNT NAATTAANGT CTCAAATACA ACTATTTAAT	60
CAACCACTGA TTAATCATAT NGTATACATA TATAAGGAT ATGACAGAGT AGAATTTNAA	120
TAAANGTAAA TAACTAATTA TAAAATAGGG GTCTTATTTG AATAAACAAT TTTGAATGCT	180
ATCACTGCTT ACCTGANCAC TNCTGCTCAT TTTGGGCCCT CTGGGATCCA AAAATTCCAA	240
AGNCCTTGGG CNTTGGGGAA CCCNCCCAG GGTGAGAAG TCTTA	285

(2) INFORMATION FOR SEQ ID NO:1106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1106:

GGCACAGGGA AATGTGTGCA GCAAGGTTGT CCTCAAGGGG CTCTTGTTCCA CGTGNCCTC	60
TACCCATGGT CCCACAGCG GGACCAGCTC CACACACAGG GAAAGANTGG NAAAGGAACA	120
CCCAAAGCCA ACCTGGCCCT GGGAACCTCC CCTTCCTGGT TTTGAACGGC TCCTGNAAAT	180
TGGNTCANTN CACACCGAAA GGACTTTTTT GGAAGGNAGC GCACCAANTT TTTTNTTCTG	240
GGAAAGATGG TGTAAGGCA GAGCTTGAGT TCCATTGCTT ATGGGAGGGG AGAGATTAGN	300
CCCTTGACA GAGCCTTCCT TCGGGGGTTN CCAGGGGNAN TNG	343

(2) INFORMATION FOR SEQ ID NO:1107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1107:

GGACAGTAAG ATCTTAATCA TCCANAGCTT CTTTAACCCC AACATCGTGA GAATTCCATG	60
AGGTNTACGA AACAAACATG GAAATNTACC TGAATCCTGG AGTACGTGCC AGGGAAGGAG	120
ACCTTTTTGA ACGCCATCAT AGAAAGTTTG AAAGTTCCCG GAGCCCGATG CTGCCCTCAT	180
GAATCATGGG ACTTATGCAA AGCCCTCGTC CACATGCACG ACAAGAGCAT TGTCACCGG	240
GACCTCAAGC GCGGAAAACN TTTTGTAAG TTTTGATTTT TTGATGATAT GGGAGAGGGT	300
NTTTTTAGAA TATGGGGTTA AATTTGNTN	329

(2) INFORMATION FOR SEQ ID NO:1108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1108:

ACTGGGTTGA TACAAAGGAT TGGTCTCAA GCTCTGAAAT TTTTCTNCT GCTTCTCTA	60
GTCTGTNGTA TTTNAAAATT CCTATAGTAA ATTTTNNAAT TCCAGAAGT	109

(2) INFORMATION FOR SEQ ID NO:1109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1109:

GAATAATTTT	CNCATCGNAG	ACCCACACCG	GGCAGCCAAA	TTAANC	GGGC	AAACGCAGCA	60
NATTTNNGGC	GGTNAGATCG	GTATCGGTGC	TGAACAGTGA	ATGTGGCATA	ACAAACTCCA		120
GATAAGTNCT	TTTTNATGAT	TACGCCACAT	CATAAAAAGA	NTAAAAAATA	TCGATTTATG		180
TCGAGTCTAT	GCAAAATTGN	TATGGATTAC	CGGTTTGCGA	GAGAGCGCTA	ATGGCCGCCG		240
TTAACTTACG	TCATATTGAA	ATTTTTCATG	NGGTTAATGN	CCGCCGGAAG	CNTTGACTGN		300
GGNGG							305

(2) INFORMATION FOR SEQ ID NO:1110:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 132 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1110:

NCCTCTTGGC	ATGCCTGTCC	TAACTTNTNG	TAACATCAGG	CCTGCCCCGA	ATCACCTGTN	60
CGAGCCACNC	CAGTGCACAG	CAGGAACTGG	TAAAGTGCCT	GGNCTGCTTC	TNCCTTTNCT	120
CCCTTTCCAT	CT					132

(2) INFORMATION FOR SEQ ID NO:1111:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 348 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1111:

CACGGNATTA	ANAAACGGTG	ACGCGGGTAG	CACCACTTCA	AAGGCCTCGC	NACGGTTAAT	60
TGCNACCACT	ACACGTTGCT	GATTCANCAC	GCGGACAAAT	ACCACCACGT	TATCTTCCGC	120
ATACAGCACC	TNANAGCCGC	CATGACGTAG	CGCCTGATTT	TTTTNACGCA	GCGCAATCAT	180
TCGCTGGTAC	AGCNNGGAATA	ACGCCGTATC	CTGCTTTTCC	ACCTGCNAGG	GGAACGGTTT	240
ACGGCAAAAC	GGATCGTTTT	TGCCATCCAG	TCCTACTTCA	TCACCGTAAT	AAATGGGACG	300
GTACACCAGG	GCCAGGTGGA	ACAGGNAGGT	NCACCGNNCA	NGGCAGGC		348

(2) INFORMATION FOR SEQ ID NO:1112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1112:

ATTTNNGATT GTNCAANACA GAGAATCTCA TCCCGNACAA GATGTAGGAG GAAGAATTAT	60
CCAGGTCAAT GGA CTGGTG AATTCGATC CACCTGAACT NTGCCACAGT GAGTCCCGAG	120
TTCCTTAGGC TTNNTGGTNT AGNGG	145

(2) INFORMATION FOR SEQ ID NO:1113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1113:

GGCCATTNAA ATTNCCCATC CTGCATGAAA TTCCCCTTGG TGTAATNAC CTGCACAATA	60
TGACTCCTCC TTTACTTCAT CATGACTTGA AGACTCAGAA TATCTTATTG GACGATGAAA	120
TTTNATGTTA AGATTGCAGA TTTTGGTTTA TCAAAGTGGC GCATGAATGT CCCTCTCACA	180
GTCACGAGTA GTCAAATCTG NCACCAGAAG GAGGGACAAT TATCTATATG CCACCTGAAA	240
ACTTATGNAA CCTGGGACAA AANTCAAGGG GCCCAGTATC AGGCACGGTT ATATATGAGG	300
CTNTGNCAGT TTTTTCACAT CGGNAAGT	328

(2) INFORMATION FOR SEQ ID NO:1114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1114:

AGGTGACACA GGAGTGGCCT TNCCCTTCGA ATCTTTCCTG GGCAACTACT CCTGTGCTGC	60
CCAGGGCACC CAGGGTGGNC AGCAAGAAGT AAGCAGGGGA AAGGGCCAGG GAATGGGGTG	120
AAGTAAGGGC AGGGCCAGGN CAGGGAAGGG AAGGTGGAGA GGGTGGGCTT TTGGGGTCTN	180

TTTCCCTTTC CTTCTCTTAA GCCCCTGNTN CAGCCCTGGG GATGGGGTCA AGACTGGGGA	240
ATCAAAGCAA GGCCCTGTGG GGCAGTTNTG GGGAGGGGGC TGAGTNTTCG ANAAGAACAG	300
TTCCAGTTAG GGGTNAACGG CCTTCCTTGA GCAATNGTTC TT	342

(2) INFORMATION FOR SEQ ID NO:1115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1115:

GGCANAGGTT TACTTATCAG TCAGACCCAT TCCGGTGGGC CTCGAAAGGT ATGTNCATGT	60
TTGGAGTTTG CTTGGTTTTN TTCTCACCTG CTTTTNACCC TTTAAGAATT TNATATGGTA	120
TACATTGTAG TAGAAATATT AGATAATGNC AGGCAAGCAA GCATCAGAAT GACCTAAAAT	180
TCCAGTACTT TGAGTACAAG GCTTTAAACA TTTTAGTATA TACATCTTTC TGGTATATGT	240
ATGTGTGTAT ATATATATAT ATATGTGCCN CACACACACA TATATCTTNT TATAAAANTT	300
TATAATCTNT ANTTT	315

(2) INFORMATION FOR SEQ ID NO:1116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1116:

AGGCACAACG TTTTNANCAG CTTTATCGCC GCTATCAGCA ATGGNCGATG AGCGCCGNAA	60
CAACACTATC TTCCAAC TTC CGCCCCGGCA CAGGCTGCCC AGGCCGTTGC GAACTTTATA	120
AGGACACGAT AATGAACGAT TTTNAATAAT TATGAAAGTG TGGTTTGTA ATTGGNAGCC	180
AGCATCTNTT TGGCCCCGAA ACCCTGNNTN AGGTTACCCC AACATGCCGA GCACGTGGTT	240
AATGCGCTGA ATTA	254

(2) INFORMATION FOR SEQ ID NO:1117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1117:

CNAGGGGCCC TNAGGNTCCC TCCTGGCCCC CACGGAACCC GTGCTNCTNT TAACTCCTAG	60
GAGATGGTTT AGAAACGTTT CCCCACCTTT GACGGCATTG NAGGCACCAG GNGCAGCTCA	120
AAGTAATGTT CATCGGAGGC CCCCAACACC AGGAAGGACT TTCTACTTCG AAGAGGGGTT	180
GAAGGAGGTT GGGTTTNATT TGGTCTNCCT TGGNTTTAGG NCCTTNGGG	229

(2) INFORMATION FOR SEQ ID NO:1118:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 177 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1118:

GGCAGGAGGG AGACCCGGGG GAGAACCAGG CGTCCAGGAC GCGCGTTGNA CCACCCTCAA	60
CACGGATATC AGCATCCTGT CCTTGCAGGT GAAGACCTGC TNCCGGGGTN CCCGGGCCCCG	120
GNGNCGGACA CTCCCGGGGT TTTCTNGTCC TGTGCACTAG GTAGATCCGT AGCCCAT	177

(2) INFORMATION FOR SEQ ID NO:1119:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 425 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1119:

TGGGCCCATN TCCTCCTCCN TCTCCTCCCT GCNATCTTTC CTCTCCTCAA ATNTCCCTGC	60
AGTNTGAACC CCGGCCTTGA AGGCTGGGAA GCAGGGAGGC CAAGAGAAGG AAGCTGTGAC	120
TCCGCCTAGC TCCTGGTTGT TAAGCACCCA TGTTGGCCA GGTGNNAC AACTCTGGC	180
GCTCTAAAGG CTGATAAAGC CCCACAGCCT GCACGTTTGG NGCCTGGGCC TCCAGCCCTG	240
ATAAAGCTGG ACCTGTNAGC ACCATGGCCA CACCTGCTGT AGGNATGAAG CGGCCACCCG	300
TNTCCCTGG GCCATTCCA NTNAAGGGTT CCTGTTTCCC TGTGACAG NCAAGCCCTG	360
GGCCACCATG NCTTAGGCCA ACCCTTCCTG GNTGAAGGAA CAAATGGNNG TTGGCCATGG	420
GCAAG	425

(2) INFORMATION FOR SEQ ID NO:1120:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 123 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1120:

GGCACGANAA GAACCCCCNG NAAAGTCTCA GGATGGNAGT TCAGATTTGG TAAGGCATCC	60
CCTAGTTNCA GCTTCCTGGC GGCCTGCTCC ACACAATNGC CTNTGGGCCC ATGGCCTTNA	120
TCC	123

(2) INFORMATION FOR SEQ ID NO:1121:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 328 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1121:

TTTAANCAGC TCAGGGGGTT TNATTTCCAA GTAGAAGGCC GGAATGGTG GCATTCCTCC	60
CANAAGTGCA CANTGAACTA TAAACTTNTT TGTGGTAGAT AGGANTGAAC AATTATCCGG	120
TTATCTNGTT TCCCTTGCCC AGAAATGGTT CTNTCCAGT GGAAATTGTG CCCCCTCTG	180
CCAGGACTGG ACACTTGGTC ACAAANTGG TAGCAGAGGA TGCTGACAGT GGTCTAATG	240
CCTGGTTTTT CCTACCACAT NTCCCGGGCG TTTGAACTCT GGTNTCTTTT AGAATTTTCA	300
GCCAATATTA GGTNAGCTTC CNTAANTG	328

(2) INFORMATION FOR SEQ ID NO:1122:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 386 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1122:

CACCATTGAT GGATACTTNG GTTGATTCCA TGTCTTTCCT ACTCTGAATA GTGCTGTGGC	60
AAAACCTTTC ATGGCCTCCG GAATCTCCTT CCTTGGTCCT GCCACAGTNC CAGCAGTTTC	120
CATATTGTTT ATTATTTGGA ATTACAGCAC CAAAGTNCCT GTTAAATGT AACTNCTACT	180
TTGGAAGAG ACCTGATTCC TCATGACAGG CATTAAATAC CTTAGTTTAG GCTAGTTTAT	240

CTGCTTGGCC CTCNAGCACG GGGAGCCCTT GGGAATAGAA GGAAAGCAGA TAATGTTTCC	300
CTGGGGTCAG TATTGGGTTG TTACCTGGGG AAGGAANTGG GAAANCTTGG GGGGTTTCGA	360
GGGGGGNCCC NGGTACCCTT TNGCCT	386

(2) INFORMATION FOR SEQ ID NO:1123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1123:

CCCAGACGGC GGCAGTCCGG CTTNCCCTTG GAAGTCNAGG CTCGGTTGTC TTTTGAAGC	60
CATGGAGAGT AACTTTAATC TGNGCTACTA CGTGGGGCAC AAGGGCAAGT CCGGCCAGAG	120
TTCCTGGAGT TTAAGTTTCG ACCGGAGGGA AGTTAAGATA TGCCAACAAC AGCAATTACA	180
AGAATGNTGT NATGATCAGA AANGAGGCTT ATGTACATAA ANGCGTGATG GAGGAACTGA	240
AGAGATTAAT TGACGACATN AAATT	265

(2) INFORMATION FOR SEQ ID NO:1124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1124:

GGCAAGAACA AGCGCCTTAC GAANGGGGAC AAAAAGGGAG CCATGAAGNA AGTGGNAAAT	60
CCATTTTCTA AGAANGATTG GTATGCTGTN AAAGCACCTG CCTATGTTCA ATATAAGTGA	120
ATATTGGAAA AGAACGCTCC TCACCANGGN CCCACAGGCN NCCAAAATTT GCCATCTGAA	180
TGGTTNTTCA CGGGTCGTGT C	201

(2) INFORMATION FOR SEQ ID NO:1125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1125:

GGAAGAAAAC CAGAAGGGCA CACTTNAANC TAATTTGGGG TATCACTAAC CTGAAGANAA	60
AGAGAAAGGG GGAGAAAACC TAGCAAACCA CCATGTCCTA TGGGAAAGTT TGCANNATGC	120
ATCGAANATT NTNTGGTGGG GCTCCNCCTC CTNTGCCATC GGGGNTTAAT ATTTNCCTTT	180
ACTTTNCCCA ATGGGGAAAC AAAGTTTGCT TCNAAAAACC ANCTCAGCGG TTTGGTGTGG	240
TTTTTTNCTG GAATCGTGGG AGGTGGCCTG	270

(2) INFORMATION FOR SEQ ID NO:1126:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 202 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1126:

GNCGCAATTT ACCTTTGCCA AATAATTACC TTTTATCTAC AATTTTNCCT GTTTTTTGGT	60
TCTTTTCAGAT CTCACTTGTA TAATGNCTTC TTTGNTAATT TTGTTATATT TTCCTTTCTA	120
TTGTCATAAG TTGGGATGAC TTAANTTANC TNCAGTCTTT GATTGTTATA GGTACTATGG	180
TATNGCAGAC CATAAANATC CT	202

(2) INFORMATION FOR SEQ ID NO:1127:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 173 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1127:

GAAANTTTTA GATANTACAT AATTATTGCT GTCCANAAAA TCTTAAAATA TATGNATTCC	60
ATGAGACAAG AGATGAAGTA TGAGGTNAAG AATACTATGT CTAAGCTGNA AAGGTACCTC	120
ATTAAGTTAT AGACAGNANT AAAATGAGGA GGGAGTATGA AACATATGGA NGT	173

(2) INFORMATION FOR SEQ ID NO:1128:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 174 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1128:



GGCAGAGCAG CAGTTCCTGA AGAAGGCGNT GCAGGGGCTG CCANGGGACT TNCTGGGNGC	60
TGCGCTCGTN GCGGTGTGGG AGCAGCTCAT GTTACATCAA GGAGGGACCT CATCCTNNCC	120
GCACTACCAC ACCTTCTGAC GANCTTCATG CATCGCCAGG GNGAGGNTGT CAAG	174

(2) INFORMATION FOR SEQ ID NO:1129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1129:

GGCANAGCTT TCCTCAGAGA CCACATCACT ATTCCATATT TAAGCAGGCC AGCATCGTGG	60
AAAGCNCTTT TCGGGCATCT GGGGCTCCAG AACCGCAGTA TCAACCTTCT TTCTNATGAC	120
TATGGAGATA TTGTTGCTCA GGAGCTTCTC TACAGGTCAG TGGAGCTTCA AACTTCAGCT	180
TATGAATGCT AGGAGAGTAC ATTGTTTCTG GACTGTTTGT ATCCTTTTNN CTCTCGTTTT	240
TCAGCGGTGC ACTGGTTTAA GGTGTTGCTCC AGCTTACATG TGTGNTNTCC TCGTCTNCCT	300
TTT	303

(2) INFORMATION FOR SEQ ID NO:1130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1130:

NGNGCACGCT GCCCCGNTNC CCCACTTTNA ATGCAGGCTG GCATACCACT GTGAACTCAG	60
GATCTAAATT TAAAACTTCA ATTCATTTAA ATTTCAAAC AAAAGCANTG TAAATATTTT	120
NCCCTATCCC ATTACCCTGN TTTGANTCAT TACACATTGT ATACATATAT CCANT	175

(2) INFORMATION FOR SEQ ID NO:1131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1131:

CAGCTCAATG TGTAAGCATT TTGGTGCCTG TCCACTAAGT TTCAGGGAGC CTCATTCTTC	60
CTTCACTCAG GGCAGCATTT GCTCTGAGAG AGGCGGCAGA TTCACAAGAG TAAGTAGACA	120
GTCTATTGAG GTTTAGGTTT AAAGTCTTCC TCCAGATACT CCAGATTGAA TGTACTAATT	180
AAAATAGCAA CTACAGTGGT GGAGCATTNA GAATGCTAAT GAATGTTTTA ACCCTTTGGA	240
AACCTGATGC ATTCCCATAG GTTCATATGG TCCATTCTCC AAAAACTGG GCATTGGTTA	300
GAATGGAGTA GACAGTAGAT GCTTAGCTTG AGGTGGGAGT GAAGCTGGGT TCCTCACCNT	360
TTTTNNNN	368

(2) INFORMATION FOR SEQ ID NO:1132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1132:

GTCCTCTCCA AACTGAACCC AGAGAATCTG GAACTCGAAC AAACCTGGGA GNCAAACATC	60
CGTAAGCAGT CAGTCGCCAA TGCCTTCATC ATCTGTGGCA CCTTGNACAC CGTCAGCAGC	120
TACACCTCAG CAGATGCTAC CGTCAACTTT GCTTATGAAC ACAGGCACAG GTATCAGCAA	180
GACCCTGACC ATCCCATTC AAGAACGCTA TAAGTACAGC AGCATGATTG ACTACAACCC	240
CCTGGAGAAG AAGCTCTTTG CCTGGGGACA ACTTGAACAT GGTCACTTAT GACATCAAGT	300
TTTCCAAGAT GTGAAAAGNC TCCAAGTGTA CAGGCATGGG CAGAAGGGGG TTGNTCAGGG	360
TNTTGGGGGG AGCAGGTNNA GGG	383

(2) INFORMATION FOR SEQ ID NO:1133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1133:

CAAAATGGGA TTTNTTCAAG GNCTGGGTTT AGAAAANTCA GCACAAGGCA TCACTGAGCA	60
TATCATACCT ACTCCTAAAG CAGACTCTAC AGGACTTGGT TATTCTNTTT AGAAGCGGTC	120
ACTATCAAGC CTCCAGAACC CATCCCTTTG ACCTGGAGGA ACTTTAAAAA CCTGTTCTAG	180
GTAGGTGGAG TGGCTGCTCC CAAAAAATAA AGCTNGGGNG GCNCTGCATA ATTTTGAGTT	240

CTTGGAACAG TTTAAATTT NGGGN

265

(2) INFORMATION FOR SEQ ID NO:1134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1134:

GGCAGAGCTC GCGTNGNCTG TGGCCGCAGC TTGAGTATGC TCAGGCTTCA GAAGAGGCTT	60
GCCNTGAGTG TCCTCTGCTG TGGCAAGAAG AATATCTGGT TAGACCCCAA TGATGACCAA	120
TGAAATCACC AATGCCAACT CCCGTCAGCA GATCCGGNAA GCTGATCAAA GATGGGCTGA	180
TCATCCGCAA GCCTGTGAAT GGTCCATTCC CCCGCTTGAT GCCGGAAAAA CACCTTGGCC	240
TGCCCGAAAG GGCNAANTNA TGGGGCATAG GTAAAGCGGA AGGGTACAGC CAATGCCCCA	300
TTGCCCAGAG AAAGGTTTAC GTGGGNTGAG GAGGAATGAG GATTTTNGCA CCGGNTGCTT	360
TCAGAAGTTA CCNTGNATTT TAAGAAG	387

(2) INFORMATION FOR SEQ ID NO:1135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1135:

GGCAGAGCGG CANGAGTGNG CGCTCCTGCT GGGGGTCACG GGAGTCGGGA AGANTGNCTG	60
GTGAACGGCT GCAGGAGGTG AGCTCACGGG ATGGGAAAGG CGACCTTNTG ACCNGCCTAG	120
TNCACGTCCC ACGTTTGTA TGGACGCCTC TGNACCCAC CCAGCTCTCT NCATCCTGTG	180
TGCA	184

(2) INFORMATION FOR SEQ ID NO:1136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1136:

AATNTTTGGC AAAGCAGTGG AACATATGTT TGAGACAGAG GATGGTTCTA AAGATGAGTG	60
GAGTGGAATG GTCTTAGCAC GTGCACCTNT CATGAACACA TGGTTTTACA TTACCTATGA	120
AGAAAGMNCC TGTCTTGTGN CATGTGCCAA CTCTTAGATG ATTACAAAGA AGGCGACCTT	180
CGCATTATGC CTGATTCCAA TGGAGTCACC TCCAGCAGAA AGGGAACCAG GGAGAAGTTG	240
TGGACAGCCT GGTAGGCAAA CAAGTGGGAA TATGGCGAAA GAAAGATGGG NTCGNAAAAG	300
GGACTNGGCA TNGTTCATTT CATCCAAGGT AGGAAGGNCC AAG	343

(2) INFORMATION FOR SEQ ID NO:1137:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 502 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1137:

GGCAGGAGCA ACAGCCTCGG NNNTACTCTG TCTGTGGCGT ANATNTCTTN ATTCCTTTAC	60
TCTCCTAATA AACTTNCTTT CCCTGTACTC CAAAGACTCG CCCTGAATTC TTTCTAGCAT	120
GAANTCCAAG AACCTCTTT TGGGGTCTGG ATTGGAAGTT NTTTCCTGTA GCATCTTTCT	180
GGTGNCCACT GAAGGGACTG NAGTGCAGAA AACCCCCACC CAAAGGCTTA NCTTTTGGTA	240
AGTGGTGGGG GCCAGTAACA TTTTCTAGT GNACCCTGAG GGGACGGTTA CTGAAGAAAC	300
CCCCCGGACC CAAAGGGAAA TAGGAGTTGC AGCACTGGTT AGGGCCAANT TTGGGTAAGT	360
GGTGGGGGTT ACCAGGTAA AGGATGGATT GGGTTTAGAG GCCCAANTAG GGGAGTCAGA	420
GTCTTTCCTA AGACAGATGG GTCAAGGCCG TTTGTGTTAA GGCAGGACAC TGACCTACTT	480
TGGTTAAAGN CCACTTAGGN GG	502

(2) INFORMATION FOR SEQ ID NO:1138:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 489 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1138:

GATCAAGTAA TGAAACTACA GAATCTNTTT GTAGATGATT CAGGTCGATA TTTGGCTATT	60
CAATTCCATC TGAATNTGC ATATGTGTTT TNATATTATN ATGAGTACAG AAAAGCAAAA	120
NATCAGTTGG ATATTGCTAA GGACATCAGC CAATTACAAA TTGATTGAC AGGTGCTTGT	180

GGAAAAAGAA CACGGTTCCA GGAAAAATTAT GTGGCACAAC TGATTCTAGA TGTAAGAAGG	240
GAAGGGGATG TCCTTTCAAA TTGTGAATTC ACTCCAGCAC CCACTCCTCA GGAACATTTA	300
ACCAAGAATC TTGAGCTTCA ATGATGACAC CATTCTGAAT GACATAAAGT TTAGCAGATT	360
GTGAACAGTT CCAGATGCCG GATNTGTGTG CTGAAGAGAT CGCTATTATT CTTGGATCTG	420
CACTAATTTT TCAAAGGATA ACCCAGTGCA CACATTAAC TGNAGTGGGG TTTCTGGGCA	480
TTTACATCA	489

(2) INFORMATION FOR SEQ ID NO:1139:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 503 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1139:

GGCAGGAGCT CGTNCGTATA ATAATTTAAT TTGGGTTTGT TGGTATAGAA ACTGTATNTN	60
CACAATAATG ATAAAGCCAC TCAGGCTCAT CTAGTCATTT CCTGGATTTA TGTGTGTAGG	120
AGTACATAAA AATANGGGCA CTGATTCGTT TTGTACTTGT CTAAAATTGT TATTNTTCAG	180
TTGTTCAAAG GTACACAAAA TGCTTTTTTNC TTTATAAGGT AANAAATACT TGGNGGTTAT	240
AAGANNTAAC TCTTAAGTAG CTTACTTTGA GTGGCTTTGA TATGTATTTN CTCATAATGG	300
AATTCATGAG CTTNCCTTCT TTCGCTTGGC CAAGATTTTT TTTTCCCTT GAATTCCTT	360
CTCCGGTGTT ATCTAGGATG TTTGCATTAC AAGCAGGCCG CTTTACCCCC TTTGTCCGTT	420
GTCACAGGTG AAAAGCCATA CAAGGGTACC CGGGGAGGCT GCGACTGGNG GTCCGGCGGT	480
CCGGATGAGC TGACCCGCCA TAC	503

(2) INFORMATION FOR SEQ ID NO:1140:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 86 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1140:

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	60
AAAAAAAAAA AANNAAANNA GGGNNG	86

(2) INFORMATION FOR SEQ ID NO:1141:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 399 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1141:

GGCAGAGGCA CAAAAACACA CACCAGAATG TTCATAGCAG CCTTATTTAT AATAGCCAAA	60
ATCTGGAAAC AACACAAATA CCCATCAACT GGTGAGCAGA TAAACAAAAG AAACAACATA	120
AATACCCATC AGCTNNTGAG TAGATAAAGA AAACAGGGTG TTATCCATAC CATGGGAATA	180
TTGTTCAGCA ATAAAAGGGG AAGAAATACT GNTGNTTGCT ACATCACGGA ATGANCTTCG	240
GAAAACATAT GGCTGGAAGC CAAAATGGAA AAACAACATA TTGTATGATT TTCCATTATA	300
TGGAATGGCC TTTATATGGA ANGGGAAGGG CAACTTTTG GAAACATAAG CCNTGGGTTG	360
NCCCAGGGTT NGGGGTTTGA ACNNGGTTTG ACTGCAAAT	399

(2) INFORMATION FOR SEQ ID NO:1142:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 420 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1142:

GGCAGAGNCT CACTGGCCGA CAGTTGCCTG CTGGGGAATT TGCTGGCGGA CTTCGTTTCGC	60
GGNCAATCCT GNACGGACAA TATTCTGCTG AAATCGTTAG CGGGATCCGT NTGCTTCGCC	120
GCGTTGATAC CCTGACCGAC TCCCTGNCCC GAAGTGC GGA TCGCGCGCAN TAATTTCCGT	180
GGTGATTTCC GCCGCGTNTC GATGATCACG CTCGACGTGG TTGTGGGATC ACTTCCTGTC	240
GCGCCATTGG GGCANAATTC ATCCACAGCA ACCGCNGNAA GATTTTTTTTG CCGCCTGTTA	300
GCAGGTAATT AACGCCGTNT TTGCCCGATT TTGTCGGAGG CGTTTTCCAG AATCTGAAAT	360
GNCCTGGTTT NTGGNCNGAG CGTTGGATGG GAACGTTACT NCGGAATTCC TTTTATCGC	420
	420

(2) INFORMATION FOR SEQ ID NO:1143:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 343 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1143:

AACNANTNAC GCAGGNACCA CNAAAATCAT GTTCCACGTG TCCAGAATGC TGCCTTACAC	60
CCCTAATAAC CAGCAGCAGC TCCTCCGGAA GCGCCACATT GGCAACGAAC ATTNTGAACC	120
ATCGTNTTNC AGGAAGCCTG GNCAGCAAGC CCTTNTGCCC CACCACCATC CGCTCGCACT	180
TCCAGCACGT NTTCTAGTG GTGCGGGCAC ACACACCCTG CACGCCACAN ACCACCTTAC	240
AGGGTGGCCG TGAAGCCGCA CCCAGGGACA CCCCTGNTTT CGGGGCCAGT TCTGCCTGCT	300
TGGGGANGGC CCCTTTCGNA GCCAACGGNG ATTTTCGGGN CTT	343

(2) INFORMATION FOR SEQ ID NO:1144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1144:

AAGCCACANA ATTATCATTT TTTNTTTTTT TGTTAGGGTG GGTCTTCTTT TTTNNTTTC	60
CTCTCTCTTT TTTTAACAAA TGCCTTCTTA TAGAAAACT TTCTAAGAGG CAACAATTTA	120
GNAATGGGAT ATTTTGAACG AATCGGCATG AGTGTAACAG NTGNATAACC TGATCTGTTT	180
GTTTTNAAAG NATTATTAAC CAAGTGGAAG AATTCCAGNA ATGANTAGTA ATTTACACTA	240
AACATGCTAT ATAAAANGNT TNAAAGTCNT GATGCTGTGG AAGCAATCTN GTGCTATATT	300
TCTACCTCCT CATTGTCTTA ATTATTGGGT AGTGGGG	337

(2) INFORMATION FOR SEQ ID NO:1145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1145:

GGCAGAGGGA AAATCATTTT CTTTATCTTC TCCACTAAAT CTAACAGCTT CATTAGTTCC	60
TTCTTTAAGA CAGAAGTAAC ACATTGTAAA GAAAATGTAC AATAGATTGC NCTCCAAAAT	120
AGCATCTATG TTGTAAAGTN TTGCAGATGG CCTTGGAAC ATCTGGTGNA ACAGGAATTT	180
GTGTAGCCTA TGTNCATTGT GCATGTGCAG TGAAGGTCAA CTGACAGAAG GAGAGCCAGA	240

AAATAAAAAA TAANNAANCT GNGAGGAAAG ATTGAGTTAT TTGATGGACT GATTGNCTCG 300  
ACACCTCTGC TTCAGAGAAA TGCCATTTTG CCAAACGGAT GGNTCCNCTG GTTATCANTG 360  
NAAGGTTAGG GCATTTGTTT TGTGGGNCCN GNTACAGAGG TTGAATGTTT TTGGGTAGCC 420  
CTGGTTTCAN NTGGGTTAGA ACCTCCGGTT TGCTTTTAAG CTGGGGTG 468

(2) INFORMATION FOR SEQ ID NO:1146:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 87 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1146:

GGCANAGGGA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAANN AAAAAAAAAA 60  
AAAAAAAAAA AAAAAAAAAA AAAAANN 87

(2) INFORMATION FOR SEQ ID NO:1147:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 381 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1147:

TTTCCTGTTT CTGAAGCNCA TTTTTTGTTA TATTTTATAA TATATCAAAA TATAGATGGT 60  
ATAAAATAAG TCCCTTCTCA TGTCTCTCCT TTAAATTCG ATTAGCTATT TATAGATCTT 120  
TATTTTCCCA TATATATGTN ATAGTAAGTT TGAGAATTAT TCAAAAAGTC CTTCTAGGAA 180  
TTTNGAATTT GAATTGATTG AATTTGTAGT TACATTTTGG AAGAATTAAC AGTTTCATAA 240  
TGCTAAGTCA TCCCAGTCAT GGAAGAGGAA GATCTTTTAA ATNATTTAAT TGAGCTTTCC 300  
CCCAACCTCA TGTTAATAGT TTTGGGGCAT NCTTTGTTAG ATAAATAGGC AAATACTTNG 360  
TTTTTGTTGG GGGNGTTCNA C 381

(2) INFORMATION FOR SEQ ID NO:1148:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 111 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148:

GGCAGNGTNA CGAAATACAG NTCCTCCCCA GATGACGCCA TTTTCCAAAG CTTNGCCCCG	60
GATATACTCT TCTTTCAACC CGGCCATGGT CTGACCCCAN TNGNCCACCA T	111

(2) INFORMATION FOR SEQ ID NO:1149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1149:

GGCAGAGAAT GCCCTTCAAG ACATGGACAA ATTTAGCTTG AAAGACAGTG GCCGTGGTGA	60
CAGTAAGGCA GGAGACAGTG ATTATAATTT GGGGCGAGAT TCTCCAATAG ATAGGCTGCT	120
NNGTGAAGGA TTCAGCGACC TGTTTCTCAC AGATGGAAGA ATTCCAGCAG TGCAGCTATG	180
AGAACTCTGG CACGGAGGAG TGCANGGTCC TGGGACACTC TGACCAGTGC TGGATGCCAC	240
CACTGCCCTC ACCGTCTTCT GATTATAGGA GTAACATGTT CATTCCAGGG GAAGAATTCC	300
CAACGNAACC CCAGCAGCAG CATCCACATN CAGAGTCTTG AGGATGACGN TCAGCTGCCA	360
GATTCCGGTG AAAAGAAGAA GAGTTTTTTC CACNTTGGN AAAGGATTCC CCAAAGNTT	420
GNGGACATTG GGGTTACCNG CACATCATTT T	451

(2) INFORMATION FOR SEQ ID NO:1150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1150:

GGCANAGGNN AATGTGATAT TGGAAGAAAA ATAGTCACAT ATATCAATGG AATATACTAG	60
AGAATCCACA GATAAAACCA TAGAAATATG CTCAACTGAT TTTGACATAG ATGAAAAGTA	120
TTTGTTATTT TACATTTGAT TGATCTTGCC TCACAAGATG GATTTTAATT TNCTTGTTGG	180
CACATACNT TATCTTTAGT CTATCTTTCA CAATGCCTGT TAATGGGATC TTAGGCATAT	240
AANTATACAT TGAACCTAAA ATACTGTTGG NNTTGATTAT AAAAGTTTTT CAGGGGGGAT	300
AAGTTATNAT TATNGGTTGA GAAGGAGGAT G	331

(2) INFORMATION FOR SEQ ID NO:1151:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 61 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1151:

GGCANAGCCC CCCCTTTTTT TTTTTTTTTT TTTTTTTTTT NNGGGGGGT TTTTTTTTTT	60
N	61

(2) INFORMATION FOR SEQ ID NO:1152:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 367 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1152:

GGCAGAGTTT NAGAACCACA ATGTTAACAA TATAGCCAAT ANGACAGTC TGCACAGCTG	60
GGTTGGACTG ATAGCTGTCA TATGCTATTT GTNACAGCTT CTTNAGGTT TTNNAGTCTT	120
TCTGCTTCCA TGGGCTCCGC TTTCTCTCCG AGCATTTCTC ATGCCCATAC ATGTTTATNC	180
TGGGAATTGT CATCTTTGGG AACAGTGATT GCAAACAGCA CTTATGGGGT TGACAGAGAA	240
CTGATTTTTT TCCCTGAGAG ATCCTGCATA CAGTACATTC CCGCCANAAG GTGTTTTTCG	300
TAAATAAGGT TTGGCCTTCT GATCNNGGTG TTCCGGGGGC CCTCATTTTT TGGGGTTAGT	360
NCACCNG	367

(2) INFORMATION FOR SEQ ID NO:1153:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 254 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1153:

ATTCATACC TACTAGGCTG ACTCACAGAC ACAGTACAAG TGGTGAAGAT GTAANGAAAT	60
TGGAACCATC ACACATTGCT CCTAGGATTG TAAAATGGTG GAGTCACTTT GGAAGAAATC	120
TCCAACGGC TTCCACAGN GTCTGANCTA AATTACNTT CCCACCAGCA GTGTATAAGT	180
NTCCCTTTC TNTGCAACCT CACCAGTATC TGTAATTTT GACTTTGCAG TNATAGCCNT	240

TCTGACCATT GTGA

254

(2) INFORMATION FOR SEQ ID NO:1154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1154:

GGNAGAGGGG CAAAGACTTG GGAAC TTAA AAGCTGAAGA TTCTTAAGAA GCTACAATGT	60
ATATAATTTN TNGTTTTATT TNATTGACTG GTTCTCATAG CATA CATATG TATGAAAAAC	120
TGAGTACTTA TCTCTTTNTA ATATTTCTAT ACCTCCATTA CCCGTGCCCCG ATTTGAAGAA	180
CTGAANTGCN GNCCTGTTCC GTGGNACCCT GG	212

(2) INFORMATION FOR SEQ ID NO:1155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1155:

GGCANAGGNA GATTCCATGC ATTGGGTCCA ATTTACTACA GAGNTTCAA TGGAGCGATT	60
TTAGTTTATG ACATAACAGA TGAAGATTCT TTTCAGAAGG TAAAAAACGG GTCAAAGAAT	120
TACGGAAAAT GTTGGGNAAA TGAAAATCTG TTTATGTATA GTTGGTAATA AAATAGACTT	180
GGNAAAAGGA GAGACATGTT TCCATTCAAG AAGCAGAGTC GTATGCAGAA TCTGTGGGGG	240
GCAAAACATT ATNCATACTT CATCCTGTGA ANGTNCAACA ATNAAAAACC AATTTATGGG	300
GCTGCTTTTN GTGCACACTA GCCTAG	326

(2) INFORMATION FOR SEQ ID NO:1156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1156:

GGCANAGNTG CANATACTAG TGGAACTGG GAAGAACTGG TGAGGGACTT GCANTTNGCC	60
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CGTAAGAAGG CTCGAGAGTC CTATGTGGAG ACAGAACTGA TATTCGCACT GGCTAAAACA	120
AACCGCCTTG CAGAGTTAGG AAGAATTATC AATGGACCAA ATAATGCTCA TATCCAACAA	180
GTNNGTGACC GTTGTATGA TGAAAAAATG TATGATGCTG CTNANTTGTT GTACAATAAT	240
GTTTCCAATT TTGGACGTTT GGCATCTACC CTGGTTACAC CTGGGTGNAA TATTCAGGTC	300
AGCTGTTGGA TGGNGGCTAG GGAAAGCTTA ACAGTNANTC GNACCTGGGA AAGAGGTCTG	360
	360

(2) INFORMATION FOR SEQ ID NO:1157:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 405 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1157:

ATAAGAAGGG TGCGGAGANG AAAAAGGGCC GTNCTGCCAT CAACGAANGG TNAACCCGAG	60
AATACACCAT CAACATTCAC AAGCGCCATC CATGGAGTGG GCCTTCAAGA AGCGTGCACC	120
TCGGGNCACT NCAAGAGAT TCGGNAAATT TNCCCATGNA AGGAGATGGG GNACTCCAGA	180
TGTGCCGCAT TGACACCAGG NTTCAACAAA GCTGTCTGGG CCAAAGGAAT ANGGTATGTG	240
CCCATAACCGA ATCCGTGTGN GGCTGTNCCA GAAAACGTAA TGNAGGATGG AAGATTCACC	300
AATTAAGCTA TATACTTTGG GTTANCCATG TAACTNTTTA ACCATTTTNA AAATTTTACA	360
GGACANTCAA TGTTGGGTGA NGAATTAATT CGTTGATTGT CAGTT	405

(2) INFORMATION FOR SEQ ID NO:1158:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 209 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1158:

TGNATAGCCA GAAAACTGNG ANAACAAGGG ANCAGTGTGT AAGGNACTTG TGCACATCAC	60
TGACTGGTAC CCCACTCTCA TTTCAGTGGC TGAAAGACAG ATTGGTGNGG ACATTCAACT	120
AGATGGCTAT GATATCTGGG AGACCATAAG TNAAGGGTNT TCGGTCACCC CGNGTAGATA	180
TTTTNCATAN CATTGACCCC GTATACACC	209

(2) INFORMATION FOR SEQ ID NO:1159:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 137 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1159:

ACTGTNTTTA TGGACTAGGA ACTTANTAAA GATGAAAGAG TTTCTNCCCT TGAAGTCCTC	60
CCNGATAGAG TTGCGACATC TCNAATCAGC GATGCACACT TGGGCAGACA CANTNATTGG	120
GCAAAGCAGT GGAACAT	137

(2) INFORMATION FOR SEQ ID NO:1160:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 403 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1160:

GGCAGAGTGG CTATAAACTT TGTNACTGAA GAAGACAAGA GGATTCTCCG TGAACATTAA	60
GACTTTCTAC AATACTACAG TGGAGGAGAT GCCCATGAAA TGTGGCTGAA CCTTATTTGA	120
ATTCCTGGGA ATGAGAAGTT TTGGATGCAG TGCTCGCTGT TGCTGGAATA GGCGGATCAC	180
AACGTGCATT GTGCCTTCTT TGTTTGGGGA ATATTTGAAT CTTGTCTCAA TGCTCATGAA	240
CGGATCAGAA ATACAGNTTT TGANTAGCAA AGNANCCTTA GCCGNAGNCT CCTTGTGAAG	300
GGAAAGTCCA TTGGGCTTTA TNCCTCTTTA AGAGTTTAGA CTGTTTGGGG TGGGTTTTAA	360
AAGATGGGGG TCTGTGAAAA TCCTTTCNTT NNTNAGGAAA TTT	403

(2) INFORMATION FOR SEQ ID NO:1161:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 348 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1161:

GGCANAGTGA TCACTCATCT AGATATCTCA NACTCTGAAA TAATATAATT NACTAATTG	60
GGAATTTATA AGTTAAATTT ATAAGGTTTT TAACAAATAT ATTTGTAATG GAATTATTG	120
AACTTTNCCA AATGAAATTG CATAAAGNAT GTGAAGGNTT GCAACAGTTT ATATTAAAAT	180

TTTTNCTGG TTTGCAATAC TTGGGTGGCC TGATGAAAAG AAATTCTTCA ACTTTAGTCT	240
CTTTCCTGGC ATTGTGTTCA TACCACTCCA TATTTTAAAA GTTGGACCNG TACTTTTGGG	300
TTTCACTTCT TTAAATGGNT GNAAAAGGAN GCCCNCCAGG TAATTTTT	348

(2) INFORMATION FOR SEQ ID NO:1162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1162:

TGTTAGTGGT GGGNAGGTGT CCTGTNAGCC CCCTCCAAGG AATTCACCAC CCAGCGAGGC	60
CACTAAAACC TCCAGAGTAA GTCAATCAGC CATACTAAGG NAAAGTCCTA AGGGGGACAG	120
ACAAGGTGAG NAAGAGGAAT CCTGTGGGCT GGAGGCTGCA GGNAATTAAG CCAAGTAGGA	180
AGGAGAGGAA TCCCAGCGGG AGGNAATGGG GGGAGCAGGG GCTTGGAAG ATGAGGACAG	240
GCTTTAGTGN ATGGTTTTTG NGGGAGACAG CTCTTNAGGT GGGAGAGCCA GGAGGTTAGG	300
GGGTTNAGAC AAAAGTTAGG AAGAGGGTTT TCAAACCNC AGGGCCCCCA CAAGGGGGGA	360
GGTTCATGA GCCCCNTGAA GTTGTTTTTN CACATTNTTT CCCGTTACAG TTTTTTTTTT	420
GCGCAANACT TTTTGGTTTT CNTCAATTTT TTCAA	455

(2) INFORMATION FOR SEQ ID NO:1163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1163:

GGCAGAGGNA TGAACAGTAC CAAACAGCAG TTTTCTCTC ATGGTCTTG AGCCTGGAAG	60
TCTGAAATCA GGGTGTGAGG AGGGCCATGC TCCTCTGAA GGCTGTAGAA CATTCTCTCT	120
TGCTTTTNCC TAGCTTCTGG TGGTTGCTAG CAATCCTTGG GCATTCCGTG GCTTGTGAAA	180
TGTNTCTCTC CAGTTCTTGC CTGTATCTTC ACATTGCCTT CTTACTATG TTTACAACAT	240
CATCGGTGGG ACTTGATGGA AGAAGGAAAG GGGGCTGTAT ACAGCTTTTG AATCCAGTAG	300
GGTCTTACCA GAGAGACTCC TTCAAGGCTG GGAGGCTCAG CAAGTGCCCA TGGTTACAGC	360
CCTGGTTTGA CAACCAGGTT GGTTTTAAAG GACCATGCAG NATTTNGGNG CAATTTCCNC	420

TGTCCCTTGG CNAAGGCCAG GGGTTGGTGA AAAAAGTCTT CATTTTCGGG TTA

473

(2) INFORMATION FOR SEQ ID NO:1164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1164:

TCGAAATCTA ATTGGGGGCG CTGACATCAT TGTGATCAAA TACAACGTTA ATGACAAGTT	60
TTCATTCCAT GAAGTAAAGG ATAATTATAT TCCAGTGATA AAAAGAGCAT TAAATTCAGT	120
TCCAGTAAAT TATTGCTGCT GTTGGTACCA GACAAAATGA AGAGTTACCT TGTACATGCC	180
CACTAATGTA CCTCAGAACA GAGGGAGCTG TGTTTAGTTA CAACTGTAAG GGGNTCCAAC	240
TTNCAAANNA ACTAGGNGGC AACCTATCTT NGGAACTTCC ACAGGCCTTG GATGGACTTG	300
TTACATAGGN AAAGTTTTTT TGGGAGGGAG TGTTTGGGGT TTTTTTATGG ATTTCAAGNC	360
TTTAAANTCA GAAGGACAAG TGGAAAAAAA TGGAAN	396

(2) INFORMATION FOR SEQ ID NO:1165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1165:

GGCAGGAGGG AAAACAGAA ATCAGCGATA CATAGGATGT AAATATACAA CAGAGNAAAA	60
TCAACAAAGC TGAGATTTGG TTCTTAGAAA AGATAAATAA AATTAAGAAC CCTCTATGAA	120
ATGAGGACTG ATCAAGAGAA AGAAAGAAAA CACAAGTGAA CANTATCANG AATGAGGAAG	180
AGGNTATTAC ATTGTNTATC AAAAAGTTAC TGAGGNTTAT TCAAAGCAC AAAANCAAGA	240
CATTAGCATT TTGTNATGGT GAATTTGACA TAGTTTGGGT TAAATGNGG ATGNTTGTTG	300
NGAGGCAAGC TTACCAAAC T G	321

(2) INFORMATION FOR SEQ ID NO:1166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1166:

GGCANAGNCA GGATTTGATT CCACGCCATC TGGTGCTGGA GGCTATGCTC ATAACCACTG	60
CTGCATTCTG ACCTCTGTAA CATGCTCATG TCATTACCTT GCTCAAAAGC CACACGTGGG	120
TCCCCACTGC TGCAGGGACG GCATACTACT GTNTCTTATT CATCTTTGTA TCTTCAAGCC	180
TAATGCATCA CTGAACTGAA ATAGCAAATC GCGGGAAGT GAAATGAAAT TNCAATGTGC	240
AAGNAATGTN TCTGTGCAAG GGATGTTCCG TCGTGCGCCA ACGTTTGCTG GGTGGACANA	300
AAAGATTGAA CCCACCANTG GGAAGCCAGC TGGGCTTCA CTGGTTCAGG TGNTTGATNC	360
CGGAAAGCAT CCAGGCCAAT TAAGCGNCCG GTTATGGCCC TGTATTGGG TTGNCACAGG	420
GTTACATTG CTGGAAGTTT GCTGAGCTGA AGGGAAAGGT TGATCGNCGT TTTGGTAAAA	480
GGTGGN	486

(2) INFORMATION FOR SEQ ID NO:1167:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 366 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1167:

GGCAGAAAGG NGAATGGCTT AAGGCCGNA GTTTNAAACC AGCCTGGGNA ACATGGTGAG	60
ACCCTGTCTC TACAGAAAGA CGGAAGAATT GGCTGAAAGT GGTGGCACAT GTCTGTGGTT	120
CCAGCTACTG GGGAGGCTGA GAACCGGAGG ATACACTTGG GACCTAGNAA GTTCAAGGCT	180
GACAGTGAAG CTAATGAATA CCTTACCACT GGCCTNCCA GCCTGGGAAG ACAGAAGNCA	240
AGCCCCTTTT TNCTCTTACA AAATTAAAT TAAAAATCCC CCACAGTNCT TTGANGGAC	300
TAATGACTNA TGCTTTAATT AAATTAGGT GGTTTTATAG TNAATTTTTT AATTTTNGGT	360
TTGGGA	366

(2) INFORMATION FOR SEQ ID NO:1168:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 224 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1168:



TTCANAGTCA AGNAATGTGT CTGTTNAAGG AATGTTTCGTC GTGGCAACGT TNGCTGGTGA	60
CAGAAANAAT GAACCCACCA ATGGAAAGCA GCTGGCTTCA CTGCTCAGGT GNATTATCCT	120
GAACCATCCA GGCCAAANAA GCGCCGGNTA ATGNCCCTGT ATTGGATTGC CACACGGCTT	180
CACATTGCAT GCAAGTTTGC TGAGCTGAAG GAAAAGNTNG ATCG	224

(2) INFORMATION FOR SEQ ID NO:1169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1169:

GGCAGAGGNC ACATNATGAT TNATTCTTCC TTTTTTTAAG ACAAAGTTTT CCCCTTTTAA	60
CCCAGGAGGC AGAGGTTNCA GTGAAGTCGA GATTGCCCA CTGNCACTCC AGCCTGGGTG	120
ACAGGGCGAG TCCCACGTTT NAAAAAGAAA AAAAAATAAA CAGCAGAAAC AACAGCCAAC	180
ACCGACATCT CTATTGGTTC AGCTTACACA ATTTTGA ACT GAAAATTTAA AAGTTGNGCA	240
AACTTTCCAC TTGATGGCTG CCAAACCAG TTCAGCTGCA GNCAAGACCN GGGTTTCAAT	300
GGGAATTTGT TAAACAAGTG GGGTCTTTT AGGGTTGCTT GCAAATTTAA TTTNTTGGTT	360
TTTGCCCTT GAAAGGGATT NNCCAAAAAC CGGCAATGGG CTTTGGNTC CCAACCCNTT	420
GGGT	424

(2) INFORMATION FOR SEQ ID NO:1170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1170:

GGCAGAGCTT GACTTTAGAT AACCGGTTGA CTATGTCCTT AGGTNATGAT CTTTTNCAA	60
TGAAATTTNT CAGGTGTCCT TTNAGCTTCT NGTATTTGGA TGCCTAGGTC TCTAGCAAGG	120
CTGGGGAAGT TTTCTCAAT TATTCCCTCG AAGATGTTTT CAAGCATTTN TCCTGCCTCA	180
NCCTCCTGAG TAGCTGGGAA TTACAGGCAC ACGCCACAAT GNCCCGGCTN AATTTTNGT	240
ATTTTTAAGT AGGAGACGGG GTTTCGCCAT GCNAGGCTGG TCTCGGA ACT TCCTGGACCT	300
CCATGATCCT GCCTGNNNTT NAGGCCTNCC CAAANGGNTT GGGATTTACA GGGNTTNAGG	360

CCACCAAGGN CCGGGCCAAN TGTGGTCCCN TTTNAAGGGG GAAGGTTACC CTATGTGGAA	420
CTGTTGNTNG GGTAACAATT TCTTGGTTAT GGCAGGCGGG GGAAAACCTG CAGGGTTNTA	480
GGGGAAAGTT NTNGGGAT	498

(2) INFORMATION FOR SEQ ID NO:1171:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 269 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1171:

NTGTNCGCCT GNNGGTCATC TTCTTCTTTC ATGTGTCAAC TGCTCNTCTG AGCAAAAAGT	60
GCTTGGTGTA TCTTGGTCTG GGGANTTATT TGGAAGACAT TATTTGTGGA ACATAATGGC	120
ATANCATTTA CATACGTTCA CCTACTGACT TTGAGTATGA ATGTGTAGGT TGTGTATATG	180
TGTGAATATA TATACACCAC GGTGTCATTC TANGTGTGTTG GAATAACTGT TCANACAGTA	240
GTTACCTNTT CCCTNGGAAT TACNATCTG	269

(2) INFORMATION FOR SEQ ID NO:1172:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 323 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1172:

AATTCGGGCA NNANCNATTA CACTTTGATA TTGCACATGA NATGACACGG GGTCTTTTGT	60
GGACCCTAGC AATGACCAAG GGCCCTGCAC GCACCCAAGC ATGTNCCCTC CCGAGTAGCT	120
GGGATTACAG GCATGCGCCC ACGATGCCCA GCTAATTTNN TTTTGTTTTG TTTTTTGTG	180
GTTTTTGTTT GTTTGTNTGT CTCAAAAAA AGTTTTTGGA ATNACCTTTT TCACCCAAAA	240
TGGGACACAA GTNAAGGAGA ATGCATTCCT CTGTNGTTTT TGTGTTGG TTTTTTTTTT	300
TTTTTTGGGG NCCCAAGNTN CCC	323

(2) INFORMATION FOR SEQ ID NO:1173:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 276 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1173:

GGCACGAGGT TGGAAGTCAG GTAACAGGTA AGCTTCTTTG ACTGAANTAA CAGAAAATCC	60
AACTCAAATT GGCATGAAAA CGATAACAAA AAGGCAGGGA GGGCTCTCAG GTTGATTAA	120
TGGTTCGAAG ATCAATGAAA GATCCAGGCT TTTACTGTCT CTCTGTTCTG CCATCCTGGG	180
TATTTGGCTT CTCCAAAGGC TGGCTNTNTC CTCTTGGTCA AGATGNCTGC CCAGAGGAAA	240
CCTNAGCAAT GGTTTTTGGT TTGTNACCTA GTGGGG	276

(2) INFORMATION FOR SEQ ID NO:1174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1174:

GGCACAGAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	60
AAAAAAAAAA NAAAAAAAAA AAAAANAAAA AAAAAANNN AAAAAA	106

(2) INFORMATION FOR SEQ ID NO:1175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 489 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1175:

CCTCTCTCC AGCNATGCCC TCCACACACA CAGGCACGTG GACAGACACC GAGTGCAGCC	60
CTCNTACCTG GGGCCTGCNT CTGCAAGCAC AGTCCCCTCC TGTATGGACC CTGGCCTACC	120
NACCAAACAC TACATGGNAG CCACTGTCCT TTTTCAGCAC CCAAACGAGG ATCTGCCTGT	180
TCCCGAGCTT CCACGTGTTT CCCAGGNCCA TTNATGGGGG CCCCCGGGGC CGCTGGGGGT	240
TAGGGACCGA GGCAATGCAT ACCACAGAAG CCCGTGCCGG GGCTTTTCCN TGGGGCCACA	300
TCCGTGNTTN NAATNGCTTC CTGGTTAATT CACACAGNTT CAGGGATGCG GNCCNTGGGG	360
GGGAAGGNAA ACAGNCCAAC CTTNGCCATT GGGTTTTANT NCAAGACGGG GGTTAGCGCN	420
TAAAAGCCTT CCAGTGCCTT TGCTTNCCCC TTNCTTCNTA AGCTTAGGCA GGCTTTTTTTT	480
TCCGGTNAG	489

(2) INFORMATION FOR SEQ ID NO:1176:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 294 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1176:

GGCACAGAAG AAGCCTCTGC NACCCTCCAG GACCTGGTCT TTAATGAGTG TGGGATCAGC	60
GATGATCAGC TCCTTGCCCT CCTGCCTTCC CTGAAGCCAC TGCTCCCAGC TNAACAACCT	120
TAAGCTTCTA CGGGAAATTC CATCTCCATA TCTGCCTTGC NAAGATGCTC CTGCAGCACC	180
TCATCGGGTT GAGGCAATCT GAACCCACGT GCCTGTGATC CTGTCCCCCT GGNAGNGTTA	240
TGAGGGAANT CCATGGGTAC CCTCCANCTG GGAANGGGTT GCCTGATCTG CATG	294

(2) INFORMATION FOR SEQ ID NO:1177:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 409 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1177:

GGCAGAGCTC AAGCNNTCCA CCCGTCTCAN CCTTTCAAAC TGCTGGGATT ATAGGTGTGA	60
GCCACTGCAC CCTCAACAAG TGTTTTTAAG GACTTCTTAT ATGCTTTTAA GGGAGAAATT	120
ATATTCAACC AAACAGACAT GGATGTNTGG CGCTTTCTGC AAAACAGGGA GGTAGGTGAT	180
GATTATGTAG TTGCAAATGA AATATAATTG GCAGCTGTGN ATTAACACTT TTGNAGGGAA	240
AGATTCTTGG TGCTCTAGTA GCTTCTAAAT AAGGAGATTT GATGTAATTT GGGGAAGTNCA	300
GAGGAAGCAA GACCTGAGAT CTGATGCGGA GAGGAAAGGA TGCTCTGCGC CAGAGGGAAT	360
TGCNTTATGC AAAGGGACCN NGGGTAAGAG GGAAGGNTGG NAAATTATG	409

(2) INFORMATION FOR SEQ ID NO:1178:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 488 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1178:

GGCAGAGTNA ATTTAGCAGT AATTATCCAT GATGATATCA TATTTCANCA GAGCCCCATG	60
ANCATAAAAA AGGTTAGCAC TGTCTCAAAT TTTAGCTCGG CAGGGAAAGA TTAAAAGCCT	120
TTTAACAAGT AAAACAATNA ATTTGAAAGT CAGAGGTGAC TGANTAACAG AGCAAGCAAT	180
GGTAAACTGC AGGTTNAAAT TTGAGTAATG GAATAGGTCC TTCTTAAAGG GGGAAAAATC	240
CATCTTGGA TAGGATTACC TCTTAAAT ATNATTTNAT TTTTNTGGGG TTTATTAATN	300
TTTGCTGGG GATTTAAGTA TTATGGTTTT AAAAAACCGG GGCTTTTGA ACCCCTTG TG	360
GTAAATTNGG GTCTTTTTNT TACCGGCCCT TGGNAAAACC CAAANCCAAA CCTGGGCAA	420
TTTTAAATTG GGGTTCCAN CCCTTCCGG GAAGGCTTTT TAAANTTTG GAAATTTTNC	480
CCCTGGAC	488

(2) INFORMATION FOR SEQ ID NO:1179:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 76 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1179:

GGCACAGGTT TTTTTTTTTT TTTTTTTAAA AAAAAAACC CTTTTTCCC TTTTTTNAA	60
AAAAAANCGG GTAAAN	76

(2) INFORMATION FOR SEQ ID NO:1180:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 405 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1180:

GGCANAGAGA GGGTGCTGTA CATTGACATT NATATTCACC ATGGTGACGG CGTGGAAGAG	60
GCCTTCTACA CCACGGACCG GGTGATGACT GTTTCCTTAT CATAAGTATG GNGAGTACTT	120
CCCAGGGAAT GGGATCCTAC GGGAAATATCG GGGCTGGCAA AGGCAAGTTA TTATGCTGTT	180
AACTACCCGC TNCCGAGACG GGGATTAATG ACGAGTCCTA TGAAGGCCAT TTTCAAGCCG	240
GTCATGTCCA AAGTAAATGG GAGATGTTCC AGCCTAGTGC GGTGGTCTTT ACAGTGTGGC	300
TTCANACTTC CCTATTCTGG GGGATTCGGT TTAGGTTTGN TTTCAATCTN AACTATTCAA	360
AGGGACCACG GCCCAATTG GTGGGNAATT TNTTCAAGAG CNTTT	405

(2) INFORMATION FOR SEQ ID NO:1181:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 277 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1181:

```
ATACCACTGC ACCCTCAGTG ACAGAGTGAG ACCCTGTCTC TGCAAATAAA AATAAAAAAC      60
TTGAAGTGGA TGAAAAGATC TAATATGAAA GGTGAAAATA TAAAGCTAAT GNATGTGTAA      120
GTATGAGCAA TAGATTGTTGGG GACTTTAAGC TGGGGAAGGA CTTCTTAAAT ATGATTCACA      180
AAGCACTTAA CCATAGGGGG AGAATGGATA GATTTGTCTA CATCAAAATN GAGGATTTCT      240
GTTNCNCGGA NGCTCCCCAC AGNTTAAGTT ACCAGAC                                277
```

(2) INFORMATION FOR SEQ ID NO:1182:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 250 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1182:

```
GGCACGAGGN AAGCACAGAC TTCGGATGTA CAAAACAAAG ACTTTTCATC AACTCTTTTA      60
GATATGCTAG AAGAGCTAAA GGAAACCATG GACAGAGAAC AAAAAAATTA GGAAAGCAAT      120
GTCTCATCCA ATACAGAATA TCAATAAAGA GGTTTGAAAT TTGTTGGAAA AGGAACCCAA      180
TTNGAAATTT TTGGAGGTG AAAAGNTTTT TTAACNNAAA ACNTGAAAAT TTCCCTTAGG      240
GGGGTTTTCC                                250
```

(2) INFORMATION FOR SEQ ID NO:1183:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 90 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1183:

```
GGCAGAGTCG AGTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT      60
TTTTTTTTTT TTTTTTTTNN CNNNAAAAAA                                90
```

(2) INFORMATION FOR SEQ ID NO:1184:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 297 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1184:

GGCANAGCCT CAGTGAAAAT ATTTCTGCAG CTATCCAAGC TAATGGTGAA ATGGTTACAA	60
AGCAACCATT GATTAGAAGT ATGCGAACTG TAAAAAGGGA AACTTTAAAG TTAATATCTG	120
GTTGGGTGAG CCGATCCAAT GATCCACAGA TGGTCGCTGA AAATTTTGTT CCCCCTCTGT	180
TGGATGCAGT TCTCATTGGT TTATCAGAGA AATGTNCCAG CTNGCTAGTG GAACCCAGAA	240
GTGCTTAGTA CTATGGCCCT AAATTNGTCA ACAAGTTTAG GGGGGGNCAT ATTTNCC	297

(2) INFORMATION FOR SEQ ID NO:1185:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 275 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1185:

AACCCTACAA ATGTAAAGAA TGTGGAAAAG CTTTTCACCG ATACTCAATC CTTAGTACAC	60
ATAAGAAAAT TCATACTGGG GAGAAACCCC ACAAATGTGG AGGAATGCGG AAAAGCCTTT	120
AACTGGTCCT CAACTCTTAT TACACATAAG ATAATTCACA GTGGAGGAAA AACCCTACAA	180
ATATGAAGGA TGTGGCAAAG CTTTGAACC AGTCCTCACA CCTTATGNGN ACATANGAAA	240
ATTCATAGTA AGAGNAACCT TTACAAATGT GNAAC	275

(2) INFORMATION FOR SEQ ID NO:1186:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 505 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1186:

GGCAGAGTCT CAATGTTGGA CCTAAGATAT TGAAGACAGG CTGGAGTCCA GAGCCTTCAT	60
TCAATCTCAG ATTTATGAAA ATAATTACTG GATTGGATTA TCATATGATG AAAGGGAAAG	120

TAAGTGAAAA TGGGATTGAT AATGGCACAT CTCCTGGGAT TAATTCTACA ATAATGCGTT	180
TTTCTTCTGG GAGAGGAGAA TGTGCCATTT TTGACCTCAA CAAGAATGGC AACTATTGAT	240
TGCATTCAAA CGTACAATTG TATCTGTGGG GAAGAGGAAT AGGACTCTAT TTTCTCTGG	300
ATTNCGGTGT GCGCCCAAGA AGGAAAAGGG TGGAAAATGG GNATGTTTTT CCCTTTTTTT	360
TGTTTTCCCC CNTAATAAAT TTNCCGGATT TATTAAATC CATTTGGCTTT TTAAACCGTG	420
GGGGGCCTTA GGTNAATTC CTTTCCAAAA GGTTTAAAGG TTGGAACCCG GGGNAGGGNA	480
AAAAGGGAAA ATTTATTTTT TTGGG	505

(2) INFORMATION FOR SEQ ID NO:1187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1187:

GGCAGAGGGA ACAATATCCT CCATGAAAA CTGCCGCACT GTGTGAAGAG GAATTTAATG	60
CATATTCATC TTCCTCCCTT TAATACGCNG CAAACCAACA TGTTTCTTTA CAGCTTCTCC	120
TGGGGAAAGA GAAGTAACCA CTGAGCTTCC AGGTTGTGAA GATATAAAAC AGCTGTTGTT	180
CATTTTGGT TGGAGCTATT TTACACTCAT GTTCATGGCC CCAGATAACA AGATCAATGA	240
AGTCATCCAA AAATTGTTCT GGGAATGAAG TTAGTACTTC CATGTTTACT CCTGTTCTG	300
ATGGAATCAC AATTAAGTTA AACCANGAGT TCNTCATCTT CCNTTGGTCT TCAACATGTN	360
AACTTTTTTA TTGACAAACN TTCG	384

(2) INFORMATION FOR SEQ ID NO:1188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1188:

GGCAGAGAAG GAGAAGTCTT TACCTGGGGT CATAATGCTT ATAGCCAGCT GGGCAATGGG	60
ACAACTNATC ATGGTTTAGT GCCCTGTCAT ATCTCTACTA ATCTGTCAAA CAAACAAGTC	120
ATTGAAGTTG CCTGTGGGTC TTACCATTCT TTGGTGCTAA CATCTGATGG AGAGGTATTT	180
GNNTGGGGTT ATAATAACTC TGGGCAGGTA GGATCTGGAT CAACAGTTAA ATCAGCCAAT	240



CCCTTGGAAG GTCCACTGGC TGCCTACAAA ATAAAGTAAG TTGTGAACCA TTGGCATGTG	300
GGCAGATGTG CTGCATGGGC ATTAGTAGAC ACGGGGGGAG GTCTATGTTN TGGGGTTTAC	360
AACGGAAACG GGCAGCTTGG ACTCGGGCAA CATGGCAACC AGCCAACNCT TGCAGATTGG	420
CAGTTTGCAA GGGCTTCNTG TNCCANGGGT ACGTCCATTT CCAATTTTGT GCGTGTATTT	480
TTAAGCTTNG T	491

(2) INFORMATION FOR SEQ ID NO:1189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1189:

GGCANAGGTT CCATATAGAT ATTGCAGATA GAAGTCAAGT TGAACCAGCA GACTACAAAG	60
CTGATGAAGA CCCAGCATT A TTCCAGTCAG TCAAGACCAA GAGAGGCCCT TTGGGAACCC	120
AACTNNNAAG GTACTGNATG CTGACCTTTC TGAACAGGCA GAGTCTTGGG CAACAGAACA	180
CTTGACAGGT CCTGAGTCTT GAAAGAGCTG GTGACGTTTA AAGTGNAAAA ATAGAAATGG	240
GCACAAAAAT AGTTTTATTT GCGATTAAGG ACTTACAGCC AGTTGCAGTT GGCCAGCAAN	300
TCTGTGCTGC ATTAACAAAC AGAACAGNGC CAGACTGTTC ATTTTCAGNA TAATGCAGTT	360
CCATTAANCT TTAAAGGGAC AAGTGTTTTA GTCNTTGGGG TTNNNATGTT CTCTTTTGAG	420
ACCTGAAGCG TATAAAATNC CTTTAAATGA GGTTTTAGTT TAAATTNGTC TTATTAAAC	480
TGANCAGTTC	490

(2) INFORMATION FOR SEQ ID NO:1190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 488 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1190:

TGGATAACAA ATCCCTACCT ATAGCCATGT GGAAGCAGCT TGTCACGTGA TTTTAACTGT	60
GTAACAATTA TTGAAGGCGA AAATAGNAGT TGGGTCATCT TTGAACACCT ACCTTTTATC	120
AATGAATATT TTTAGACTGT NCTTCAGTAT CTGAGTCAGA GTTTATTGTA ATTTGTTATT	180
TACACCAAGG TGGCATCTTA GTCTACCTTC AGTGAGACTT GCGTTTCAGG GGAGGGGCGT	240

ATGTNCATCC TCGGTCTCCG TTATGTAAAC GGTCTGATCT GTNAAAATAG TGGTAGCACA	300
TGCCACGTGG GATAGTTGGT GGAGATGATA GATGGAGTTT AAGCACAGGG CCCAGCCTGT	360
TCAGCAGTAG CTACTATTAN TGTTGCCCAT TTCCCCTGCA ACTGAGGTGA GAGGTTTNC	420
NCGAGTTTTA AAGCTGACTG GGCCCACAGT TAAACGGTAA CAGACCAGTT TTTTCAGGGT	480
GTCAGCCC	488

(2) INFORMATION FOR SEQ ID NO:1191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1191:

GGCACGAGGA ACTGCTTGAG AGCTTTTCTT AATTGGGAAA AGAATGCCCC GGTAGATGTT	60
GGCTTCATGG TTTCTAAGCT GCTTTTGACC ATACAGTTAT GTCCAAAAAC AGAATTTCAA	120
CCTAGTGAAA AATTTGGTGA AGACCTAAGT GATAACACTT GGAATACAT ATTTNCCATT	180
GATCTGCTCT GCTGCCATCA GAAATGGATC TGGACGCATG ATAACATCAT AAGTAAGGAG	240
CTGTGGCCTG TGATGGATAA ATGGATAAAA TACAGAAAAG GACATGCAAA CATTGCGTAT	300
ACTCCTGATA TTATTATAGC CTCCAATTAC TGAGGCTGAT TGGTCGTTTA GGCCAATTGG	360
GTTTGAAAGA AGGGTTTTCC ATCTGCTGTG AAAAAATATT AAGTTCGGTT ATTGGTATGT	420
TTATTACAGC ATGCTCACGG TGAAGGTTAT TACCCNTGGG GGTATACCAG TTTAGCAGCC	480
CGTGTATGCT CCTTTGTGAC	500

(2) INFORMATION FOR SEQ ID NO:1192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 403 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1192:

GGCACGAGGT TTTTCAGAGAC ATAGAGGATA GCAAACAAGC TCAATTTTTTA GCCTTGGCAG	60
TAGTATACTT TATCTCTGTT CTTATGGTCT GCAAGTACAG AGACATTTTG GTAACCCCAA	120
AATGAAAGGC ATAGCCAGTC ATGTACAGAA ACTGGCAGTG GAAAATGAAG AATGTATCAC	180
TCTCTGAAAT CACACCAGCA GCATTCAGCA CTTTGAAC TA CGGCATCAGT GGGAAGGAAT	240

CTGNAAGGCA CATCATCTGC TTCGAAGGAG GGAAGTCAAGC ATTGGGGGAA GAAACAGCCA	300
CTGGTTTAGG AAGCCATGTG GGAAGTAACT CNTCACACAG NACCTTCCTG GTGTTTCACTN	360
GCAGGNCCCA GTTGCAATCA GCGAGGTGCT ATTTTANTCT TTC	403

(2) INFORMATION FOR SEQ ID NO:1193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1193:

GGCAGGAGNA AGAAGCTTGC CTTATGCATG CTAATGTTAC ACTGCCAAAG CCATCACATG	60
ACCCAGCTGG GTGCTAGAGG TACAAGCACT TGGNTATTAG GGGTGGCATT TGGGTACCAT	120
CCAGTATAAC AGAGTGGTTT ACCACCTTAT ACACATTGTA TATGATTTCT TGCAGTCAGT	180
TTTGTGGAAG GGAGTGCATT TTATTCCATT TTGTTTTGTC TACAGTGGAA TTTTGTGTT	240
ATAACTATCT TCCTCCTTTT AAAAGTTGGC AACCATAATA TTATACTTCA TATTTTGAGA	300
TAATGTTTAG ATTTTACCCA AAAAGTTGGC AAAAATAGTN NGGANTTNCC CTTATGGCCT	360
TNCACCCGGG TTTCTACTAA TGGTTAAAC	389

(2) INFORMATION FOR SEQ ID NO:1194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1194:

GGCAGAGGNA ATTTCAATTGG GNACAGCAAC CATGGCAGCC AATCTCCCAG GAATGTGGAG	60
GAGAGGATGN TTGCAGTCAT TTAAAGGTGG AAAGGCTTTT GTGNCN	106

(2) INFORMATION FOR SEQ ID NO:1195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1195:

GGCAGAGCCC AAGCACAGTG ACTCACGCCT GTNAATGCCA ACACTTTGGG AAGGCTGAGG	60
TGGGAAGATT GCTTGANTCC AGGATTTTAA GGCCACCCGT GGCAACATTA AGACCCCATC	120
TCTACCAAAA AAAAAAAAAA AAAAAAANG GNNCCCCN	158

(2) INFORMATION FOR SEQ ID NO:1196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1196:

GGCACGAGCG TTANCGNCGC NTNCGGTGAG TCAGTCCGCC CAGTGCACCA ACTGCGTGCA	60
GGACGACACG GCCAAGGCCA AGATCACCAT CGTGGCAGGC GTGCTGTTCC TTCTCGCCGC	120
CCTGCAGCCT TGCNTCGGAG GCCAGCCCAC CCCCAGAAGC CAGGTAAGCC CCCGCGCTGG	180
NACTGGGGCA GCTTCCCCAG CAGCCACGGC TTTGCGGGCC GGGCANTCGA CTTTGGGGCC	240
CANGGGCCAA ACTGCATGGA CTGTGAAACT TAACCTTTTT GGAGCAAGGG GGCTTGGGTT	300
ACCGNCNATA ATTTNACCAA CCCGTTGGAG NCCCATTTGG GCCGTTGNCC CCAATGTTTG	360
GGTTTGGGNA AGGGACCGGN AATCCTTGA AGGGGCATTT GATATTTTTT CAATTAAAAG	420
CTTTTGGTTT TTGNATTGGN AAAAAAAAAA AAAN	454

(2) INFORMATION FOR SEQ ID NO:1197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1197:

ATGAGCCCC NCGCCCGGCT ACCTGAACCT CTTTGTGACAA GTNCTGATAT GAAGGCCCCA	60
TATCAGCTGG GGCCACGGCA GCAGCCCATG CAGGNGGGGC AGNCTGGGNG TGGCTGGCCA	120
GGGNAGGGCC TGGGTGGGNG CTTCAAAGCT GGTGGGNATG CGGGTGGGTG TGGGGCCACA	180
AGAAGGAAGA GGGGTATCCA GGGTGCCCC AGTTCCTACG TGNAGGAATG GTGTCTCCCA	240
AGAGCCATGG TGGCCTCCGT GGGGACAGTG AGANTAGAGG CTTGTNAGGN GGCCCTTTCA	300
CTTGGCNTNG AAACCTCACTG GGT	323

(2) INFORMATION FOR SEQ ID NO:1198:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 316 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1198:

GGCAGGAGGT TTTCTCATAT ACATGATGGT GTATGTAATG GTTAAGGTAT ACAAGGTGGT	60
TTGCCCATGA AAGTCTATTT AATCTCTAAC AGACATGAAG AGTGTTATTA ATAGAACCTT	120
TCCCCAAAAT GTTGTAGGGG AAAATGTCCC AGTTCCATGT GGAATTGTCA GAACAAGCCT	180
CAGCCTCTTC GAGGATTTCA AAGTGGCTTT CGTCTTTTAA GTTGATGTCC TATCTCTCTC	240
TCTGTGCTCC TTTTTTTTN AACTTTGTGT GCTTGAACA NGGACCCCTT GCCACTTTNA	300
AAGCTGAGTN ATTNAT	316

(2) INFORMATION FOR SEQ ID NO:1199:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 492 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1199:

GGCAGGAGCT CGGCCTNTNT TNCAAGTTTC TCCAAGGGGC TGGCGGCGGC CAAGACTTGC	60
GGGGTNTAGG GGTGCTGCGG GCGGTGGAAG ATCTCGTCGN GGGCACCCAT TTCCACCACC	120
CTGCCCTCGC TCATCACCGC CACCCGGTGG GCGGATGCGT TCCACCGCCG CCAGTCGTGG	180
GGAGATGAAC AGGCAGGCAA AGCCTNACTG CGCCTGCAGN TTCGGATACA GCTTCAAGAA	240
ATCTGGCTTC TGGGATGGTC ATGTCCAACG CCGAGATCGG CTTTCATCGGC AATCACCAGT	300
TCGCGGGTGT CCGCACCAGN GCCCGGCCAA TGGNCACGN TTNGACGCTG GTCACCGGAC	360
AANTGGTGCG GGGAAGGGGT TCGACAAATT TTTCCGCCAG CCGATTGTTC CANCAGGGTT	420
TTTGGCCAAC CGTTCAAGAC GTTTNGGGGN TTTCATGCCC GGGGAAATTG GCGNAGGNTT	480
TTCGGGGAGA TT	492

(2) INFORMATION FOR SEQ ID NO:1200:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 478 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1200:

GGCACGAGCT TGTATTTGTC TACTGACAGC CCCTTGGTAC TATTTAGGTT GGGGGAGGGG	60
ACCTAAAATA AATAGACTTT AACATTTCCC TTGGGTGCTA ATCATAGTTG GAAGTTGAAT	120
TTAAGGTGAT TATTTGGGTG ACAATTAAAA ACCTAAGGAA AACCAGAAAT CTTGGTAGTG	180
GAAGAAATGT GTAAGGTCAC CCCAATCGGT AGATTTTAAT GAACGTTGTG GAATGTTGGG	240
AGAGGGGATG TTAAGTTGAA TGCAGAATTT CACTAAGTAC TTAGTGTAAG TTTTAAGGAT	300
GTTNGCTNNT TTTNATCNAA GGAATTCCAT GTAATGGCCC CAAAGGGCAG TTTTACNGG	360
TTTTAAAAAA TTNGGAATTA ATTTTACCA TGACCATTCT TGGAAATTCC CAGGNAGTTT	420
TTNTGTGTAG GGACCCTTTT TNAAAAATTN CCTCCCGNTT TTTTAAGGGG GAAATTAA	478

(2) INFORMATION FOR SEQ ID NO:1201:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 391 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1201:

CCAAGACAGA CTGCAGGTTA CGGCCTGACA TCAGAGCCAT GGAAAATGGA GAGATAGATC	60
AAGCTAGTGA AAGAAAAAAA ACGACTTGAG GAAAAACAAA GAGCAGCCCG CAAAAACAGG	120
TCCAAGTCAG AAGAGGACTG GNAGGACGAG GTGGTTCCAT CAAGGTCCTA ATCCCTACAA	180
TGGAGCACAG GACTGGATTT ACTCTGGGCA GCTACTGGGA CAGAAATTAC TTCCAATTTG	240
CCTGACATTT ATTTAAATG CATACAAGTC AGGGTGTTTG GCTAATCTAC AATAAGTCTT	300
TAAANCCCAT GTTTTTAAAA TTTTTTTTCC CCTGGGTTTC TNACTTANCT TTTTAAAAAA	360
AAATGGGNAA AACCTCCTG GGGTTAACNG G	391

(2) INFORMATION FOR SEQ ID NO:1202:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 441 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1202:

GGCACGAGGA AATTCATTG GGAACAGCAA CCATGGCAGC CAATCTCCCA GGAATGTGGA	60
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GGAGAGAATG AATGGCAGTC ATTTTAAAGA TGAAAAGGCT TTGGTGACCA GTCAAAATTC	120
AGACTTACTG GATGATGAAG AAGTTGAAGA TGAGGTGTTG TTAGATGAGG AGGATGAAGA	180
CAATGATATT ACTGGAAAAA CAGGAAAGGA ACCAGTGACA AGTAATTTAC ATGAAGGAAA	240
CCCTGAGGGA TGACTIONATGA AGGAAACCAG TGCCCTGGAG ATGAGTTTGC AAGACATTCC	300
CCAGTTGAGG TTTTAAAGGA GGGNAGGATT TTTAAAGTNG GACTTTTCTT GCTCTTAGGT	360
TCCATNTTAA GGGCANTTTC ACCAGTTTGG CCNTCCAAAT TGAGGGGAAT TTGGGAGGTT	420
TATTCCATTN TTCTTNAAAG G	441

(2) INFORMATION FOR SEQ ID NO:1203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1203:

GGCACGAGGT GGAATAGAGA AACTTAATGA GTGTTTAAAC CAAGCTTTTC AAGAGACCGT	60
TTCCCAGGCA CATACTGCG GGGCGTCTCA ACATCCTGTC ACCATTGTNC TTGAACTCAC	120
TTCTTCAACA CCACTCATGT GGACTIONATG GAAATAGGTG ACATAAGCCA GACTCTTCCT	180
CATAATGCCT GTCCACAGTT TTTTGCTAAT ACATAATAAC TGATTAAGAA AGACAATGTT	240
TCCAGTAAGG ACAGTGGTGA CATATTTAAG TAGATGAGTA ATGAACCTTG GCTTGTAAGT	300
GTCCTTTCTG CAGAATAGGG AGGGAAGAGT TAAAGCTGGT ATCCCCTCGG GCTCTTAGGC	360
ACCTGTTAAA CCCCAGGCCC AGGGGATCCT TCCGTCCTGT CCCTGTGAGT GCTTCAGCCC	420
AGGGACACAC AGAAGGGGCA TGTTTCATGG GTCCGAAGGA CCCGTTTAGT TTCATGTGGA	480
TTTCCAGACC TGATTGCA	498

(2) INFORMATION FOR SEQ ID NO:1204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1204:

AGAATATTGG TAATATATTG CAGAAAGTTG TGTGCAGAAA ATTGACAATN ATTTGGCCTT	60
TAGTAAAAAC TTTTACTCTT TCAAAAGTTA CTATTTTAAA GCATGGTATT ATTTTGCATT	120

ACAAAATGGT TTTATTTTCT TAGTGGTGAG ATAGAGGAGA AATTTGTACC TGCTCTTCTG	180
AATCTGAAAA GTTGTTTTCA ACTTTTACAT TACTTCCTTG TTTCTTTCTA TTGGTTGAGT	240
GTAANTGAAA AGTTTCCCAT TNACCATGCT GGCTTTGNAA ATTGAGACCN NATGTTGAAA	300
ATTT	304

(2) INFORMATION FOR SEQ ID NO:1205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1205:

GGNANAGGCG CGGCAAAGGG CCTCGTNAGT NGTGTTTCAGN TTGCCCCCTGG GGATCTNCTG	60
TGTCTTCAGC GCCCAGCCCT GCGTGTTCTT GGTGAAGCAG TTTACATCA GTCTCTCCAG	120
ATAGCACTAC GAATGTATTC CGCTTCTGAA ACAGGATCCC ATGCCAGTTT GGAACACTTT	180
CCCAATCTTA GTTCAGAAGT GGCTTGATG ACCTGTTTCAG GGGTCACATG AAGGTCTCGC	240
CATTTCTTGG GTCCTCTTCA GAGGCCNGAA AGTTCTAAAG TTCTGAGTCC CCGGCCAGGG	300
TCCTTTAANA CCTTGGNCAC AGAGGCTGTT TGGGCAATGT AGAGGCTGNC TCTGTGTGTG	360
GTTTAAGTAA ACTGGAATGN GGACATGACG NGTTG	395

(2) INFORMATION FOR SEQ ID NO:1206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1206:

GGCACGAGNG AAAAGTCGGT GCGCTGGTCC TGCCTCATTA ATCCAGGGGT TGCAGTGCTT	60
TGAAGCCCAG TCGTTGTTGG TTTTNTGAT GNAAATACCT GTNAAGATGA GTGGNCGGGG	120
N	121

(2) INFORMATION FOR SEQ ID NO:1207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1207:

GGCACGAGGT TGTGTGGTGT TTTTGGACAG ACGTTATTTT CTTTTTTGTA GAGTAGCCTG	60
TTTGTAAGTT TAAAGTGTTC ATTTTCTCTCC TTTGCAGCAT CATGGCCAGC CCAAGAACCA	120
GGAAGGTTCT TAAAGAAGTC AGGGTGCAGG ATGAGAACAA CGTTTGTTTT GAGTGTGGCG	180
CGTTCAATCC TCAGTGGGTC AGTGTGACCT ACGGCATCTG GNATCTGCCT GGAGTGCTCG	240
GGGNGNACAC CGCGGGTTTG GGGTTCACCT NCAGGTNCAG TGTCTGCCG CTCTGGGTTC	300
T	301

(2) INFORMATION FOR SEQ ID NO:1208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1208:

TGGCAAGCTG GGGCCCGGCC TGCGGGTGCT GGACGCGTCC TGGTACTCAC CAGGCACCCA	60
AAAGGCTCGN AAGAGTACCT CGAGCGCNAC GTACCCGGCG CCTCTTTCTT TAANATAGAA	120
GAGTGCCGGG ACACGGCGTC GCCCTACGAG AATGATGCTG CCCAGCAAGG CTGGNCTTCG	180
CCGAGTATGT GGGCCGCTTG GGNATNCAGC AACCACACGC ACGNGTGGTG TATGAATGGT	240
GAAACACCTG GGNCAGCTTC TATGCTCCCC GGGTTTGGTG GATGTTNCCG TGTGTTTNGC	300
CACCGCACCG TTTTCAGTGC TTCAATGGTG GNTTCCGGA ACTGGTTGAA GGAGGGCCAC	360
CCGTGAACNT CCNAGCCTTC AGNCCAGAA CCGGCCTTTT TCAAAGCCAC ATGGGACCGT	420
NNCTGNTTCA AACNTAGAG TCAGTGTTGG AGNAACTTGA ATTTAAGAGG TTTCCACTGG	480
TG	482

(2) INFORMATION FOR SEQ ID NO:1209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1209:

GGCAGAGCGG GGGTCTNGGG AGGCAAGTC CNTGGCAAGC CGTCTTCTGC TCAACAACGG	60
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AGNCAAGTTG CCCATCCTNG GGTGGGAGC TGGTNGTCCC CTCCAGGNCA GGTGNNCTGA	120
GGACGTGAAA GATGGCCATT GNACGTCGGG TACCCCCACA TCGACTGTGC CCCATGTNTA	180
CCAGNTTGAG CNTGAGGTGG GGGTGGCCAT TTCAGGTGCA GCTCAGGGNG NAGGTGGTTG	240
AAGNGTGAGG TNGCTTCTTC ATCGTCCAGC AAGNTGTGGT TGCACGTTAC CNTGGAGAAA	300
GGGCCTGGGT TGAAGAGGAG CCTTGCCCAA GAGNACCANT TCANGGGACC CTG	353

(2) INFORMATION FOR SEQ ID NO:1210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1210:

GGCANAGGTT NTCCCTTCGC GNCCCAAACC ACATCCTGGA GCGCACTCTC CAGCGTGGCT	60
GGNAGCGNGG ACT	73

(2) INFORMATION FOR SEQ ID NO:1211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1211:

TCCAGCCTNA CTTCTGGGC ATAGAGTCCT ATGGNATGCA CGAACTACC TTCACTCCA	60
TCATNAAGTG TGNACGTGGT ACATCCGTAA ANGACCTATA CGCCGTCACA GTGCTGTCTG	120
GNGGCACCAC CATGTACCNT	140

(2) INFORMATION FOR SEQ ID NO:1212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1212:

AAAAGAAAGT TTCCCAGAC AAGATGNTTN AANTGCAAGC ANAANTTGAT GAGGAGAGAA	60
AAGCACTTGA AACAAAGCTC GACATGGAAG AAGAAGAAAG AAACAAGGCT AGAGCTGATT	120

TAGAGAAACG GGAAAAAGAT CTTCTTAAAG CCCAACANGA GCATCANTCT TTGCTGGAAA	180
AATTATCTGC CCTGGAAAAG AAGGTAATTT TTGGTGGGGT TGACTTGTTG GCCAAAGCTG	240
AGGAACANGA GNANCTTCTT GAAGAATCTA NCATGGAAGT GGTGGNAAGG AGGAAAAGNG	300
CAGNGCAACT TNGCAGAGAT CTTGAGGAAA AGAGCAAGNN CGCTTGGATA TTGANGNAAA	360
TATACCCGTT TGCAAGTGGT AGCNCGGGN AAGTCCAGA AGTTAAGGAA GTTTGGCCCT	420
GCTGATGGTG CAAATCCNGG TNGGTTGTCT CCACCAGACC TTCGGGGNAT T	471

(2) INFORMATION FOR SEQ ID NO:1213:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 58 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1213:

TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTNGGGGG GGNTTTTTTT TTTTNNC	58
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(2) INFORMATION FOR SEQ ID NO:1214:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 277 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1214:

GGCAGAGCGG CACGAGNCCT TGCACCTGGN CTTCGCGTCT CAAAGGTGGG ATGCAGATCT	60
TCGTGAAAGA CCCTGACTGG TAAGACCATC ACTCTCGAGG TGGAGCCAGT GTNCACCATT	120
GAGAATGTCA AGGCAAAGTA TCCAAGGNCA AGGGAAGGGC ATCCCTCCTG ATCCAGGCAG	180
AGGTTGATNC TTTGGCTGGG NAAACACTGT GTANGATGGG ACGCACGGTG TCTTGACTAA	240
CAACATCCAG TAAAGAGTTN CACNCTGGCA CCTGGTG	277

(2) INFORMATION FOR SEQ ID NO:1215:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 153 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1215:

NTGCGGGGAC TNGCTGGAGC AGCGGTAGGG GGAGCNTGTA GANCCGCTGC GTCCCTTCAC	60
AGTCCGGAGC CCGGCCGTGC GCTGNCCGTA GGAACATGA CACTTTTCCA TTCCCGAAAC	120
CGANTCCCGC AGGGGGTACA GCGNMNGTCT GCC	153

(2) INFORMATION FOR SEQ ID NO:1216:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 270 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1216:

GANNNCATCA ACAAGGAAAA TANCACTAAG TTGAACATTG TAAACCTCCA GATCACGGAA	60
GACCCTGGCG AGTATGAATG TAATGCCACC AACGNCATTG GNTCCCCTCT TTTGTAACTG	120
TCCTNAGGGT GTGGNGGCAC CTGGGCNNNA CTNTGGCNTT NNTTGGGAAT TCTGGCTGAA	180
TTATNATNNT TGTGGTGATC ATTGTTGTGT ATGANAAGAG GAAGAGGNCA GATGAGGTTT	240
TGAACGATGA TGAACCAAGT GGACCAATGG	270

(2) INFORMATION FOR SEQ ID NO:1217:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 387 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1217:

GGCCTTTAAG GCTTNACCCA ACGTNATCAA TCACCGATTT CCACGGTAGC AGACGCGCAT	60
CCTGAAACAT CATTGCTTG TTTTCCTGAN TTTAAGCCAG CGGTGTGGTG CCCGCAAACA	120
CATCGCCTGN GGTTGGCGTT TCCANACCTG CCAGCAGGCG NCACAGGGGT ACTTTTGCCA	180
CCACCGCTGC GGCCACCAC CGNCACAAAC TGACCTGCCG GAATATGTAA AATCCAGTTG	240
GTTCCAGGGA CGATATTTTC CGCGTNAATG TTTGCTTTAC TGCATTGAGC AACAATGGTT	300
TGNCCCTGGT TTCAAACGGG GCAGTTATTN CATACCGTGG GCCTCCTTTC AAATGATTAA	360
GCCGGGTTTC CCAACGGNAA CCCNNGG	387

(2) INFORMATION FOR SEQ ID NO:1218:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 104 base pairs
  - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1218:

CCAACCTACG GTTGNTTCGT NCTTTAACCC CTACACGTTT CCCATTATGC CGTTGGNGAT	60
GAGTGGGANG ATTGTTTGNT TCGGGTTTAA ACTGTTGTGC CCGT	104

(2) INFORMATION FOR SEQ ID NO:1219:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 336 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1219:

AGGGAGAAAN TGGCCAGATG ATGAGCTGCA CATGTTTTGG GAAACGGAAA AGGAGAATTC	60
AAGTTTGANC CCTCATGAAG GCAACGTNTT ACGATGATGG GAAAGACATA CCACGTAGGA	120
GAANCAGTGG CAGAAGGNAA TATCTCGGTG CCATTTGCTC CTGCACATGC TTTGGAAGGG	180
CAGCGGGGCT GGCGCTGTGA ACAACTGCCG CANACCTGGG GGGTGAAACC CAGTCCCGAA	240
GGCACTACTG GGCCATCCCT ACAACCAGTA TTCTTCAGAG GNTACCATCA GGGGACCAAA	300
CACATAATGTT NAATTNNCCC CATTNAGAGT CTTTCA	336

(2) INFORMATION FOR SEQ ID NO:1220:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 429 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1220:

GGCACGAGAG AAAACTCATT CTGGAGAAAA ACCCTATGAG TGTAAGTAAGT GTAAGAAATC	60
TTTTGTGCAC CTGTCTTCCC TGATTGANCA TTGGAGAATT CACACTGGAG AAAAACCATA	120
TCAATGTAAG GNCTGCAAAA AGACCTTTTG TCGTGTGATG CAGTTCCTC TGCACAGGAG	180
AATTCATACT GGTGAAAAAC CCTATGAATG CAAGGAATGT GGAAAGTCCT TCAGCGCCCA	240
TTCTTCTCTT GTTACTCATA AGAGAACACA CAGTGGGGGA AAAACCGTTT TAAATTGCAA	300
GGAATNTGGG NAAAGCCTTT CAGTGGCGGA CTTTTCCCT TGTTTACTCC NTANGGGGAC	360
ACACATTGGG GNGGAACCCT TTACNTGGCC TGCCCTNGGG GAGGGCCTTT AATATTTCCCT	420

CCCCATTTT

429

(2) INFORMATION FOR SEQ ID NO:1221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1221:

GGCACGAGCC ATAGTGGTNA TCAGTGCCTC TNATGATGAC GTGGGTGAGA ATGCTCGTAT	60
CACCTATCTC CTGGAGGACA ACCTNCCCCA NTTCCGCATT NANGCAGACT CAGGNGCCAT	120
TACATTACAG GCCCCATTAG ACTATNAGGA CCAGGTNACC TACACCCTGG NTATCACAGN	180
TCGGGNCAAT GGNATCNCAC AGAAGGCAGA CACTACTTAT NTGGAGGTGN TGNTCAATNA	240
CGTGANTGGC AATGCTCCAC AATTTNTGGC CTNCCACTAT ACAGGGNTGG TNTCTNAGNG	300
NTGCCCCANC TTTCACCACT GTCCTTCAGT TCTCAGCCAC TTGCCNGGCT GCTNATGCCA	360
ATGAGTCCGT GTNCAGTACA CTNTCCAGAA TGGTGTATAG ATTGGGTGTG GTAGGTNTTT	420
AA	422

(2) INFORMATION FOR SEQ ID NO:1222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1222:

GGCAGAGTGA AGCCTCCTGA CCTCCAATAC GGTGCACTCT GGTGAGGGAC AGTGGGTGGG	60
GTGGGCCAAG GAGGGGCCAC AGGGTGGGGG CAGATGCTGG AGTGTCCCTC ATATGCCTGC	120
AGACACCCGG GAACTACATC TGTGAAGTTC TGCGCCCGGT CTTTCCGCAC TAGCAGCAAC	180
CTTGTCATCC ACAGACGTAT CCACACTGGA GAAAAACCCC TGCAGTGTGA GATATGCGGG	240
TTTTACCTGC CGCCAGAAGG TTTCCCTGGA ACTGGGCACC AGGGCAAGNT TGCAGAGACG	300
GTGGGTTGCC TTGCGNTTTC CCCTGTGAAT TTTNCGGGN AAGGCTTTTN AGGAAGNCCA	360
GACATTTTTT GCAGCCCACC TTGGCAAAAT TTAACCCNGC CTGTTTTTAG GCCCTT	416

(2) INFORMATION FOR SEQ ID NO:1223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1223:

GGCACGAGGN TGGCTTTTGC CTGTAGTCCC AGCTACTCGG GAGGCTGAAT GAGGTGGAAA	60
AATGGCTTTT TTTTTTTTTT NNNGNG	86

(2) INFORMATION FOR SEQ ID NO:1224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1224:

GGCACGAGAA ATTATGGATT CTTTCAAAGA GAAAATGGAG AATATTGACT ACAGCAACGA	60
GGAGCACATG ACCCTGCTGA AGATGATTTT AATAAAATGC TGTGATATCT CTAACGAGGT	120
CCGTCCAATG GAAGTCGCAG AGCCTTGGGT GGACTGTTTA TTAGAGGAAT ATTTTATGCA	180
GAGCGACCGT GNAGAAGTCA GAAGGCCTTC CTGTGGCACC GTTCATGGGA CCGNGGACAN	240
AGTGGACCAG GCCACAGCCC AGATTGGGT CCATCCAAGT TTGTGCCTGN TCCCAATGTT	300
TGAAACAGTG ACCAAGCTCT TTCCCCATGG TTGNNGGNGG TTCATGNTG	349

(2) INFORMATION FOR SEQ ID NO:1225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1225:

GGCAGCCGAG GTGGCAATGC TACACCTCAT TTTTATGCG GGTTTGCCAG GGCAAGCCCG	60
GCACTCGACC GATAGTCAAT GAGGATTATG TCAGCCACCA GCGCACGCNC ACCACCAGAA	120
CCACGACCAG AATCAACCAG ACCCAGTGCT TCAAATGCTG GTCGAGATTG TGCCACCACG	180
GNGCAATCAC CTGACCACCA GCGTAACCAA TAGTGGTAAA AATCAACGCC CAGGCAAATG	240
TGCCGAGNAT TTTCAGCGGC AGAANATTTT CGGCGGCACT GGTGGNAC CATTACGCGT	300
TGGGCCATTC ACCCGAAAGC CTNACTNAAN GGGGTTACCA TGACAAACAG TTACGGNTGG	360

NGTTGGNTNA GTTTTTGN GN CCCGTTTCATT TTGTGCNGNT GTTTTGGGGA AACGGNGTTA 420  
ACATGCCTTG TTTCAGTTAG TTAGATTCTT GCCGTNATNT TTGTTTCAGGC GTTGNACGGT 480  
CNGGCCAGGT TAT 493

(2) INFORMATION FOR SEQ ID NO:1226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1226:

GGCACGAGCC ACAATGGCTG AGCACTTCCT GACGTTGCTG GTAGTGCCTG CCATCAAGAA 60  
AGATTATGGT TCCCAGGAAG ACTTCACTCA AGTNTGGAAC ACACCATGAA AGGGCTCAAG 120  
TGCTGTGGCT TCACCAACTA TACGGATTTT AAGGACTCAC CCTACTTCAA AGAGAACAGT 180  
GCCTTTCCCC CATTCTGTTG CAATGACAAC GTCACCAACA CAGCCAATGA AAACCTGCAC 240  
CAAGCAAAAG GCTCACGAAC CAAAAGTAG AGGGTTGCTT CCAATCAGCT TTTGTGTGAC 300  
ATCCGAACTA ATGCATTCAC CGTGGGTGGT GTGGCAGCTG GNATTGGGGG CNTGNGNTGG 360  
NTGCCTG 367

(2) INFORMATION FOR SEQ ID NO:1227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1227:

GGCANAGAGT TAACGGAGGC AAGTTGGATG TCGGGAATGC TGGGGGGAAN TTTTGGGAAG 60  
AGAACAGGAG CCTGGAAGGC TGAACCTGCA GAAGCTAAAG NACGAGCTGG CCAGCACTAT 120  
GNCAAAAAGT AGAGAAAGCT GAAAACCAGG TTCTNGGCCA TCGGGGAACA GTTCTNAGAG 180  
GCCTCACCAA GNGTTACGN ACCGATTTC TGGAGGAGGC AC 222

(2) INFORMATION FOR SEQ ID NO:1228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1228:

GGCAGAGCTG CAGGGCCCCC AGGAGCATCC CTGNTCACCC CTCTGCNCCC TCCCCACCAG	60
AGCTGAAGAT CCCTGAAAAC GCCAACGTCT TCTATGCCAT GAACTCTACT GCCAACTATG	120
AACTTTGTCC TGAAGNAAGC GGNCCTTCAC CAAGGGAGTG AAAGGTCAAG CCACGGTAGG	180
CCAGCTTCCA CCCTCCCTTC GCATGGAAGC AGAAAGGGAC TCAAGATTGC CAAGGGCATC	240
TTCCTGAGGG GCATCCTCCC AGGGTCTGGC TGGCTGGTTA GCCAAGCACT TATGGGACCA	300
GAGTGGGCCC AGGCCAGTTG GGGGGCCTTT CTTCCCAACT GNNCAGCCCA GGGTACCCCA	360
GATTTCANTT TCANCCCGGA ANTTTT	386

(2) INFORMATION FOR SEQ ID NO:1229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1229:

TAACGGCGTC GAAACCTATT TTNAAGTCTA TGTTAACGGT CAGTATGTGG GTTTCAGCAA	60
GGGCAGTCGC CTGACCGCAG AGNTTGACAT CAGCGCGATG GTTAAAACCG GCGACAACCT	120
GTTGTGTGTG CGCGT	135

(2) INFORMATION FOR SEQ ID NO:1230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1230:

GGCAGAGCGA AGTTTTTTTT TTTTTTTTNA GGNGGTTTTT ATTNAAAGTN CTTNTTTTTT	60
TGGGGT	66

(2) INFORMATION FOR SEQ ID NO:1231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1231:

GGCAGAGNAA CGAACATTTA ATCTGCTGAT TGGCAAGAGA CAAAGACCAA TCCATTTAAG	60
TTTTGATATT GAATGCATTT NACCCTACAC TGGCTCCAGC CACAGGGAAC TCCTGTTGTG	120
GGGGGACTAA CCTATCGAGA AAGGCATGTA TATTGCTGAG GAAATACACA ATACAGGGTT	180
GCTATCAGCA CTGGGATCTT GTTGAAGTC CAATCCTCAG TTGGCCACCT CAGAGGAAGA	240
GGCGAAGTCT TACAGNTAAC CTGGNCAGTA GATGTGNATT GCTTCCAAGN TTTGGTCCAG	300
ACAAGNGAAG GGGGGGCATA TTTGTTCTTT GGGCCAACCT NCCTACTTCC CAGTTTCACC	360
AGTTGGATTC AGAAAATTCA AGCACGTGTG NAGAANTTTN GGNGACA	407

(2) INFORMATION FOR SEQ ID NO:1232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1232:

GGCAGAGGNA CGAACTCATG NAAAGATACT GTCCTAATTC CGTATTGGTC ATCATTGATG	60
TGAAAGCCGN NGAACTTAGG GCTGCCTACA GAAGCGTACA TTTCAGTGGN AGNAAGTCCA	120
TGNATGATGG GAACTCCAAC CTCGAAAACA TTTGAACACG TGAACCAAGT AAATTGGAGC	180
AGAGGAAGCT GAGGAAAGTT GGAGTTGNAC ACTTGTTACG GGATATCAAA GACACGACGG	240
TGGGGCACTT NGTCCCAGCG GATCACAAAC CAGGTCCATG GTTTTNAAGG GGCNTGAAAC	300
TTCCAAGCTT CTGGGTNTTC AGGNGCTACC TGGNAAAAAG TCGCCACAGG CAAGNTGNCC	360
CTTCAACCAC CAGTTCCNTT TACCAGTTGC AGGACGTTTT TCAACCTGTT GCCCAATGTT	420
CAGCTGCAGG GGTTCNTCAA GGCTTTTACC TGANGGCCAT GGCCATTGTG GTAGTTTATT	480
GGCNCGTTAT C	491

(2) INFORMATION FOR SEQ ID NO:1233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1233:

CAGGCCTTTG CGCCTTCATA CTGCACCGAG TTTTGCCCAT CAATGGCTTT NACCACGTCT	60
TGGTAAGTTC ATACGTNAGA ACCCAAGCAT CGATCTGCGA ACTTTAAGCC AGCACAGAAT	120
ATGCACGTTT TGAACAGGGA TGATTTTAAA TCTEGATATA GTCTACGGTG NAACCCCGTC	180
CATCACCTTA TGAGAAAGAT CCCGCTTGCT GTTGAAGAAC TTACGCCACT GTNTTCTCCC	240
CAACTGGGCT GAGCGGCTAA AGAAACCAGA GGATCTCTAT GCGTTGGACA TTGGATTGAG	300
TGCGGTGTTG CAGTTTGTTA CCCNTNGGAA AAGGNNGTTT TAGGGGGGNT AAAAT	355

(2) INFORMATION FOR SEQ ID NO:1234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1234:

GGCANAGNNG GAGTAGGAAA ATCTTGCTTG CTTTCATCAAT TTACAGAAAA AAAATTTATG	60
GCTTNTTGTC CTCACACANT TGGTGTTGGT TTTGGTACAA GAATAATCGA AGTTAGTGGC	120
CAAAAANTAA AACTGCAGAT TTGGGNTACG GCAGGNNCAG GAGCGATTTA GGGCTGTTAC	180
ACGGGGCTAC TACAGAGGTA GCTATCGGGG AGCCCTTNAT GGTNCTAT	228

(2) INFORMATION FOR SEQ ID NO:1235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1235:

AGACTGCCCT CATCCACGAT GGCCTAGCAC GTGGNAATTC NCGAATTGCC AANGCCTTAG	60
ACAAGCGCCA AGCCCATCTT TGTGTGGCTT GCATCCAAC NTGGTGTGCC TATGGTATGG	120
CAAGTTGGTG GTGGCCCTTT GTTNCTNNNC ACCAAATCAA CCTAATT	167

(2) INFORMATION FOR SEQ ID NO:1236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1236:

CCAGGNTTGC TGATTTGGCG AACGGTAGCA ATGATCATCA ATGAAGCCCT TGAATGCGCT	60
TCAAAAAGGC GTGGCCTCTG AACAGGATAT CGATACCGNC ATGGTNCTTG GGGTGAATTA	120
TCCATATGGC CCACTTGCCT GGGGAGCGCA ACTTGGCTGG CAGCGNAATA TTAAGGCTCC	180
TTGAAAATCT ACAGCATCAC TATGGCGAGA AACGCTATCG CCCATGTTCA TTGCTGCGCC	240
AACGGGGTTT NCTGGGAGAG CGGTTATGAA GTCATAAGGC CTGGCAAAT GCCCATGCAA	300
TGTATGAGAA CGATGCCTGC GCCAAAGNTT TGGCNGGACC ATTATCTTCA ATGGATGAAG	360
GCTTTGCTGT TAGTGGACCN GNACCTTCAT TGCACAATGC TTAACGGTTC NTCAAGTTGC	420
CAGGGGGGCA GTATTTTTC TGGGTGATAN NGCTTTGCNA CGCTGAATAG CCAGGGTTGC	480
ACNGTACCAT T	491

(2) INFORMATION FOR SEQ ID NO:1237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1237:

AACCACTGGT ATCACATGGN CATGAACCTAC CGCGGGATGA TCANTATGCT GATCTNCTGC	60
GGTTGTTTCG GGCAAAGCGG TGGCGGCTGG GCACACTATG TCGGCCNGGN AAAAAGTGGC	120
CCCCACAAAC CGGCTGGTTG CCACTGGCCT TTGCGCCTCG ANTGGNAACC GACCACCGCG	180
CCAAATGAAC AGCACCTCGT TTTTCTACAA TTCATTCCAG CCAATGGCGC TTATGAAAAA	240
GTCTCTGCTC CAGGGAGTTN ACTTTCACCG CTGCGCGATG CCATAAAGTT ACAGCGGTCA	300
TCTGATTGAT TTCAACGTTT GNGCCCGAGC TATTGGGCTT GGCTANCTTT TTGNGCCNTG	360
ATTGGGGGGT TAACCCGTTT GGNATTNAAA GTTGAAGCCG ACAAGGCCGG ATTTTTCCTCC	420
CACAG	425

(2) INFORMATION FOR SEQ ID NO:1238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1238:

GGCANAGGTG ACGTGCGNCC AGTACACAGC CCTGAGTTGG GATGTTGAAT TTNTCGATCA	60
CGCCATAGAT GGTATCCAAC ACGCGGCTTA AGTTTTCCAC GTCGTCAGTC ACCGGGTTAN	120
CGCCGATCAC CGCATCGCCC ACCCCGAAGG AAAGCCCTTC GTAGATTTGC GCGGCGATAC	180
TTTGACGTC GTCACGGGTG TCATTTGGCT GCAAACGGGC GCTAAAGGTG CCCGAAATAC	240
CGATGGTGGT ATTGGCCTTT TTGGATTACC GGCATTTTCT TCGCGCCGTA GGATTCAGGT	300
CCGCGTTGGG AGCAAAATCT TTCGTTANCG CCGGGGACCA TTTCCGAGGT TCANCCCTT	360
TGCGGGTNAA AGGCAATGTC GTTCCACGTT GGTTCANCG TTCAGCAACA TATTNAAGGA	420
TTCGTNGATG CTTCCATTTT TAANCTGGTT TAAGGCCTTT GTTAAAANGG TCC	473

(2) INFORMATION FOR SEQ ID NO:1239:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 328 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1239:

GGCANAGGNN NAAATGGATT GATTATGTCA AGNGCCAGG CATGGTAAGG AGCAAAGAAG	60
GTTCACTCTG GACAGCACTA AGGAACTTTG GTTTAGGAAA GAAGAGCTTA GAGGAACGCA	120
TTCAGGAGGA GGCCCAACAC CTCCTGNAG NCAATAAAAG AGGAGGAACG GNACAGCCTT	180
TTGGACCCTC ATTTCAAGAT CAACAATGCA GTTTCCAATA TGCATTTGCT CCATCACCTT	240
GCGGAGAACG CTTTGAGTAC CAGGATAGTT GGTTTTCAGC CAGCTGCTGN AAGTTNACTG	300
NGATGNAAGT NCACATTACT TTGGGGGG	328

(2) INFORMATION FOR SEQ ID NO:1240:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 247 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1240:

GGATCCCCCG GNCNGCAGGA ATTCGGCACA GGTCAAAGNC CACGGCGAGT ACACGATGGA	60
AGCAAACAAG GACTANAAGG ACTATAAGNA CGATGAGCTG CCAGCCAAGG AATGACCCAA	120
ATTCCCCNCT GCAGCCCGGG AACACCCCTG CAGCTGTTTG AAGGGTCGGA GGAACCGCCG	180
CAGTAGNNTA GNACGCCCAA AGTGGTGGAG GAGCAGGAGT GCCANGGNGC ACTACACCGT	240

GTGCCAT

247

(2) INFORMATION FOR SEQ ID NO:1241:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 283 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1241:

GGCANAGGGA CCTTCCCACC TCAGTCTCCC AAGGTGCAGG GATTATAGGC GTGACATCTN	60
TCTGGCACCA GCCCCAGNAG CTTTCAATG AATGTGTTCT ATGTGGGAAG TGGGTATGTN	120
GTGGATTTTT GTAAAGCTTA TCCTNTAGAT TTCTTGAAC CTGNGATGNN ATATCTCTTC	180
TCAGTTTTGG AAAATTCTCA GCCATTATCT CTTTACACAT TTCTTCTGCC ACATTCTTTC	240
TGTTATTNCT CCTTCTGGGG GCTNCAATTT ACANATNACG NTA	283

(2) INFORMATION FOR SEQ ID NO:1242:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 280 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1242:

AGATGAACGA NCAGACTCAG GCGATGTGCT TTATGGCAGG CGCAAACCTCG ATTTTTTACG	60
GTTGCAAACCT GCTGNACCAC GCCGAATCCG GAAGAAGATA AAGACCTGCA ACTNTNCCGC	120
AAACTGGGGN TAAATCCGCA GCAAAC TGCC GTTNTGGGCA GGGGGATAAC GGAACAACAG	180
CAACGTTTTG GAACAGGCGC TGATGAACCC CGGACACCGA CGGNATTTTT ACAACGCGGC	240
ACATTTATGC NGCTGGGCAA GNNGAAANTT TAAACGGGGG	280

(2) INFORMATION FOR SEQ ID NO:1243:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 103 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1243:

NCCGACCNTA ACCATATCGG TAANTTTAAN CTTATCGGCC TTAAGCCACT GCCCAACCAC	60
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ATAGCTGGTC ATAATTTTAG TNAGGCTCGA GGGTTCATT TTN

103

(2) INFORMATION FOR SEQ ID NO:1244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1244:

NATTCTCAAA GGNCTCAAGT TCAACCTCAC GGAGACTTCT TAGGTCAGAA ATTCACCAGA 60

NCTTCCANCA CCTTCCTNCG CCACCCTCAA TTCAGTCCAG GGANTGAGCT CNAGCTGA 118

(2) INFORMATION FOR SEQ ID NO:1245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1245:

TTGGCACCAA AATNCTGCAC CTAACCGTTG NACAGGCACG TGGCTTTAAT GCTGAACACG 60

AATGGAAAAC CNTTTTTTAA TGGTNTGGTT GANTTCATGA CCTCNGGCCC GATANGANGT 120

TTCCGTGNCT GGAAGGTGAA AACGCCGTTN AGCGTNACCG NAATCTGCTG GCGCAACCA 180

ATCCGGCAAA CGCACTGGCT GGTACTCTGC GCGCTGATTA CGCTGACAGC CTGACCGAAA 240

ACGGTTNCCA CGGTTCTGAT TCCGTGCAAT CTGCCGCTCG GAAATTCGCT TATTTCTTTG 300

GCGAGGCGAA GTGTGCCCGN GGACCCGTTA ATAATTTCTG AATNGCCGNT GCAAAGTNGG 360

TTTCCGTGCG GCCAAATTN 379

(2) INFORMATION FOR SEQ ID NO:1246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1246:

AAAGGAACGA CCTGGCTTNT AAGCAGGACG AAGGGCCCCCT AGACGGCAGG CACGGTCCAA 60

AGTCCAGCCC CTAAACNAG GTGGTGTNTA AAGCCTTTTT CCGCTTCTTC CGTGAAGAT 120

TGTGGGAACA TGACTCTTTG TTCCTAACGT CGGGCGAGCN TAAGGAGAGA ACCCTGCAGC	180
GGGAGGCCTT CCGCAAAGCT GTCTCCTCCA ANAGCCTCCG NNACTTCCTG GAAGGTTTTT	240
CATGGAGGAC TTCAAATGTT TTCGGGGGCT TTCATTCCAG GAGCGGGAAG TTGCGNCCGG	300
CAGGTATGGC CAAAGGGTCT GTTTTNNAGG TTCCGNAGGN CCCAGAAGTT ATTTGGGGAA	360
AACAATTTCC CCA	373

(2) INFORMATION FOR SEQ ID NO:1247:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 386 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1247:

TTAATTCANG CGTACCATCG TACCGAAGTA TGCGTCCGGA TCAAAACCAA AGCAGGCACC	60
GTGTTTGGA TATTCGTAGC GTTCCAGGCA GGAAGTTCCG CNAGCTCCTG GNATGGNCTT	120
CACTTAGTTT AGCGGCCGTT TCCAGTGAAT AATCCGGTTT CCGGCGGATG TAACACATTC	180
GGCTGGCGCG CGCTTTCTGG TAGATTCGGG ATTGGGNCGA GTAGCGCAAC CGAAAGCGCA	240
TCCAGCGGCG TTCATCAACA CCACGGGCAG CAACCGATTT TAGGCAATCC TGGGCCACNG	300
ACCATGTACG GTTCAGAAAT CCAGCTTTTG TTTGGTCGTT TTCGGTTTTG CAGGCGGACC	360
NTCCNTCTGG TTTNTTAACG GNTTTC	386

(2) INFORMATION FOR SEQ ID NO:1248:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 428 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1248:

ATCTGGNAAG GCGATAAAAA GCCGATGCAG GGGCGGNAG ATATTCAGGC TCGTCGACTG	60
AAACTAAAGA NCTGATGCCC GATGTGGAAC TGAATGCAGA AGACGCTGGG GGAAATGAAA	120
CGGTGACGCG NNACTACGCG GTAGCGTNAG ACTGCGGTGG CGGCACTTTT AGGCAACANT	180
AACGGCAACC TGGAAACTTT TGATGAATGA CGGGCTGGTG AAGCCGCAAC CTGATGGGAG	240
ATTGTTGGGC TGAATGTCGG CAACTTACAT TGTCGGTGCG ATATTTGGTT GATGATGAGG	300
TGCGGGTGAA ACTNCGNCGG CGGGGGAATT CTGAAATAAT TGCCACGGG GTTGGGCGGN	360



GCCCCCAAAA TTTTGTGCTT TTCGNTAACT GAGAACNCGT TTTGATTNAA TNTTAACCCG 420  
GAAGGCAA 428

(2) INFORMATION FOR SEQ ID NO:1249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1249:

GTTTTNCCTG ACGGGAGANC GACTGCNAGA ATTCAGGAAT ATACAGCAAC GAAGGCTGAC 60  
GTGGATCGAA GGAATCGCC CCGACCATCA CCGGATTTTT AATGCCCTGC CCTTTGGCAT 120  
CGGCAACAG CGCGGCGAGT TTTTCCTGGN AGGGAAGTGT GCGGGCGAAT CCCC GTTCCA 180  
CAGCCGGTTN CATCGANGCG GGCGAAAACA TCCTGAACGT GCGTGAAAAC TGCGGGTANN 240  
GCGGACATTA ANGGA AAAA 259

(2) INFORMATION FOR SEQ ID NO:1250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1250:

TTTGCGTGCA ANGAAACGTG AACTCGCGAA ANTGGNATAT TTGCTAATCT ACTCGCCGCA 60  
TTTTTAATTG ACGACATAAT CCAGCCATCG CTGATTTGCC CCCCCAGAAG TGCCGGATCC 120  
GAAAAGAAGA ACTGAACTCG TTGTGGAGAA TAACAAAAAT GGTCACTCTG AGCTTACAGG 180  
TGGCCATTCG TGGGNACAGT NATCCCTGAA CAGCCTACAA AACGCAATTG AAAGAACGCG 240  
AAGGGCATCG TGCTTGAACG NGGGCACCGA GGCGTCGCAT TGTTCAGAT GGTTC AACC 300  
CTTGAAGTTA AGCGCTTTAT GGGNTAAATT CCCCCGATA TNCCGGTTTG TCCAAGTTCA 360  
NGGATGGGTT AAGGGCANCN GG 382

(2) INFORMATION FOR SEQ ID NO:1251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1251:

GGGCACAGTG TNCTGAGATC TGAGTCAGTA TCATTNATAT AAATGTCCTT CATAATGTTT	60
AGCACAGTGG GTTATCCGTN ANCCCAAGTA TCCTGTGAAT AGTCAAATTG GCTTTGTCCT	120
GTGTTGGGAA TATGGNGGGA TAGTGAAATC CATGTGGTTA TGTCTCTTA TGTGCCGGAT	180
GAAAAAACT GATTAANCAG ATGTGTGTAA TTGCGTTCCC AAGTTCCAGA TAGCAAGGGA	240
TTTATCGAAT CCAGCTCATT TCTGAGTATA CACAGATTCA ANGAAGANTT GAGATATTTA	300
AGAGNTACCN ATATTTGNAA AA	322

(2) INFORMATION FOR SEQ ID NO:1252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1252:

AAGCTTATCG ATACCGTCAA CACCCTGAAA NAAGTGGCTG CCCAGGTTNN CTGAATCAGC	60
AACTGGAAAC TCCCCGCTTC CCCTTCCCGT ACAACACGCC AACCTCTAAA GAAGTGTA CT	120
TGTATCGGGA GATCTTTGAA AGAACTATTC CCGNTTCCAA GNGCCGNTGA AGTGCGTGCC	180
GGGCGGTCCT TCCATCGCTT GTTCTTCCGC TAAAGCGAAT NCGNTTGGGA ATGCAAGCGT	240
TTCAAGAAAA ATGGGACGGT TCCGTCTGGT NCGCGNGGTT GGTGTTCCAC CAGTTCGGCG	300
TATTAGGTTA AGAAATNCGG NAACCGCCCC CGGTGGAATT CCGGGGTCCG GTTACCCAAT	360
TTCGNCCTNT TAGTTGAGTT CGTTTTTACA TTTNCATTGG GCCT	404

(2) INFORMATION FOR SEQ ID NO:1253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1253:

GGCAGAGCCA AAGTGCAGAT ATTACAGGTG TGAGCCACTG TNCCTGTCCA TTTTCTAAGT	60
TATTTTATAA ATAATTAACA CAAGTAAACA ATGAAAAACA ACCTTATTAG AACTTTAAT	120
AAGAATTTAA CCATAGCAAA CCCAATTTTT TTTATCCTGT AAGTTCCTTG GTTTTGAAGA	180

CACATACATA TTCAAAATGA GAAAAAGTCC TTTGGANTAT AATCATCANT TGCTATATAC	240
AAACCTGTAA ACATATACAT TATATAAATC CTGATTTNCC CGGTTTAAAA TGGAATCTCT	300
TAATATGGTC CGGGGGTTAN CCATNANTTC TGGGTTTTTG GCATTTNAAT TGTTCCAAAG	360
GGCCGTATTT TTGGAAACT TTGGATGGGC TAGNATTTT	399

(2) INFORMATION FOR SEQ ID NO:1254:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 500 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1254:

GGCANAGCCA AAGGGNCGGC ACAGCACGGT GCAGCGCTCC AAGTCCTTCA GCCTGCGGGN	60
CCAGGTGAAA GGAGACCTGC GCCGCCTGCC AGAAGACCGT GTACCCCATG GAGCGGCTGG	120
TGGCCGACAA GCTCATTTTC CACAACTTT GCTTCTGCTG CAGACTGTCA CACCAAGCTC	180
AGNCTGGGCA GCTACGCCGC GCTGCACGGG GAGTTCTACT GCAAACCCCA CTTCAGCAG	240
CTGTTTANGA GCAAAGGCAA CTACGNACGA GGGGTTTGGC CGCAAGCAGC ACAAGGAGCT	300
TTGGGCCCCAC AAGGAGGTGG ACCCCGGCAC CAAGACGGCC TGAGGGCTCT TTTAACTTTC	360
CANCCCCTTT NNGGAAGGTC TTGTAGCCGN CAGGGGAAAG TTGGGAAGGA GGTGAGCTT	420
GGGGTTTNTT TGGGGGGNCC AGTTGGNAAG GGGTTAGGGT TTTTCAGGGT AGGGGNCCAG	480
GNAAGGTTTT TTCCAGGATT	500

(2) INFORMATION FOR SEQ ID NO:1255:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 439 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1255:

CGANATGCCG CCACCGCCAC CTGCCCTTTN AGCGCATCTT TNACCCCAAC CACCGCCACT	60
TCGGCAACGN CCGGAATGGC TGGAGATACT CTNTTCAATC TCGCGCGTCC CCAGCCGATN	120
TNCCNGCAAC GTTAAATTAC ATCGTCAGTG NCGCCCGAGA ATAAAGTGAA TAACCGTCAG	180
CNTCACGGAT GCCCCAGTCA AAGGTGGCGT ACACCGNGCG GGAAAACAGC GACCAGTAAG	240
TTTTACAAA GCGGCCGTCG TCGCCCCAGA TGGTCTGAAT ACACCCCGGC GGCAGGGCCC	300

TTCACCACC AGCATCCCTT TTTCGTTGAN GCCAAAGGTT TGCCGGTGGA TTTCATTAAG	360
CAATGCAAGT TATAGNCCTT ANATTGGNAA AACGGGGNTT TCCAAAGGGT TGGNCTTTTG	420
TTCAGACGGG GGAATGGCC	439

(2) INFORMATION FOR SEQ ID NO:1256:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 205 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1256:

CAACAGATGG GTAATGGCAC CAACGAGAGC CTGATGAAAG GGAGGGCGAT CCTCCAGTTC	60
AAATATAAGG TCAGAACCTG CATGGTTTAT ATCAGACATC CCTTCACTCC TTTTAAAGTA	120
AATTTGAATC ATCTGAATTA GTAAAATAAA TTCCACGAA TTTGGGGCGC AGGACGCCTT	180
GAGAACGGCT TATCTCATTT TCGCA	205

(2) INFORMATION FOR SEQ ID NO:1257:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 503 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1257:

GGCAGAGGGA AAATNAAGTA CTCTTTTCAG TTGTGGATCG CAATGATGTC AGCAAAGGGA	60
CATGATGGGA AGGAACCTGT GAAATTTGTA GATTTGCTTG GTGACCATGG GAAACATGTN	120
CAGTCCTCTG TGGGAGTTGA TCAAATGGTG CCTGGGTCTG TCAGTGTACA CCATCCCTTC	180
CATTGGACTG GCTTTGTTGG AAGAAAAGCT CAGATATAGC AATGAGAAAT ACCAAAAGTT	240
TAAGGCAGTG GAAGAAAGCC TGCGTAAAAG AGCTGGTGGA TATGCTAGGT GATGATGGTG	300
TGTTCTTATA TNCCCTCACA TCCACAGTG GGCACCTAAG CATCCATGTN CCTTTAACA	360
CGGGCCTTTC AACTTTGGNT TACAACAGGT GTTCTTTCAN TGNCTGGGT TTGCCNGTNA	420
ACCCCATGCC CATNGGACTG AATGCCAAGG ACTCCTTTAG GCATCCAGTT GTNGGNGTAC	480
CCTTAAGGTC ATTTGCCCCG GTG	503

(2) INFORMATION FOR SEQ ID NO:1258:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1258:

AGNTGAANAN NCCACAACCC TGACTCCCC GACGTCCACC GTGAATCCAC ATCCGCANCG	60
AGACCTCCGT GCCCGACCAT GTGTCTGGTC CCTGTTCAAC ACCCTCTTCA TGNAACCCCT	120
GCTGNCTGGG NTTCATAGCA TTCGNCTAA	149

(2) INFORMATION FOR SEQ ID NO:1259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1259:

AGCTAAAAAA CGTCGCTGCG GTAATGGTGA CAGNGGCANT GTCTCCGTTT GGNACGNCAT	60
GGGCAAACCA TCGATGTGGT GGTTTCTTCC ATGGGAAATG CCAAAGCTT NCGTGGAGGT	120
ACGTTGTTGN ATGACACCGC TTTAAGGGNC GTTGGACAGT CCAGGTGTAT GCGCCTNGCG	180
CATGGGCAAT TATTC'TGGTT GCGGNC'GCA GGAAGCCTCC GCTNGCGNNT ACAGTGT'TTC	240
AGGTTAACCA ACT	253

(2) INFORMATION FOR SEQ ID NO:1260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 489 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1260:

ATATGCCGCA GAAATTTGGT CTGTATGAAG ATCTCACGGT GATGGAGAAC CTCAATCTGT	60
ACGCGGATTT GCGCANGTNC ACCGGCGAGG CACGTAAGCA AACTTTTNCT CGCCTGCTGG	120
AGTTTACGTC TCTTGGGCCG TTTACCGGAC GCCTGGCGGG CAAGCTCTCC GGTGGGATGA	180
AACAAAACT CGGTCTGGCC TGTACCCTGG TGGGCGAACC GAAAGTTT'G CTGCTCGATG	240
AACCCGGCGT CGGCGTTGAA CCCTATCTGC ACGGCGCGAA CTGTGGCCAG ATGGTGCATG	300
AGCTGGCGGG CGANGGATGT TANTCCTCTG GAGTACCTNT ATTTTCGACG AAGCCGAGCC	360

ATTGCCTGNA CGTGTTAATT GATGAACGAN GCGNATTGCT GTTTTCAGGG NNGAACCAAA 420  
AGCCTGNACA CAAACCNGGC CGGACGCAGT TTTTGATGAC CATTACAGG AGGGCAACNC 480  
AAANNTTGC 489

(2) INFORMATION FOR SEQ ID NO:1261:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 69 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1261:

GGCANAGGGA GAAGCAGGAG CTGTCGGGNA GATCAGANGC CAGTCATGGC NTGACCAGCG 60  
NGACCTTAT 69

(2) INFORMATION FOR SEQ ID NO:1262:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 283 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1262:

GGCANAGGAG ACAGGCAGTA TACAAATACT ATAAATACAC TGGAGGAAAA CATAGTGGGG 60  
CTGATTATAG TCGATTTTTG CTCTTTTATT TCCGGTAACA GTAAAACAAC TCTGNATAAG 120  
AAAAGGTTTG AACATGAAGG CAGACCTGAA GCGNGTNAGG NNAGTGAGCT ATGCAGCTAA 180  
CCAGGGTAAG AGTTCCAGGT AGTGGGGATA GCAAGTGCAA AGGCACTATG GNAAAGGNTC 240  
ACATGGNNAG NGGTGTCAGC AAGAAGGGCC ACTGTAGCCA GAG 283

(2) INFORMATION FOR SEQ ID NO:1263:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 279 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1263:

GGCANAGCAA GAAGGCAGGC GAAACAAACC GCCGTCAACA GATCCCAGAC TACCGTACTC 60  
CTCCNANTNT TTNAGAAGGA TCGCTTTCAA GACATTGCCA CCAGGGAACA GCTGGCCAGA 120

GAAGACGGGC CTCCGGGAAG TCCAGGGATT CAAATCTGGT TTCAGAATCG AAGGGCCAGG	180
CACCCGGGAA CAGGCTGGCA GGGTACTTAC CAGGCAGGCG GGCTTGATTG TTGGGCCCCA	240
GGCGGGGTTT TAACCCTGNT TNCCTNGTGG NTCNGTTTT	279

(2) INFORMATION FOR SEQ ID NO:1264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1264:

AGCNTGGGNT ACGACGTGGA GAACGACCGG NAGGTGAGGC CGANTTCAAC CGCATCATGA	60
GCCTGGTCGA CCCCAACCAT AGCGGCCTTN TAACCTTCCA AGCTTTCATC GACTTCATGT	120
CGCGGGAGAC CACCGACACG GACACGGCTG ACCAGGTCAT EGCTTCCTTC ANGGTCCTAG	180
CAGGGGACAA GAACTTCATC ACAGCTGAGG AGCTGCGGAG AGAGCTGCCC CCCGNACCAG	240
GCCGAGTNAC TGCATCGCCC GNTATGGTGT CCATNACCAG GGGCCCTGAA CGCCGTGGCC	300
CGGTGGCCNT CGAA	314

(2) INFORMATION FOR SEQ ID NO:1265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1265:

GGCAGGAGGA GACAGGTCTT AGTCAATTTG GTAAGTTTAT TTTGCCAAAG TTAAGGACGT	60
GCGCCTGCAA CACAGCCTCA GGAAGTTCTG ATGACACGTG CCCAAGGTGG TCTGAGCGCA	120
TTGGNTTTTA TACATTTTAG GGAGATATGA CACATCAATC AATATACGTA NNATGAACAT	180
TGGTTTTGGT CTGGGAAAGG TGGGACAAC TGAACAAAG GCAAGACAAC TGGNAGTAGG	240
NAAGGGAGCT TCCAGGTCAT AGGTAGNTTA AGAGACAAAT GGTTGCATTG CTTTGTAGTT	300
TCTGNTTGGG CCTNTCT	317

(2) INFORMATION FOR SEQ ID NO:1266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1266:

GTCGTTGNTG TTGTTGTTGT TGNGTATGCN GCAGAATTTN ACCAGNTGAT CTTAAAACCA	60
CACAGTGATA ATACAAGTTA CCAGCTATGG TCAAACAGTA TTGAAAAAGA NGATCAAAGT	120
TGGAGGACTC ATATTTNCCA ATTTNAAAGT TGCTTTAANG CTNCTNTAAT CAAGATGCTG	180
TGGTACTGGC ATAAAGAAAG ACATATATGT TGGTGGAATA GAATTGAGAA TCTAGNAANC	240
TTTACATTTA ATNAGTCAAT TGATTTTCCA GNNGAATGCT ATTAAGACGG TTA	293

(2) INFORMATION FOR SEQ ID NO:1267:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 379 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1267:

GGCAGAGGGN CCTCTCAAAG TGCTGGGATC ACAGGTATGA GCCACTGCAC CCAGCCAATA	60
CTGTATATAT TTTTTTTAAT GGACCAAGGC CACCACAATG TGAGCAGAAA GGTCAAATAG	120
TCTGTTATGT GGGAGAAATG TGTACAGTGN ACTTTGTTTT TTAATTTCCC CCAGTTTTCT	180
AGTTTTCTGT TTTAGAAGAC ATGCTGTCAC AATTAACAAC TCTTACTNAA TAAGNACTTG	240
NTCAATTTGA AATGGTCTAT ACCAATTATG NAAATATGGA GGAAAGTTAG GGCATTAGGA	300
CTTACAAGCA CGTACTTCN TCTTAAGTGG CTTAGGATTC CCAAGCTGT NAACANTGCT	360
TTTTTTCAGC TGTTNCCN	379

(2) INFORMATION FOR SEQ ID NO:1268:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 351 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1268:

GGCANAGCGN ACAGGGGGCG CTGTTTTCGT GGAAATCCCC CGGCTGCGAA CCTGGGATCC	60
CTGACCTGGA TCAAGTCTCC GAAGCTGGCA GAGTCCATTC TGCATCACCG GTCTTGGGCT	120
TTGAAGAAGC TAGGAGAAAT TCCGCTTCGG CCATCACGCT ATGGAAAAGT GGATTTTTTTT	180



TTCTTAAGTC AATTTTTTTTT TTTTGAAAAT ATGAGACTTA GTAGGTTTGG GAAGTGGGCT	240
AAAAGAACAT TTGATATTGT AAATTGGACC CCCCCTTTGA AGGTGACAGT GTTTTTCCCC	300
TACTTNAAG CGCCAANTTT TTTTNTGGCA CTATNAAAAG CTATTTACTA N	351

(2) INFORMATION FOR SEQ ID NO:1269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1269:

GGCANAGGGA ACTAGTTCTC TCTCTCTCTC TCCATGACCC CGCAGCTTCT CCTGGCCCTT	60
GTCCTCTGGG GCNANCTGCC CGCCCTGCAG TGGAAGGAAA GGGGNCCCCA GNAGCTNCTG	120
AACACTG	127

(2) INFORMATION FOR SEQ ID NO:1270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1270:

CAGTTTNAGG CGCAGAATAT CTNNGGAGGC GCTGCGCCCC GGTAAAGGTG CCGGAGAAAG	60
TAACGNGGGC GGCGGCAGTT GAACGACGTG ATTCTGCCCN GAATGCCGCA TCACGCTGCC	120
AGGCTTCGNT TTCGCGGTAT TGCTGGTACT CTTCCACTAC ATCANCNAAA GCGTNAAAT	180
GGCGAANAGG NCGTTGGTTC GCCACGCAGC CATGTGCAGT NAAATATTGG CGATCTGGCG	240
GGTAATGGCC GGGAAAACTA AAAGCCATCG NACCAGCAAA TGGTGATAAC GCTGNTTACC	300
ANTACCAGCG GTTTATNCGC CCACCTGTTN TCAGCTGATG AAAGACCATG GTTTTACCGT	360
TATCGACGGG CNATTCTTGT TGCAAATCCG CCTGGTATTA ATGCCTGGGC CATTACCNTG	420
CGGGNTCATG TTTGGTTCNT AGGGTCGTTA ATTTTGGCN ATTCGAACGT TNAA	474

(2) INFORMATION FOR SEQ ID NO:1271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1271:

GGCACGAGAA AGAACGAATT GGCAGCCCTG TCTACACTGG CCCTCTCTCA GGTGCATCAT	60
AACCTATTCC ATTCAGGCTT TTNACTCTCA GCACTTAGGG GCAGTTATGC TTGGCATAGT	120
TTCCAAAAAC TTCCATTTGC CAAATCTAAA AGTCAGTCTT CTGTTCTCAT CTTGAAAATG	180
AATTATTAAA TTATGTATAT TTGGGCGGAG GCACTTGTTT TCCCTTTGAA GTCAGGGACC	240
CCCTGTTTTA TACCCTATGA TTATTGTTAA TGTTTCTGTT TCTCTCAGTT TTAAGACAAT	300
TATCTCCTAT ATTGATGAGC AATTTGAGAG GTACCTGCAT GACGAGAGCG GCTTGAACAG	360
GCGGCACATC ATTGATAATT AGGGTGCATT GTTGCTTTTA CTTTATTTCA CCTTTTGGAC	420
ATGGGTAAGT AATTGTTTAT CGTGGAGAAA TGCTTTACTA CATGGGGTTG TAAGTTTACC	480
CAAAC TGGGG ATTTTAATAT	500

(2) INFORMATION FOR SEQ ID NO:1272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1272:

GGCACGAGAA GAACGACATC AGAGATGAGG ACAGCATTCG TGCTCCTTGC AGCCCTGGNT	60
GTGGCTACAG GGCCAGCCCT TACCCTGCGC TGCCACGTGT GCACCAGCTC CAGCAACTGC	120
AAGCATTCTN TGGTCTGCCC GGCCAGCTCT CGCTTCTGCA AGACCACGGA ACACAGTGGN	180
AGCCTCTGAA GGGCTTCCCC GAAAGTTNTG GGNACCAGGT CCAGGTGGGC ATGGAATGCT	240
TGATGACTTG GGAGCAGGCC CCCACAGACC CCACAGAGGA TGAAGCCACC CCACAGAGGA	300
TGCAGCCCCC CAGTTNCATG GGAAGGTTGG AGGGACANAA GCCCTTTGGG TTCCCCGGGT	360
TTTCAAATTN CTTNNGGTTT TT	382

(2) INFORMATION FOR SEQ ID NO:1273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1273:

GTTCGCCTTC CGCTTTNAGG ATTTGCAACT GTTTTTAACC TTCGGCTTTA AGGATTTCCG	60
CCTGACGGAT CCCTTCCGCT TCAAGAATGT AAGCNCGTTT GGNACGTTCC GCTTTCATCT	120
GCGCGTTCAT TGAAGAGATA AGCTCTGCCG GTGGGCGCAC GTCGCGAATT TNAATACGGG	180
TNACTTTAAT CCCCCACGGG TTGGTGGCTT CATCGACAAT ACGCAGCAGG CGTGAAGTTT	240
GATGCTGTCTG CGCTTGAGAG AGCATTTCTGT CAAGTTCCAT TGAACCCAGC ACGGGTACGG	300
GATGTTAAGT NCATGGTCCA GGTTTGATGG TTCGCCAAGC TTCCAGATTG CTTGACTTTC	360
ATAAGNCNGC GCGCGGGGGG GGTTNAATTC ACCTGGAATT AAAAGGCACA CGGGCGTTTCG	420
ATTGGTNACC GTTTGGCGGT TATCCTTTTC GGGGATAACT TTCCCTGGGG AAGGGGNTAT	480
TCGAG	485

(2) INFORMATION FOR SEQ ID NO:1274:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 439 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1274:

CGGGGGNGAA TCANTTTNTG GAATACTTTG GTGAGGCGCT GTTCCGTGCC GACTTGTGCA	60
CGCCGACGTA GCGATGGGCG ATCTGCTGAT TCACGAAGGC GCGCCATGCA TTGCACAGCA	120
ACATGCGGCA AAAGTNTTTA ATGCCGATAA AACCTACTTC GTTTTAAATG GNACTTCATC	180
TTCTAACAAA GTGGTTTTAA ACGCNC'TGCT AAACACCGGG TGATCTGGTG CTGTTTGATC	240
GCAATAACCA CAAATCTAAC CACCACGGGG CGTTGCTACA GGCTGGTGGC AACACCGGTT	300
TTATCTGGGA AACGGCANTA AACCCGTNTG GCTTTATTTCG GTGGGCATTT GATGCGCACT	360
GT'TTTNNAAG AAAATTTACC CGCNGTGAGT TGATTTCGGGG AAGTTCCAGG GGGGGGGCCC	420
GTTACCCCAT TTGGNCCNC	439

(2) INFORMATION FOR SEQ ID NO:1275:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 509 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1275:

CAAGGGGCGC CACAGCNGAG GGAGCTGGCC GAGGTGGATG TGGACTGGCT GATCGTTTCT	60
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GGTCGCGGCG CAGTGGTGTG CGATAACACC GAATTCCGCG TGGTGAAGTC ACGTACTCAG	120
CNGNAAGCGT ATGTTTTTGC ACCGGCTACG CTGTCCAACA TTTACTACGG TTCCTCGCC	180
GTAACAGCC GTTTCATGTC TTTCGGTGAT GGTGTGGCGC AACTGGGCCG CTCGCTGGAT	240
GTTGATGCCA ATACCAACGG TCAGGTGGTG ATCCGTGGAT AGCGCCATCA ACGGAAGTTT	300
TNAACACGGC TGAAACCGTG GGGCCGATGC GGTGTTTCTC TNAATCGTGC CNTTTNNGGG	360
GNAATAACCG GCANCGTAGN TGATTAACGN ACGAAATACC AGCGCAATCT GGAATNGNCA	420
CTAANTACAA CCGCATGTGG GGGATTACAN TAAACCCGGG CGTTGGGTAA TAAAATGGGT	480
TNNCAAGGGC GAGAAATTAA GGGCAATTN	509

(2) INFORMATION FOR SEQ ID NO:1276:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 362 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1276:

AAAATTGGTC ATCTGTTTGA CTACATCCTG TTTGANTCAG CATGGGTCGG CTATGAACAG	60
TTTATTCCGA TGATGGCGGA CTGTTGCGCG CTGTTGCTGG TTCTTAATGA GAACGATCCG	120
GGTATTCTGG TTACGCAATC TGTGCATAAA CAACAGGCTG GTTTTTNTCA GACTTCACAA	180
ATTCATAAAA AAGACAGCCA CATCAAAGGG CAANAGCGTT ATGTACCGCA CAAACGCATG	240
AACAACGCCT TTNTGAATGC ACGCCTCCAC CAGCCCGTTT CTATCCGCTG TTTGCCGCAC	300
TGNANTATCC AACGCCAAAN TGNCATGGAA GGTGTTTCAGC GGTTCGTAAT NATGTGGGAT	360
GG	362

(2) INFORMATION FOR SEQ ID NO:1277:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 56 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1277:

TTTNTTTTTT TTTTTTTTTT TTTTTTTTTT TTTCNCCAGA TGGNGTCTCT CTCTNT	56
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(2) INFORMATION FOR SEQ ID NO:1278:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1278:

CGGTTCCANA CTGTAATTGG TTTCCATCGC CACTTTGCCA CGCAGCACTT TGCATTTNCA	60
GGTCGCACAG ACGCCGCCTT TGCAGGCATA GGGCAGATCC GCCCCCTGGG GCAATGCCGC	120
ATCGAGAAAT GCTTTCATCG TCGGCATTAA GCACGATTTC CCGATCCCGC CCATCCTGAC	180
GTACAGTCAC TTTTNTCCG TNACTTTGCA CGTTAAACGC TACGTTTGAA CGCGCGTGCC	240
AGGGGTATTA AACCGCTCCA AATGAATGGT TTTTCTGGG CATTCCCAGT GGCTTTTTAA	300
GGCGGTTTTTC CGGGTNCATC CATTCAATCG NCGNCGGGNC CACAAATAAA ATGGCCTCNT	360
CCTTAAAGAC	370

(2) INFORMATION FOR SEQ ID NO:1279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1279:

GGTTTCGCCA GTGAACGAAC TGCTCACCCA TCAGGCGCAT CGNCATATCC ACACCTTTGC	60
GGNTCAGCGG TTCACCNTTN TTACCGATAA TGCGGTTTCTAG CGAAGCGGGA GAGGCTGGCT	120
TCGTTATGGG TGGAAACCAG TTTGCCAGTA AACAGCAGCC CCCAGGTGGC GGCATTAACA	180
AACAGTGACG GGCTACGAAC CAATGTNTGA CTGCCAGTTA ACCGTTGCTG ATTTTTTCGC	240
GGAATTAAAC GCGTCGGGGG TGGGCTTTGT CGGGGAATAC GCAACAACGG TTTCCGCCCA	300
GACACATTCN GCGGCCAAGG CTTTCCTGCG NATTGACCAG CGGAAAAATT CCTGGCAATT	360
AANCCCTTGG GACCATAACC TGGGNGGACC CATTGGGNAT TTTTTTGNAT TACGGCGTTT	420
TTTTCCGGCC CANTTG	436

(2) INFORMATION FOR SEQ ID NO:1280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1280:

TGGCGCAGGC NCTGTTTGCT GATCCGGATN TTCTCCTGCT CGACGAACCG ACCAACAACC	60
TCGACATCGA CACCATTTCG TGGCTGGAAC AGTGCTGAAC GAGCGTNACA GCACCATGAT	120
CATCATCTCG CACGACCGTN ACTTCCTTGA ACATGGTCTG TACCCACATG GCGGATCTGG	180
ATGACGGCGA GCTGCGNTTT TATCCGGGTT NTTGNCGNAT GGAGTACATG ACGGCGGCGA	240
CCCAGGCGCG TGAAACGTNT GCTGGCCGNT TAACGNCAAG ANGAAAGCGC AGATTGNTGA	300
GTTGCAATCT TTGGTTTAGC CGCTTTTAGG GC	332

(2) INFORMATION FOR SEQ ID NO:1281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1281:

GGCCATCCNC TGGGCCTGCA GGTGCATGAN GTCGCTGGTT TTATGCAGGA TGATAGCGGT	60
ACGACCTCGC GGCACCGGCA AAATATCCGT ACCTGCCCTG CACCCGTNTT CTCCAGCCGG	120
GCATGGTGTT AACCATCGAA CCGGGTATCT ACTTCATCGA ATCGCTACTG GCACCGTGGC	180
GTGAAGGGCA GTTCAGCAAG CACTTCAACT GGCAGAAAAT TGAAGCACTG AAACCGTTTCG	240
GCGGCATTTCG TATCGAAGAC AACGTGGTGN TCCACGAAAA CAACGTGGGA AAACATGACC	300
CGGGATCTGA AACTGGCGTG ATGGAAAGCT GGTTAATTCC TGCGGCACCG GTCACGTTTCG	360
TTGGNGAGNT CAAAAAGAGC CGGTTTCATA ACGATGTTGG GNGCATACCG TGGCGTTTTA	420
GGCGGCGAAA GNTTTTTTTT GAATCGGTTC GGGAAGAAAA CCCCNTTNN CCGGAACATT	480
TTTTTTGGGT TGGTTC	496

(2) INFORMATION FOR SEQ ID NO:1282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1282:

TAATGAAGAA AACTCCNGGN TGTGGATNTA CCGCAAGCTN GCGGCGGGC TACTCGGAAT	60
TTTAATGGTA CCGGTGCTCG CGGCCTATAC CACCTATNCT NTGGNAGATA AACCGGCGTT	120

ACGCCAGGCT TTGCGGCTGG ANTTGCNGCC AACATGATCG GCTCCGGGTT TNTCGGCGCG 180  
GTCGTTGGCG GNTTGATANC CGGTTACTT 209

(2) INFORMATION FOR SEQ ID NO:1283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1283:

TACACACAGG CCAAAGAATC CTGGGAGATG GATACCAAAG AAAAATTGGA GCAGGCTGCC 60  
ATTGTCAAAG AGAAGGGAAC CGTATACTTC AAGGGAGGCA AATACATGCA GGCGGTGATT 120  
CAGTATGGGA AGATAGTGTC CTGGTTAGAG ATGGAATATG GTTTATNAGA AAAGGAATCG 180  
AAAGCTTCTG AATCATTTCT CCTTGCTGCC TTTCTGAACC TGGCCATGTG CTACCTGAAG 240  
CTTAGAGAAT ACACCAAAGC TGTTGAATGC TGTGACAAGG CCCTTGGA CTGACAGTGCC 300  
AATGAAGAAA NGCTTGTATT AGGAGGGGTG AAGCCCAGCT GGTTCATGAA ACGAGTTTNA 360  
GTCAGCCAAG GGTGGACTTT TGAAGGAAAG TGCCTNGNAA GTAAAACCCC CAGANTTAAA 420  
GGCTGCAAGA CTGGCAGATC TCCCATGTGG CCAGNAAAAA GGGCCAAGGG NGCACAACGG 480  
AGCGGGGANC CCCAGGATTT T 501

(2) INFORMATION FOR SEQ ID NO:1284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1284:

GGAGCCGGGG AATCTGCGCC ANTTGATGAT CCCGGAACAG CAGAGNCCTG CTGGAGACGT 60  
TTACGCTGTT AGTCGCCAAT GCCCTTNAGC GGCTGACGCT AACCGCCAGC NANGAACAGG 120  
CGCGGATGGC AAGCGAACGT GAACAGATCC GCAACGCCCT GCTGGCGGCG CTTTCGCATG 180  
ATTTACGCAC GCCGCTTACG GTGCTGTTTG GTCAGGCAGA AATCTTAACG CTCGATCTGG 240  
CAAGCGNANG ATCACCCAC GCCCGCCAGG CCAGCGAGAT CCGTCAGCAT GTGCTGAACA 300  
CTACCCGACT GGTGAATAAT CTA CTGGATA TGGCGCGAAT TNCAGTCCGG CGGCTTTNAT 360  
TTGAAGAAAG AGTGGTTAAC GCTGGAAGAA TAGTCGGCAN GCGCTGCAAN GCTGGAACCG 420

GT'TTTNNNTT GCCCNTCATG TTTNNTTNNN CAGAACCNTG AACCTAATNC CAGTTGAANG 480  
GGCCATTNTT NNAACGGGTG CTGATTAATC TG 512

(2) INFORMATION FOR SEQ ID NO:1285:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 485 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1285:

ATTGTTTTTAA AAAAGATTAT ATCTTTACGT CCGTAACCGG AGATTTCCCG CAAAGCCAAT 60  
TTACCGATAA TGAAATATCG TCTTTTATAA GGATATCTAA GATGCGTAAA ACAGTGGCTT 120  
TTGGCTTTGT CGGTACCGTA CTGGATTATG CCGGGCGCGG CAGTNCAGCG CTGGTCAAAA 180  
TGGCGTCCGA CACTCTGTTT ATGCCAGCAA GAATCGTTGG TCATCGATCG ACTGGAATTG 240  
TTGCACGACG CCCGCTCCGC GCTCGCTAAT TTGAAACGCT TAAACGCGAT TATCGCCAGC 300  
NTTTCGCCAG AAACAGNAAG TGGTGAGCGT TGAGATTGAA CTGCATNAAC CCTGGGATTT 360  
CGAAGAGGTC TACGCCTGTC TGCATGATTT CGCCCTGGTT AAGGAGTTTT CAGCCAGAAA 420  
AGGAAGANCT TTTATTTTAC NTCACCACCG TTACCCAGTG GNNGCNATTT GCTGGTTTTN 480  
GCTGG 485

(2) INFORMATION FOR SEQ ID NO:1286:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 334 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1286:

TATAAGCAAC GTGATGCCCT TGTGGGTCGC GCTTTTAAA GATCCCCTAC TTGNNGANCT 60  
CTTCAAACGT TGGCAGTTCA GGAATNGCTT CCCGCGACTG GGCATACAGA TGCCGNATCC 120  
ACTCTTCCTG GGTACGGCCT TCAGTAACT GTTGCTCAAC GCCAAGACGT TTNCCANTT 180  
CGCTGGTTCA TTTCATAGAT GGTCTTACAT TCAAAGCGCG GNTTAATCAC CTGATCGTTG 240  
AAAATCACGT AAGGCNTATN CCCGAGTAT GCATCCAGCG NAAAGTCCAT CTGTTNCGGA 300  
AGCGGTNCAG TCAGGCAGCA GGATGTCCAG CATA 334

(2) INFORMATION FOR SEQ ID NO:1287:



(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1287:

TGACTCACTG CTTTGCAACA CTCCGTGCTC TCATCGCCAA GTTTGGAGAC TTACTCTTCG	60
AAGTGGAGGT GGAACAGTGT TTCGACCTAT GTCACCAAGT CCTGCANCAC TGCAGCAGCA	120
GCATGGGATG TCACCCGGAG ACAAGCCTGT GCCACCCTTT ANCTCCTCAT GAGGTTTCANT	180
TTTGGGGCCA NCCAATAATT TTTCAAGNTT AAAGATTCAA GTAACCCAAG GCCCN	235

(2) INFORMATION FOR SEQ ID NO:1288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1288:

GGCACGAGGG AGCCGGCGCC CGNGGAGCA AGAGGAGGAG GAGGAGGAGA GGTCGGAGCC	60
GTCTCCAGGA GCCCTTAGAG ACCGAGTCCC GGCGGCGACG GCGGGGCAGC GCACCGGCAG	120
GCGGNTTCAT TCCACTTAAA ACCTGAAAAC ATTGGACCAC ACAAAGTCTT ACTGATTTCA	180
GGTAAAAACA ATAATTGAAG ATGTCCAGCA AAACAGCAAG CACCAACAAT ATAGCCCAGG	240
CAAGGAGAAC TGTGCAGCAT TNAAGATTAG AAGCCTCCAT TGAAAGAATA AAGGTTTCGA	300
AGGCATCCAG CGGACCTCAT GTCNTACTGT GAGGAACATG CCAGGAGTNA CCNTTGCTGA	360
TAGGATTACC AATTTTCAGAA AACCNITTCA GGNTAAAAAA ATTGCTNCTN TTNTATGGAT	420
NGAGAAACAG TTCTTGGCTT TTTCCCAACA NGGCAATTAT GAGCAGTCTT GAGGGGTTTA	480
CNTCAGTTAT TTGGTAACCA TGTT	504

(2) INFORMATION FOR SEQ ID NO:1289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1289:

AGCGAGGCAC GCAGCCTACT AGGTGTGGCG GCGACCCTGG CCCCAGGGTTC CCGTGGCTAC	60
CGGGNGCGGC NAACCCGCGC GNGAGCCGAA ACGCCCGGTG GNCNAGACCC CGAGGACCTC	120
	120

(2) INFORMATION FOR SEQ ID NO:1290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1290:

GGCAGAGCTT CACAATAGAA GTGGAAAGGG CCCTGAGAGT NTTGGATGGT GCAGTCCTTG	60
TTCTCTGTGC CTGTTGGAGG GGTACAGTGC CAGACCATGA CTGTCAATNG TCATTGANGG	120
CGCTACAACG TTCCGTTTCT AACTTTTATT AACAAATTGG GACCGAATGG GCTCCAACCC	180
AGCCAGGGNC CTGCCAGCAA ATGAAGGTCT TAAACTTAAA TNCATAAATG CAGCGTTTTA	240
TGCAGATACC CATGGGNTTT NGGAGGGTAA ATTTTAAAG GTNTTGTTAG GATCTTTATT	300
NGAGG	305

(2) INFORMATION FOR SEQ ID NO:1291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1291:

GGCAGAGGNC GCTTCCTGGG CCGCTTTGGT CTGCAGCCCC AAAAAACCAA ACTNNTTGGG	60
GCAACCACCC TGCGCCTTTT TAACATTCCG CAGCGCTGCA GAGAGGGACA AGGCCCTGCG	120
CCGTTTTGCA TGGTGCCCTC TGGGAAAGGC CGCCCACTCA GTGTGCGCCT GTCCCCGGCC	180
CAAGGGCAGC CCCATGGCCA GGAGGAGGCG ACAGGAGGGT GAGAGTNAAG CCACCAGTGA	240
ACACGAGTGG CCGACGTGGT GACCCCTCTA TGGACAGTGC CCTATGCTGA GCAGTTGAGC	300
GGNAGCAGCT GGAGTNCGAG CANGTGCTGC AGAAATTGCC AAGAAATCGG GAGCACCAAC	360
CTGCCTTGTT GCCTGGTTGT TGAGCAAGGC ACAAGCACAA CAAGGCTGTN NCCGTTGAGG	420
GGGTCAGNCT TANCCCNCAA TT	442

(2) INFORMATION FOR SEQ ID NO:1292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1292:

AAAAAATGGG ACCTCGGCGA CATCCTCGGC GCGAAAGGTA AGCTGTTCAA AACCAAAACC	60
GGCGAACTGT CTATCCACTG CACCGAGTTG CGTCTGCTGA CCAAAGCACT GNGTCCGCTG	120
CCGGATAAAT TCCACGGCTT GCAGGATCAG GAAGCGCGCT ATCGTCAGCN TTATCTCGAT	180
CTCATCTCCA ACGATGGAAT CCCGCAACAC CTTTTAAAGT GCGCTCGCAG ATCCCTCTCT	240
GGTATTGCGC ATTCCATGGT GAACCGCGGC TTTATGGAAG TTGAAACGCC GATGATGCAG	300
GTGAATCCCT GGCGGTGCCG CTGCGGTNCC GTTTANTCAC CCACCNTAAC GGGTTGGATC	360
TTNGACATGT TACCGCGTTA TCGGGCCGGA ACTGTAACTT CAAGGGTTTG GTGGTTGGTG	420
GNTTCGAGCG TGTATTCGAA TCAACCGTAA NTTTCGTAAAG AGGTNTTTC GTANGTN	477

(2) INFORMATION FOR SEQ ID NO:1293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1293:

TTAATGGTAC CGGTGCTCGC GGCCTATACC GCCTATTCTN TGGCAGATAA ACCGGCGTTA	60
GCCAGNNTTT GCGGCTGGAC TTGCCGCCAA CATGATCGGN TCCGGGTTTC TCGGCGCGGT	120
CGTTGGCGGN TTGATAGCCG GTTACTTGAA TGCCTGGGT GAAAAATCAC TTGCGTCTTA	180
GCAGTAAAT TCAATGGATT CCTGGACTTT TTATCTCTAC CCGGTGCTCG GTANTTGGGA	240
GCGGGCAGTC TGATGCTGTT TGTGGGTGGG GGAAGTGTTC GCCTGGGATC AATAACTCGT	300
TTAACCGCCT GGCTTGAACG GTCTTTTCAG GAAGTAAACG GGCTGTTTGC TTGGGTGNCC	360
ATTCTCGGTT TTAAGGGGTT CCCTTTGAAC CTTGGAGGGG CCATGAATAA AAGCCGTAA	420
GCANTTCTGC CCGGGGGNAA TGGGGAACGG GGTTTAAGGN CCNTATGCCA TTTGGGCTCC	480
GTNAAAA	487

(2) INFORMATION FOR SEQ ID NO:1294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1294:

AGCTCAATCC CGNCNCCGAC AAGACCCAGC GGNTTGGTGC CGGACTGTNG CGATTTTCCG	60
TCCTNTTGCT TCGCGACCAA AGCCAGGCAG TGTTCAGCAC GTCGTGGGCG ACCNNGNCCT	120
CTCAAGTCGT CCGTGGTATT ATCACCCGNA CG	152

(2) INFORMATION FOR SEQ ID NO:1295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1295:

GGCAGGAGCC GGCNTCCCCC ATCCCCCGGT TCGGACCGNC GAGCGCCGGC TCTCCCCCTCC	60
CTGAGCACCG ATCCCAAGTT CCAGCTAGAG AAGGTGGGCG GCACGCAGCC CGGCGGCCCC	120
TCCCAGCTCC CAGCGATTG AGAGGGAAGA TCTGATCTCC TAGAATTAGA GTTGGTACAG	180
AAACCATTTC AGCTCCAAAA ATGTTGGAGG AAGATATGGA AGTCGCCATA AAGATGGTGG	240
TTTGTAGGGA ATGGAGCAGT TGGAAATCA AGTATGATTC AGCGATATTG CAAAGGCATT	300
TTTACAAAAG ACTACAAGNA AACCATTGGA GTTGATTTTT TGGAGCGGCC AAATTCAAGT	360
TTAATTGATG ANGATGCAGA CTTATGTTAT NGGGCACTNC AGTCAAGGAG GAATTTTGNT	420
GCAATTACAA AGGCCTACTT ATCCGGGGAG CCCAGGCTTG TGGTGCTCGG TNTTCCTNTA	480
CCACAGGTAG GGGATT	496

(2) INFORMATION FOR SEQ ID NO:1296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1296:

AGCGGTTCAT CCCCTTCCGG CGTCAGAGGA AAAGGTTAAT TTCTCTCCCA CCACCTGGGT	60
TTCGACGATT TGTCCGTTGT CCATAACCGT TACCCGCTGG CAAAAGCGTT CTACCAGGCG	120

TGAATCGTGG GTGAATGAAC AGGCAGGCGG TGCCAAACTG TTNNTGTAGC TTTTTCAGCA	180
GGCGAATGAA CACCCGCCTG TGAACACGAG ATCAAGGTTA GAAACGGCTT CATCCAGAAT	240
CAGTAGTTTC GGTTCGACCT TCANCGCGCG ACCAGGCAGA CGCGCTTGTA GCTGGCCGCC	300
GTTTAACTGC GGTGGGNCTT TNTNGAGAAC GCTGTTTATC GAGATCGACC GNCTTCAGNA	360
NTTTCGTTGG CGGGCGNCAT TTGTTCCGGA TTTTTCCTAA TGATTAGCAA GTTGGCGCAT	420
CGGTTACAGN AGNTTTCGG GAAGGTTTTT CGGGAATTCA GGGGTTNTGG GNT	473

(2) INFORMATION FOR SEQ ID NO:1297:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 351 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1297:

GGGGTAATAC AGGCCAGACC ATTCTTGCCG TTNATGTTCA GACCGTCGGA ACCGCACACA	60
CCTTCACGGT AGGAGCGGCG GAANGACAGG CTGGGATCTT TCTCTTTTAG CTGGATAAGC	120
GCATCCAGCA GCATCATGTC GCGACCTTCA TCCGCTTCCA GGGTGTAATC CTGCATACGC	180
GGANATNCAT CAACATCCGG GTTATAGCGA TAAATTNANA AACTCGAGTC TCATTTTCCT	240
GTCTCCGCAT TAGTTAAGTA CGGAATCTTN GGTGCGGGAT TGCCNGGGCG GCATTTTCGG	300
GTTTCCCATG TTTGAACGTT TTCGGNGGCG TTCANNGGAT TTCCCGAACT T	351

(2) INFORMATION FOR SEQ ID NO:1298:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 357 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1298:

TGCATAGTCT GGCAGGATCG CTGGATGTNG CCGATCGCCA AATGGTGGA ATCGTCNGCG	60
GGCTGATGCG CGACTCGGGN ATTCTGAATN CTCGATGAAC CTACCGCCTC GCTTACCCCT	120
GCGGAAACCG AACGCTTGTT TAGTCGCTTG CAAGAGCTGC TTNCTACTGG CGTGGGTATT	180
GTTTTTATCT CGCATTAAAG TGCCGAAAAA TTCGCCAGAT TGCCGNATCG AAATTAGCGT	240
GATGCNCGAG CGGGAACCAT CGCCTTNAAG GGGGCAAAAC CAGCGGAACT GTTCTNACCG	300
ACGACATTTA TTTCAGGCCA TNCACCCAG CGGGTAGNGG GAAAAATCGG TCTTNTG	357

(2) INFORMATION FOR SEQ ID NO:1299:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 458 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1299:

GGCANAGCCT GATCCGACCC CGTCCCGCNG CGCGCCCGNC AGCCATGAGC TCNACGCATT	60
GCAACAAGGG CCCCTCGTAC GGGCTGTCGG CCGAGGTCAA GAACCGGCTC CTGTCCAAAT	120
ATGAACCCCC AGAAGGAGGC AGAGCTCCGC ACCTGGNTCG AGGGACTCAC CGGCCTCTCC	180
ATCGGCCCCG ACTTCCAGAA GGGCCTGAAG GATGGGAACT ATCTTATGCA CACTCATGGA	240
ACAAGCTACA GCCGGGCTCC GTCCCCAAGA TCANCCGCTC CATGCAGAAC TGGCACCAGC	300
TAGAAAACCT GTCCAAC TTC ATCAAGGNCA TGGTCAGNTA CGGGCATGAA CCTGTGGACC	360
TGTTTCGAGGG CCAGGAAGT TTTTAGAGTT GGGAACATGA NGCAGTTGCA NGTGTTTTTT	420
TTTNGNCCTG GGTGGGAAG GNCAAGATTA AGGGGTTG	458

(2) INFORMATION FOR SEQ ID NO:1300:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 71 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1300:

GGCAGAGCAA CAAAGGAGCC AAGGGNGACC GAGGCTTGCC TGGNACCCAG AGGCCCCCAG	60
GGNAGCTCTT N	71

(2) INFORMATION FOR SEQ ID NO:1301:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 348 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1301:

TTNGCAACCA CGATTTTCGC GTCGGTTGGG TTTTCCAGCA GGTATTCTGC CAGCAGTTGC	60
TTCATCTCCT GTTCAACCGC CGATTTCACC TCAGAAGAAA CCAGTTTGTC TTTGGTCTGG	120

GAGGAGAATT TCGGGTCCGG CACTTTCACG GAAACAACCG CAATCAGGCC TTCACGCGCA	180
TCGTCACCGG TGGCGCTGAC TTTGGCTTTT TTGCTGTAGC CTTCTTTGTC CATGTAGGCG	240
TTNAGGGTTA CGGGTCATCG CCGCACGGTA AGCCTGCCAG GTGAGTACCG CCGTNCACGT	300
TGCGGGATGT TGTTGGTAAA GCAGTNAGAT GTTTTGCNTG GGANGCCN	348

(2) INFORMATION FOR SEQ ID NO:1302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1302:

GGNAGAGCGG GATCAGAACA AGTACAAGGA GGCTGCCCAC CTGCTCAATG ATGCTCTGGC	60
CATCCGGGAG TAAACACTGG GCAAGGACCA CCCAGCCGTG GCTGCGAACA CTAAAACAAC	120
CTGGNCAGTC CTGTATGGCA NGAGGGGCAA GTACAAGGAG GCTGAGCCAT TGTGCAAGCG	180
GGGCACTGGN GGTTCTGGGAG AAGGTCCTGG GCAAGTTTTC ACCCANATGT GGGCCANGCA	240
GTTTAGGAAA NNTGG	255

(2) INFORMATION FOR SEQ ID NO:1303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1303:

GGCAGAGGAG GAAGGGGTCT CGTCGGAAGG CGCTGGACGG GGGTGACCGG GAATCGGGNA	60
CAGGGACAGA GATAGGGACA NGGACAGGTC ATCCAAGAAG GNCCGNCCCC CCAAGGAGTT	120
CGGCGNCTTC CTCAGGG	137

(2) INFORMATION FOR SEQ ID NO:1304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1304:

GGCANAGGTA AACAAAGGGTG AACCTGGTGT GGTGGTGCT GTGGGCATGA CTGGTNCATC 60  
TGGTCCTAGT GGACTIONCCAG TAGTGAAGGG GTGCTGCTGG CATACTGGT AGGGCAANGG 120  
NAGTTAAAGG GTNAACCTGG T 141

(2) INFORMATION FOR SEQ ID NO:1305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1305:

GCATATTGTT GCGGTTAGTN AGGCAGTCCT GGAACNNCGN CGGCGCTTTC TTGAAATCCG 60  
CTGGTTAAGN CACCGGCGTC GCTGGCGAAT CTGGTATTAC TCGGTTGGTT ACTCGGCGTG 120  
CAATATGCCC GTGCGNCATA AATATNTNTA GTGGTCGGCA ATATCCTCAA CATTGTGCTG 180  
GATGTCTGGC TGGTGATGGG GCTGCATATG AACGTGCAGG GCGCGGCGCT GGCGACGTTT 240  
ATTGCGGAAT ATGCAACATT GCTGATTGGT CTGCTAANGG TCGTAANAT CCTCAAATA 300  
CGCGGAATTT TCCGGCGNAA TGCTGAAAAC TGCCNTGGCG AGGNAACTTN CNTTGGTTTG 360  
NTGGGGGTTT AACCGGATA TCAAGCTGCG TTCNCTGTTG TTGCAANTNG TTTCGGGGG 420  
ATCANCTACT TGGGGCCNAC TGGGGGGTGC CTTATCNTTT TAACGGGTT 469

(2) INFORMATION FOR SEQ ID NO:1306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1306:

GGCANAGCGT TTGCGNAGGC TGTTCACCG CCCTGGGAGG CAGCAGCTTC TTCGAGAAGG 60  
AATGGAGCCC NNTTTTGCCC CGAGTGCTAC TTTAAGCGCT TCTCGCCAAG ATGTGGCTTC 120  
TGCAACCNGC CCATCCGACA CAAGATGGTG ACCGCCTTGG GCACTCACTG GCACCCAGAG 180  
CATTTCTGCT GCGTCATTGN GGGGAGCCCT TNGGAGATGA GGGTTTCCAC GAGCGCGAGG 240  
GCCGCCCCCTA CTGCCGNCGG GACTTCCTGC AGNTGTTTCG CCCCAGGTTG CCAGGTTGCC 300  
AGGCCCCATC TTGGTTAACT ACATCTNGGN GTTCAGGGNT TCTGGGACCC GGANNTTTTC 360  
GTTTNCANGG NAATGTTTGG GGCCTTTTTN GGGGGGNATT TTTTNGAGC AANAAGGCN 420



CCCTTTTGG AGAAACCATT TCCAGGAAGA AGGGGTGTT TTGGNCAAGT TTGGGTCCCC 480  
TNTAANC GCC TTTGTT 496

(2) INFORMATION FOR SEQ ID NO:1307:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 200 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1307:

TCCGGTATGT NCAAGCTGG TTTNCTGGG GACGACGCTC CTGAGNTGTG TTTCTTTCCA 60  
TCGTCGGGTG CCCNAGNTAC CAGGGCGTCA TGGTGGGGCA TGGGCCAGAA GGACTCCTAC 120  
GTGGGNACG AGGCCAGTG GCAAGCTTGG CATCCTGACC CTGNAAGTAN CCCATTGAGC 180  
ATGGGNATCG TTAACCAACT 200

(2) INFORMATION FOR SEQ ID NO:1308:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 477 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1308:

CCGCAGTTTC GCTTCGGCGA GNGTGTGTG AACCACTTAG CGTCCGTTGG ATCAGCGCAT 60  
CCAGCTGCGG GTCATTGAGT TGTTTCCACC ACTGCGCCTG AGNCCAGCCG GAGCTGCANA 120  
GAATGAATAT CGTCGGCCAG TTTGAATTTG TTCCGGTTTG AGCTGTCAGT GGCATAGGGG 180  
CAGCGCGGGT TAAAGCAGGC AGCCGTTTCGG GCGGTTTCGTA CTTGCCGGGA ACGACACCTG 240  
GCAACGACGC CAGACGTTCT TTGTCCTGAG CAAATTCTGG CAGCGCACGC AGCAATGCCT 300  
GAGTATAACG GGTGACGCG GCGCATGGTA AGATGGCGTG CCGCATTCAC CGGTTTTCCA 360  
CCAACTGGGC TTGCATAACA TCACGATGAT TTTANTGTTG CCCGTTTCCG NCAACAAGGC 420  
CAGTTCATGG GTAATTAAAC ANCAGGGCCA GTTNTTTTTC TGGTTTNAGT TCCCACA 477

(2) INFORMATION FOR SEQ ID NO:1309:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 489 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1309:

AGCCACCAGN GCTGGGACGC GCGGGCANGG CGGCGGCGGC GGCCCTCCGG CAAAGCGAAG	60
GCTGGNAGNT AGGAGAAAAGC GGTCATCAGT ACCTCTCAGA TGGTTTAAAA ACCCCCAAGG	120
GTCAAAGGAA GAGNTGCACT ACGNNGTTCC AGATAGTCCA AAAACTCCAA AATCTCCCTC	180
AGAAAAACG CGGTATGATN ACGTCTCTTG GTCTGNTCCA CCAAGNAAGT TCATTTTCAGC	240
TTCCTGCAGC CAGTTCACCC GATGGGGTAT TGGNATTTGN AACAAGGTCA GNCAGNNGTG	300
CTNAAAAGTG CAAAAGAGGN AGGTTTTTTG NTTATNCACC AACGTTTTGG TAAGGNCTNC	360
CACCTGNNTT AAGAAGTAGT TNTAAAAACA ACGTNCCAAT GGGTGGGGTT GCATTCTGTT	420
CTGAGGTTGG GGGNATGTTT NGCCCATTTT CAAGGTCTGT TCAAAGGAGT NACCCGGTTC	480
AGTCAGGAG	489

(2) INFORMATION FOR SEQ ID NO:1310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1310:

TTTTTCTGG GCGGCCGCTG CGACACGGGA CTGACTTNGG GATGGGAAGT GGAGTNCCCG	60
GAGCTGCTAC CGTGGCGGCG GCGCTGTGAG GAGCAGCCAG GGGGAGGCAG CTGCGGCTCG	120
CCNNTGAAGT ATCCGGGAAA GCGCCACCAT GGGGCTCCGT GAAGAAGAGC ACCAAGAACC	180
CCCCGTTCT CAGCCAGGGA ATTATCCTG CAGAATCATG CGGACATCGT CTCCTGCGTG	240
GGGATGTTCT TCCTGCTGGG GCTTGTNTTC GAGGGAACAG CAGAAGCATC CATCGTGGTT	300
TCTCACTNTT TCAGCACANT GTTGTCTGTA CCCTGCAGCA GAGGGAACAA GCCACGGGGT	360
TCAAAGNCCC CCTNTTTTTT ATGGTGTTC AAGATTNNGG CCACGGTTTT TTTNTTACAA	420
GGTGGTGGGC AATCATNTT CATGNCACAT TTCAGGAATA NGTGTTTGGN TAAATTAAC	480
AAGAGAATGC	490

(2) INFORMATION FOR SEQ ID NO:1311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1311:

GGCACGAGGT TGGGCTCCCG CTGGAGTNTG CGTTGGGGGC GGACCAGGAG CGGTGGTCTC	60
NAGGGAGGTC GAGGCTGGGG CTCCCACCCG GATTTGGAGC AGGGTCGCCG CGGCCAGCT	120
GAACCCGCCG GCNTTTGTAC GTTGTGTGCC CACTCAGGGA GCCATGGACA ACTGTTTGGC	180
GGCCGCAGCG CTGAATGGGG TGGACCGACG TTCCCTGCAG CGTTCAGCAA GGTTGGCTCT	240
AGAAGTGCCT GGAGAAGGGC CAAGAGGAGG GCGGTGGACT GGGCATGCCC TGAAGCNTC	300
CCAAAGGCTG CATGGGGGTC CTTGCCCGGG AAGTGCCCCA CCTAGNAGAA ACAGCCGGCA	360
NCCGGCCCCG ANCGGTTTTT CCCGGGGGNA AAGAGAAGAG AGACCCCAA CCTTTAGTGN	420
TTTCCTTTCA GAACAATGGC TGAATTCAT GGATTNTATT TCAATTCANT NTGGGAATA	480
NTANTTCATT GTGGCC	496

(2) INFORMATION FOR SEQ ID NO:1312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1312:

GGCTGCTGGG TCACGGCGAT TCGCCGCCAA CCGTACCCGC TGGTACTGCG CGACTGNTTN	60
AACGCTTAAC CGCTGCGCAT GAAATCAGGN ATATCGACCG TTTGCTGGAG GTGCTGCATG	120
GCAACGGTTA ATAAACAAGC CATTGCAGNG GCATTTGGTC GGGCAGCCGC AACTTATGA	180
GCAACATGCA GATCTACAGC GCCAGANTGC TGACGCCTTA CTGGCAATGC TTNCACAGCG	240
TAAATACACC CACGTTACTG GACGCGGGTT NTGGANCTGG CTGGNTGAGC CGCCATTGGG	300
GNAACGTTCA CGCGCAGTGG GCG	323

(2) INFORMATION FOR SEQ ID NO:1313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1313:

ATGGCGATAT CGGCGGCGAG ATCGNGATCC GCATCATCGA AAACGATCAG CGGTGATTTA	60
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CCGCCCAGTT CCATGGTCAC TTCTTTCAGG GAAGAGGCCG CCGAGTTAGC CATCACTTTT	120
TTGCCGCTGG NGACACCGCC GGTAATAATGA AACTTTTGGC AATGCCCCGA TGCTCGGTCA	180
GATAATTGCC CCGGTNTNCG GGGCCCAAGN CCNGGCAACA AGGTTAAATT ANG	234

(2) INFORMATION FOR SEQ ID NO:1314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1314:

CAGGAAAGAC TATGGAACGG AGCGTCANCG TCGTTTATC AATGCCGAGA ATATCCAGCC	60
ACTGCTGCAC CAGTTTTTGC TGGCGATCCG AAACGGCCTG ATAAATGCCA ATCGAATCAA	120
AATAGCCAGA AAGAATCACA TTACGCACGG TAGTCTGAAC CCGTAATCC AGATGCAAAC	180
TACTGCTGAC GTAACCGATA TGCTTTTTGN TATCCAGAT GGTTTCGCCG CTGCCGCGAC	240
GTACGTCCGA AAAAGCGTCA AATCGTTGCT GTTAACCTTG CGGATGATNC GNCAGTTAAC	300
CAGGGTTAAT AAACGTGGNT TTTTCCNGCA CCATTGGGC CCGACAATTT GN	352

(2) INFORMATION FOR SEQ ID NO:1315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1315:

GGCACGAGCT GCGGCGNCAG NAGCAGCAGC AGCAGCGNGN GGNAGAGGNG GTGGCGGCGG	60
GGTGGACAGC ACGGCCGAGG CTGCCAGAG GCGCCTCCTC CACACCCCCC GCTGCGGCAG	120
CACCGNGAA CAGATTTTTT AAAAAATGGA TTTGGCCAAC CATGGACTTA TTCTACTGCA	180
ACAGTTAAAN GCTCAGCGAG AGTTTGGTTT CCTGTGTGAC TGCAAGGTTG CAGTCGGGGA	240
TGTATANTTC AAGGGCACAG TAGATNCAGT TACTTANCTT CATTGCTACC AATTAACCTT	300
TANNATGTTG TTTGTA	316

(2) INFORMATION FOR SEQ ID NO:1316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1316:

TGTCACTGGT CCAGTCTCGG AAGGCAGGAA TCACTTCTGC AATGGCTACA CGCACTTCTC	60
TTAAGGACGA NGAGCTGAAA TCCCACGTNT TTAAGGAAAC CCTGCAGGCC TTAATCTACC	120
CCATTTTCGTG CACCACTCCT CATAACTTTG AAGGTCTGGN NGGCCACTAC CCCAACCTAC	180
TGCTATGAAG TGTGAAGGNC CTGCTCTGGG GCATTGTCCG GCAGGATGNC GCCTGCAGCG	240
AAATGTGGAG TCAAGTGCCA TGNGAAGTGC CAGGTATCTG GTTCAATGNT GGACTGNCTG	300
CCANCGGGNT GNANATAAGA GCTGTGAAAC ATGGAGCTGA GGGACCGGTA CCCAGAACNT	360
NNNCNTGGGC CNGGAAGGNA CCGCATGGAA GATCCGAGTG GGGAATTAAN GNCAGAGATN	420
NTTTGNAAAG TTTTTCGGG GANTNTTTTC ACAGTGGAAC AAAGTTGCCC NGTGNCAGTA	480
GNTTG	485

(2) INFORMATION FOR SEQ ID NO:1317:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 100 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1317:

GGCAGAGCTC GGCNAGANAG AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	60
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AANAAAGNNG	100

(2) INFORMATION FOR SEQ ID NO:1318:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 502 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1318:

GGCANAGAGA AGGAGAAGGA GGAAGTGGAC AGGGGCTGCC GCGAGTCCAA GCGCAAGGTG	60
GCCGAGTGCC AGAGGAACT NAAGNGCTG GAGGTGGCCG AGGGCGGCAN GGCAGAGCTG	120
GAGCGCCTGC AGGCCGAGGN CACAGCAGCT GCGCAAGGNG GAGCGGACTG GGAAGCAGAA	180
GCTGGAGGAG ATGCGCAAGA AGGAGAAGAG CATGCCCTGG NAACGTGGGA CACGCTTCAG	240

CAAAGACGGC TTTCAGCAAA GAGCATGGTT AATTACCAAG CCCGAGAAAG TACGGTAGGA	300
GGATTCANAG GAGGTTGAGG GGAGCAGAAA CACAAGACCT TTCTTGGGAA AATTACGGGT	360
AAACAGNTTC AAGCATTTTG GGCATGTTTT CGCCGTTGGG GTTGACAGCC AAAATTACCT	420
TTCAGACAAN TTCCACTTGT TTTTCGAGGA GACAGCCCTT TACCTGGTCN TTTGGTGCTT	480
TGACCTAGAG TTGGAGGGAA TT	502

(2) INFORMATION FOR SEQ ID NO:1319:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 50 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1319:

GGCAGAGTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTNT TNAAAANAAA	50
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(2) INFORMATION FOR SEQ ID NO:1320:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 256 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1320:

GGCACGAGCC ATGATGACGC CCACGGGNNC TTCCAGTACG ACCATGAGGC TTTCTTGGA	60
CGGGNAGTGG CCNAGGAATT CGACCAACTC ACCCCAGAGG AAAGCCAGGC CCGTTTGGGG	120
CGGATCGTGG ACCGCATGGN ACCGCGCGGG GGACGGCGAC GGCTGGNTGT CGCTGGCCGA	180
GCTTCGCGCG TNGTTTCGCA ACGACGCAGC AGNGCACATA CGGGNNTCGG TGAAGCGCGG	240
CCTGGGACAC GTACGA	256

(2) INFORMATION FOR SEQ ID NO:1321:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 403 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1321:

GGGGTAATAC AGGCCAGACC ATTCTTGCCG TTCATGTTCA GACCGTCGGA ACCGCACACA	60
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CCTTCACGGC AGGAGCGGCG GAANGACAGG CTGGGAATCT TTCTCTTTTA GCTGGATAAG	120
CGCATCCAGC AGCATCATGT CGCGACCTTC ATCCGCTTCC AGGGTGTAAT CCTGCATACG	180
CGGANATNCA TCCAACATCC GGGTTNATAG CGGATAAATT GAAAACTCGA GTCTCATTTT	240
CCTGTCTCCG NATTAGTNAA GTACGAATCT TCCGGNGGGA ATGNCCGGGC GCATTTNCGG	300
TTCCATGTTT GACGTTCCGN GCGTTCATGG GNTTCCGAAC TCTGGGCAGA TACAGGGNAN	360
TGGGCACANC CATTTTTTCA TCATCAAGAT TCGGGGAAGT CGA	403

(2) INFORMATION FOR SEQ ID NO:1322:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 471 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1322:

GGGGTAATAC AGGCCAGACC ATTCTTGCCG TTNATGTTCA GACCGTCGGA ACCGCACACA	60
CCTTCACGGC AGGAGCGGCG GAANGACAGG CTGGGATCTT TCTCTTTTAG CTGGATAAGC	120
GCATCCAGCA GCATCATGTC GCGACCTTCA TCCGCTTCCA GGGTGTAATC CTGCATACGC	180
GGANATGCAT CAACATCCGG GTTATAGCGA TAAATTNNA AACTCGAGTC TCATTTTCCT	240
GTCTCCGCAT TAGTAAGTAC GAATCTTCGG CGGGAATGCC NGGNCGCATT TTCGGTCCA	300
TGTTGACGCT TCGGGGCGTC ATGGGTTCCG ACTCTGGNCA GATACAGGGA GTGGCACAGC	360
AGTTTTCATC ATCAGTTCC GGAAGTCGAA GCGGTTNTGG CGCCAAGGTT TTTCGTANGG	420
AATTTTGCAG AACAGCNTTG CNTAGGCGTT TCCNTCAGTT ATCCATTCCA G	471

(2) INFORMATION FOR SEQ ID NO:1323:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 429 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1323:

GGCANANAGA AAGATCCACG ACTTGGCCCT GGAGCTCTAC ACGCAGAGAT CGCTGCTGGT	60
GATGGGGCGG GGCTACAACCT ACGCCACCTG CCTGGTAAGN AGCCCTGAAA ATTAAAGAGA	120
TAACCTACAT GCACTCAGAA GGCATCCTGG CTGGGGAGCT GAAGCACGGG CCCCTGGCAC	180
TGAATTGACA AGCAGATGCC CGTTNATCAT GGTCATTATG AAGGATCCTT GCTTCGNCAA	240

ATGCCAGAAC GCCCTGCAGC AAGTTNACGG CCCGCCAGTG GNCCCCCATT TNTACTGTGG	300
NTCCAAGGGA CGATNATTGA AAGTTTCCCA AGTTTGCCTA TTAAGNCAAT TCGAGGTTGC	360
CCCCACATTG TGGGAANTGC CTTCCNGGGG ATTCTGAGGC GTTGATTTCG GTTGCNATTG	420
NTGTTCCCTT	429

(2) INFORMATION FOR SEQ ID NO:1324:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 494 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1324:

GGCACGAGCN CGCGTGGNTC GCGCACACGC AGCAGCGGCA CATACGGGAC TCGGTGAGCN	60
CGGCCTGGGA CACGTACGAC ACGGACCGCG ACGGGCGTNT GGNTTGGGAG GAGCTGCGCA	120
ACGCCACCTA TGGCCACTAC GCGACCGGTG AAGANTTTCA TGACGTGGAG GATGCAGAGA	180
CCTACAAAAA GATGCTGGCT CGGGACGAGC GCGGTTTCCG GGTGGCCGAC CAGGATGGGG	240
ACTCGATGGC CACTCGAGAG GAGCTGACAG CCTTCCTGTA CCCCAGAGAG TTCCCTCACA	300
TGCGGGACAT CGTGATTNCT GAAACCCTGG AGGTCTTGGA CAGAAACAAA GATGGCTATN	360
TCCAGGTGGA GGNGTACATC GCGGATCTGT ACTCAGCCGA GCCTGGGGAG GAGGAGCCGG	420
CGTGGGTTCA GACGGAGAGG CAGCANTTNC GGGACTTNCG GGATCTGAAC AAGGGTTNGG	480
CACCTTGATT GGGA	494

(2) INFORMATION FOR SEQ ID NO:1325:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 160 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1325:

GGCANAGCGG CAGANCANCC ACACAGAGAT GGAACATGAA GTGGCTTGCT TTGGACATCA	60
CCCCATTAGG TAGACAGCAA TGGACTGTCG CCTCTTTGTN CCATTGGCCT CTGGGACGGT	120
ACATCTCGNN CTCGTGATCT TGAAAGTTGC CCTNTTTTGN	160

(2) INFORMATION FOR SEQ ID NO:1326:

- (i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 343 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1326:

GGCANAGGCA AGAGTGTCTG GAACAGGNTC GGCTGCTTGG CTTGCTGATG CCATTTAGGG	60
CATTTNGTGG TGTAAGTTC AAATGGAGCA TTGACCTTCA AAAGNGAGTG ATAGAATCTG	120
GGCCAGACCA GTTGAATGA CAATGAGATA TACCAAGTTT ATTCCCTCCTG AATTATCACA	180
CACCTCCTTA TCTCACTGGC TGAGGCANAG GTAACCTACC ACCGATTGAA GGCCACAGGA	240
TGAAGTTTCT GGTGTTGGCT ACTGGATGGG TTGTGGGAGA CTGATGTCAN GGGGCAGGNT	300
GTGGTTAGGA TTNTGGGTGA GTACCTAACT GGGCATGGNA TNC	343

(2) INFORMATION FOR SEQ ID NO:1327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1327:

ACGAGCAGGC TATTCTTTGG AGAAGGTATT TGGGCTTCAA TTNAAGGAAA TTGATAAGAA	60
TGNCCANTNT TACANTCTTA TCAGCACCTT AGAGCCCACT TATGTCAGGN CATTCTCGGA	120
ACGNNCTAAG GTACTCACCC AAGCTGGGTC TGCTCATGGT GGCTTGCTTA AGCATCATCT	180
TCATGANNTG GTAAATCGGT CCNGTGGAGN CTGTCATGTG NGGAG	225

(2) INFORMATION FOR SEQ ID NO:1328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1328:

GGCAGAGACT GACCACAGCC CATGAGCAGT TCAAGGCCAC CCTCCCTGAA TGCCGACAAG	60
GAGCGCCTGG CCATCCTGGG CATCCACAAT GAAGGTGTCC AAGAATTGTT TAGACCTACC	120
ACGTGCAATA TGGCGGGCAC CAACCCCTNA CACAACCATC ACGCCTCAGG AGATCAATGG	180
CAAATGGGNA CCACGTGCGG CACTNGTGCC TCGGNAGGGA CCAAGCTCTN ACGGAGGAGC	240

ATGCCCCGNCA G

251

(2) INFORMATION FOR SEQ ID NO:1329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1329:

GGGNGAATTT CAACAGNCAA CAAAAGAACC TTTCAGTGAG CNGTGCNGCT GCTTCTNTGG	60
CCAGTTCACG CTCTTCTGTA TTGAAAGACT CGGAATATGG NTGTTTGAAG TTTCCACCAA	120
GATGTANGTT TGATCATCCA GATGCAGATA AAACACTGAA TCACCTTATA TCGGGGTTTG	180
AAAANTTTGA AAAGNAAATC AACTACAGAT TCAAGANTAA GGCTTACCNT CTCCAGGCTT	240
TTACACATGC CTCCTACCAC TTACAATACT NTCACTGNAT TGGTTNACCA GCGCTTTAGT	300
AATTCCTGGG TNGATGCGAT TT	322

(2) INFORMATION FOR SEQ ID NO:1330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1330:

AGTTGTTCCG AGGTGACACA GTGTTGCTGA ANGGAAAGAA GAGACGAGAA GCTGTTTGCA	60
TCGTCCTTTC TGATGATACT TGTNCTGNAT GAGAAGATTC GGAATGAATA GAGTTGTTTCG	120
GGAATAACCT TCGTGTACGC NTAGGGGATG TCATCAGCAT CCAGCCATGC CCTGATGTGA	180
AAGTACGGCA AACGTATCCA TGTGCTGCCC ATTGATGGAC ACAGTGGTAA GGGCATTACT	240
GGTAAATCTT CTTNCGAGGT TATTACCTTT AAGCCGTNAC TTTCTGGGA AGCGTTATCC	300
GACCCCATCC GGNAAAAGGN GACCATTTTT TCTTNGT	337

(2) INFORMATION FOR SEQ ID NO:1331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1331:

TGCAACAAAT GGTTTATAAC CTGCCGCCAG ACATTACGCT GGTGAAAGCC ANAGTCTTGC	60
TGATATGAAN CCGCAGTGNA TAACTTCTAC ACCGCCGAAA AACGCTGTGC CTGAATGCAC	120
CGCGTAATCC GTTCCGTGGC GTGAAAGCTG TGCAAACCGA NTAAACCGAT AGAACCTGTT	180
TATGCTAATC GCTTCTTTGA ANGTATTAAG CGAAAAGCAT TCAGCCAGAG CACGCTGATG	240
CGTTTACTTT CCAGCATCAG TGGGCAAGGC TGGGGGCAAN CAGCCCGANG CGGCGGAAGT	300
TTTANCGGTT AGCGCCAANT TAAAAGGCGT TACGGGTAAT GGAATTGTT GCGGACCN	358

(2) INFORMATION FOR SEQ ID NO:1332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1332:

GGCAGAGCAA CCACGGTGTC GCAGGCCAAG GNAGTNCTGA GCGCCGAGCA GCTGCCAAGC	60
GAGGAGGTGC ACGCCGGCCT GGGCGAANCT GCTGTCCTCA CTCAGCAACT TGACGGCNCG	120
CAACGTGAAC CTGGATGCTG GGCAGCCGAC TGTTCNCGGA CCCAGCTCAN TAAGCTTTCG	180
CTAATGAACT TCNTGNG	197

(2) INFORMATION FOR SEQ ID NO:1333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1333:

CNTGGTNAAC CTGCTCCATN AAACAGGTCC GTNAAAATNT TTAATGTGCG CAATGGAAGG	60
GCAGATCCTT ATCGCCGACC TCAGGGGTCA TGAAGGTCC TGTTTGGCAA GTGGCCTGGG	120
CTCACCCCAT GTTACGGCAA CATCCTGGCA TCGTGCTCCT NTGAACCGGA AATCATTATN	180
TGGAGANAGG AAAACGGCAC TGGGAAGAAG AGCCACGAGC NGGGGGGACA CGANTCCTTC	240
ATTGAAANTC GGTGTGCTTG GG	262

(2) INFORMATION FOR SEQ ID NO:1334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1334:

CTCTGGAAGC ATTACTTCCA GANTNNCCCA GGGTCTTATT TTTTGGTAG ATAGCAACGA	60
TCGTNAAAAN TTTCAGGAAG TAGCAGATGA CCTGCAGAAA ATGCCTTCTG GTAGGTGNAT	120
TTGAGNAGAT GGCAGTCCTG CTGACTTTTT NCAAAACAAAC AGGNTTTGNC CAAATGCTAT	180
GGCCATCAGT GGAAATG	197

(2) INFORMATION FOR SEQ ID NO:1335:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 57 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1335:

GGCACAGGNA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AANNANN	57
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(2) INFORMATION FOR SEQ ID NO:1336:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 379 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1336:

GGCCCCGTCC CGCCGCCCGC CCGCCAGCCA TGAGCTCGAC GCAGTTCAAC AAGGGCCCCT	60
CGTACGGGCT GTCGGCCGAG GTCAAGAACC GGCTCCTGTC CAAATATGAC CCCCAGAAGG	120
AGGCAGAGCT CCGCACCTGG NTCGAGGGAC TCACCGGCCT CTCCATCGGC CCCGACTTCC	180
AGAAGGGCCT GAAGGATGGT AACTATCTTA TGCACACTGC ATGGAACAAG CTACAGCCGG	240
GGTCCGTCCC CAAGATTCAN CCGGTACCAT GTCAGNAACT GGTCACCAGC TTAGTAAAAC	300
CTGTNCCAAC TTTCATTCAA GGNCCATGGT GCAGGTTGGG GGATGNAACC CTGTGGAACC	360
TGTTTCNAGG NCCAAGAAC	379

(2) INFORMATION FOR SEQ ID NO:1337:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1337:

GGCACGAGGA CCCGAGTTCA CCAGCATCCC TGCCTGCTAC TGGTGGGCTG TNATCACCAT	60
GACGACGGTG GGCTATGGCG ACATGGTCCC CAGGAGCACC CCGGGACAGG TAGTGGCCCT	120
GAAGCAGCAT ACTGAGCGGC ATCCTGCTCA TGGNCTTCCC AGTCACCTCC ATCTTCCACA	180
CCTTCTCCCG CTCCTACCTG GAGCTTCAAG CAGGAGCAAG AGAGGGTGAT GTTCCGGAGG	240
GCGCATTCCT CATCAAAACC AAGTNCGCAG CTGAGCGTGT CCCAGGGACA GTNAACATCT	300
TGTTACGGAA GTGACCTNCT NCGGNACACC AG	332

(2) INFORMATION FOR SEQ ID NO:1338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1338:

GGCAGAGCCA GTNTCCGCGC CTCCACCCAG CTCAGGAACC CGGGAAACCC TCTNTTGACC	60
ACTATGAAGC CTCCCGTCCA GCCGCGCGTC CCGTGTCCCG GGTCTTCGG GCTCCTTGTC	120
CGCGCTGCTC GGCTGNCTGC TCCTGCTGAC GCCGCCGGGG CCCCTCGCCA GCGNCTGGTC	180
CTGTCTCTGC TGTGCTGACA GAGCTGCGTT GCACTTGTTT ACGCGTTACG CTGAGAGTAA	240
AACCCCAAAA CGATTGGTAA AACTGCAGGT GTTCCCCGC AGNCCCCGCA NTGCTTCCAA	300
GGTGGGAAGT GGTAGCCTT CCCTGAAGAA CGGGGAAGCA AGTTTGTTTT GGACCCGGAA	360
GNCCCTTTTT TTAAAGGAA AGTGCATNCC AGNAAATTTT TGGGACAATT GGNAACAAAG	420
AAAAAATTGG GTNAACCAAA AAAGG	445

(2) INFORMATION FOR SEQ ID NO:1339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1339:

GGCAGAGGGN AGCTCTTGGG GAGCCCGGAA AGCAGGGATC TCGGGGAGAC CCNGTGAATN	60
CAGGACCCCN TGGAGACTCT GGTACAGCCA GGCCCCAAGG GNAGACCCCG GNCAGGCCTG	120
GTTTCANCTT ACCCAGGACC CCGAGGNGCA CCCGGTAGAA AAAGGCGGAG CCCGGTNCCA	180
CGNGGCCCCG AGGGAAGGCC NAGGCGAACT TTGGTTTGAA AGGAGAACCT GGGTAGGTAA	240
AGGAGAGAAA GGTAGAGCCT NCGGTATTCC TGTTTCCCCC TGGTGNAGCC AGTTACCTTC	300
GGGGGGGCCA AGTAGGTAGT TCCCANGGAC CTCGNAGN	338

(2) INFORMATION FOR SEQ ID NO:1340:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 417 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1340:

GGCANAGTGA ACGCCACCT GCCGTTTGCT GTCATTGGCA GCACAGAAGA ACTGNAGATA	60
GGCAACAAGA TGATGAGGGC GCGGCAGTAT CCTTGGGGCA CTGTGCAGGT TGAAAACGAA	120
GGCCCACTGN GAACTTTNTG AAAGCTGCGG GAGAATGCTG ATTCGGGTCA ACATGGGAGG	180
ATCTGCGGGA GCAACTCCAC ACCCGGGCAC TATGNAGCTG TATCGCCGCT GTANCTGGNA	240
GGAGATGGGC TTCAAGGACA CCGACCCTGG ACAGCAAACC CTTCAGTTTA CAGGTGGACA	300
TATGNAGGCC AAAAGGAACG AGTTCCTAGG GGGGAANTCCC AGNAAAAAAG AAGAGGNGAT	360
GNGGACAGTT GTTCGTTCCA GCGAGTTCAA AGNGGAAAGG AAGCGGGTTT CCAAAGG	417

(2) INFORMATION FOR SEQ ID NO:1341:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 279 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1341:

GGCANAGNAA ACACCCCAT ATCAAAATGG TGATGGAAAG TGGGGACTGG ACTGGTTGGT	60
GGAGACCTTN AGGTGCTGGA GAAAATAAGA TGGAATGATG GGCTGGACCA ATACNTCTG	120
AACACCTCTG GAGCTCNAAC AGAAATGTGA AAGGAAATGT AATNCTGATN CGGTGTTTGC	180
ATTCCAGTTG CGCAATCCTG TCCACAATGG CCATGNCCTT TTTGAATGCA TGACACTCGT	240
CGNAGTTCNC TNAGTAGAGG GGGCTACAA CACCCGGTT	279

(2) INFORMATION FOR SEQ ID NO:1342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1342:

GGCANGAGGG ACAGCTAGCC CTGCTGCCCC GCTCCACTGT GCTTCTGCCC TTGGCCTGGG	60
CTGCTACGTG GCTGCCGCTG ACATCCAGGA CCTGGTCTCT TGCCTTGCCT GCTTAGAAAG	120
TGTTTTTCAGC CGGTTCTATG GCTTGGGGGG CAGCTCCACA AGTCCTGTGG TTCCTGCCAG	180
CCTGCACGGC CTGCTCTCTG CTGCCCTGCA GGCCTGGGNA TTGCTGCTCA CCATCTGCCC	240
TAGCACCCAA ATGNAGCCAC ATCCTTGACA GGCAGCTGNC CCGGCTGCCC CAGNTNCTTG	300
TGCCAGTGGA AAGTNTGAAC CTGCGGATNG TTGCCGGTGN AAACATTGGC ACTGCTCTTT	360
GAAGCTTGCC CGGGAACCTN GAGGAGGGAT TTGTTTTTAG GAGGACATGG AGGNCCTTTG	420
CAATGTTCTG GGAATTTGG GCCATTGANA NTAACAATAC CTTGNCAAGG TTGATTCGTT	480
GGGGGCAAGG TTNTA	495

(2) INFORMATION FOR SEQ ID NO:1343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1343:

GGCAGAGGGC TCTGTCATTG ATTATNAACT GATTGACCAA GATGCTCGGG AATCTCTATG	60
AACGCTGGAG TGAAGAGGAA AGGAACTGAN TGTTCCCAAG TGGATCAGCA TCATGAACCG	120
ANCGGANGGN CCCACCTCC AGAAAGTATT TGAATAGSTA CAAGAGTTAC AGCCCTTATG	180
AACATGTTGG GAAAGCATCA GGGAAAGAGG TTAAAGGAGA CCTGGGAAAA TGCTTTCCTG	240
AACCTGGTTC ATGGCATTCC AGAACAAGCC CCTGTGNTTT GCTGATCGGC TGTATGACTC	300
CATGGAAGGG NCAAGGGGAC GCGAGATTAA GGTCCNTGAT TCAGAATTCA TGGTCTTCCC	360
GCATTGAAGT TGGNCCTGTT TGGAAATTTA GGTCTGGATT TCAAGGGNAA GTANGGGCAA	420
TTCCCTGTAC TTTTATNTTC CNGCAAGGCA	450

(2) INFORMATION FOR SEQ ID NO:1344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1344:

GGCANAGCCC CTTTNTTGAA GCCAAGAAG AGTTTGCTCA TAAGACCCTG GCAATGGATG	60
TNATGAAACC CCGGAGAAAT GATCCTTTGT TGA CTGTCCT TACTCAGGAG AGTTATGTAC	120
TGTGGNAAGA TGTAGAGACC ATAATCAGTG GAACCACTTA CAGTGGCTTC CCAGTGGTGG	180
TATCCCGGGN AGTCCCAAAG ACTTGTGGGC TTTGTCCTCC GAAGAGATCT CATTGATTTC	240
AATTGGAAAA TGCTCGAAAG AAACAGGGTG GGGTTGTTAG CACTTCCATC ATTTATTTTC	300
ACGGGGCATT CTCCTCCATT GCCACCATAC AATNCACCCA TTNTAAAGNT TTGGGAANAT	360
NCTCGG	366

(2) INFORMATION FOR SEQ ID NO:1345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1345:

GGCAGAGTAA AAGCAGACAA CCAGAGGCTA AAGGNTGAAA ATGGGGCCTT GATCAGAGTT	60
ATAAGCAAAC TTTCCAAATA AAAAAAAAAA AAGCAGCANG NAATGGTGTT GCACATATTA	120
GTAACCCAGT GGAACCATAN TTNGTN	146

(2) INFORMATION FOR SEQ ID NO:1346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1346:

GGCAGAGCNA GGNGCCAGTC GTGTGAGTCC AATCCTAACC TGGGCTATCC CTGCAATCAT	60
GTCATGCTCT CCTGCTGTGA AGGGTGAAGA GCCTCTCATA GTACCTGAAG GTTCGCCGAC	120
CTCCAGAGNC CGCAGNTGCA CCACGGAGAG TTTCAGAGGC AGAGATGGCG GGCCGAGAGC	180



TCGNTTCACT GGGCACAGAG GCCGAGCTGC CGAACAGNCT GCCGGGCGAT GTACCAGGAT	240
GAGTGCCTTC TCCTNCCGGG GNGAGCTGTG CCAGCACCTT TGGCATCAAT AATTGTGGGT	300
TTTTTACCAT GTGGCTGGTT TTTCCTGGGT TTTTCAATGG CAGNACGNTG GGCCGCAATT	360
NTNCGNCCA	369

(2) INFORMATION FOR SEQ ID NO:1347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1347:

GGCAGAGGNA GGGGAGGCTC CAGCCCTCGG NAGTAAATAT CTTCCCTTCC AACCTGGTGT	60
CAGCAGCCTT TCGCTCATAC TCTACCACCT ATGAAAGAGA GGAATATCAC CGGAACCAGG	120
GTGAAGGTGC CCGTGGGGCA GGAAGGTGGA GGGGATGAAC ATCCTGGGCC TTGGTAGTGT	180
TTGCNATCGT CTTTGGTGTG GCGCTGCGGA ACTGGGGGCC TGAAGGGGAA GCTGCTTNTC	240
CGCTTNTTNA ACTCCTTTNA ATGAGGCCAC CATGGTTCTG GTCTCCTGGA TCATGTGGTA	300
CGNCCCTGTG GGCATNCATG TTTCTGGTGG CTGGCAAAAT TCTGGAGATG GAGGATGTGG	360
GTTNATCTTT TGCCCGCCTT GGNAATAACA TTTGTGCTGC CGTTGGTNAA GGCATCCNGG	420
GNTCC	425

(2) INFORMATION FOR SEQ ID NO:1348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1348:

GGCAGAGTG GAGGCCTTTA ACTTTAACGA GTACCAGCCA GAAATGCTCG AAAAGTTCCG	60
GAACATGCNC NGCAGCACCC CTACGTCCTC ACGGAGGACA CCCTGAAAGG TCTACCTGAA	120
NCAAGTTCAG ACAGTCCTCG CCGGACAGNG TGAAAGGTGG TCATTNNATT TTNCTGNTGG	180
AGCAGACGGA GAATCTGGCT GATTACACA GNGGCATCTG AGAAACCTCC GCCAAGAAAG	240
GAGTCCGTGC CCTTGAATCC TGGTGGGCCT TGAAACGANN TGGTTCAACT TGGAAGCGGC	300
TTAATGCATC TGGNGTTTGG GNGAGGGTTT ATGTNTGA	338

(2) INFORMATION FOR SEQ ID NO:1349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1349:

GAACCCACTN AGGNGACACC AATCTTNGAC TTCCAGATGG AACATGACAT CNATAAAAAG	60
GNAAGTGAT GGCATCTATA TCATAAATCT CAAAAGGACC GGGAGAAGNT TCTGCTGGNC	120
AGC	123

(2) INFORMATION FOR SEQ ID NO:1350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1350:

GGCANAGCCT GGNTTAAANG GACACAATAG ATTTCAAGGT CTACCTGGTA TCGCTGGTCA	60
CCATGGNGAT TTATGGTGCT NGTGGTTCCG TGGGA	95

(2) INFORMATION FOR SEQ ID NO:1351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1351:

GATACTCTAA CCGTTTTAGT AGTCGCAGCC TCGAAATGAT AGACGAAATG CTCCACCTGT	60
AAGANCAGAA AATCGTCTTA TAGTTGAGAA ATTTATCCTC AAGAGTCAGC TGGGCAGGTT	120
TGTTGAAATA CAGTTTTGAA GTTATTTTGN ATGTGGCTTT TAAAAAAGT TTANTGGGTA	180
GCTCAATGTT GTATTGTTTT ATTAAANGTA GTTTTGAANT TAATGGGTTT NATGGG	236

(2) INFORMATION FOR SEQ ID NO:1352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1352:

GGNACGAGGT CTGGCTCCCG TCCCCGCAAG CAACCACCCC GGAAGCACAC TCGTNCCTGG	60
NCTGTCCTGA AGCTGCTGCT GCTGCTGCTG CNATTTGGTG TGGCGGGAGG GCTGGTTGCT	120
TGTGGGGTGA NAAAGCTGCA GCAGCACCCC CTCTGCNACC AGCNTGAAAC ACCATCTTAT	180
GAANAATGNG GGTCCAGGGT CTACGCCGCC ATNAGATTCC TCCAGTGGGT CCTCCAAACC	240
GAA	243

(2) INFORMATION FOR SEQ ID NO:1353:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1353:

AAGGAACCTC TGAGAACTT AAGGTTGACA GNTNTNTCCA GCCCTNNACC TGCCTAGTCC	60
TGGGCCCTGG CCCTTTTTTT TGGTGAAGGG TCTGCTGTGC ACCATCCCCC ATNCCTAACG	120
TGGGCCCACC TGGCCTACAA ATTTCGGGGT GAGNGGTGTT TAAGNCAGGT GCGGAGGGT	180
TTCCAAGGGA CCGAAANGTG GTTTTTTCAA CCNTNTG	217

(2) INFORMATION FOR SEQ ID NO:1354:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 321 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1354:

GGCACGAGCG GACCTTCATC ACCATTGGAG ACAGAACTT TGAGGTGGAG GCTGGTGA	60
TGGTGACCAT CTCAGAACTG GGCCGTGGAG CCTATGGGGT GGTAGAGAAG GTGCGGCAGG	120
CCAGAGCGGG CACCATCATG GGNCGTGAAA GCGGATTCCG GGCCACCGTG NAACTCACAG	180
GAGCAGAAGC GGCTGCTTCA TGGGACCTGG NACATCAACA TGCGCACGGT TCGGACTGTT	240
TTCTAACACT GNTCACCTTC TNACGGGGTC ACTTATTTCA GAGAAGGGTG GACGTGTGGG	300
ATCTNNCATG GNAGCTTCAT G	321

(2) INFORMATION FOR SEQ ID NO:1355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1355:

CGGTTGCGCA ATGGGNGAAT ACTTCCGTGA CCGCGGTGGA AGATGCGCTG GATCATTTAC	60
GATGACCTGT CTAAACAGGC TGTTCGTTAC CGTCAGATCT CCCTGCTGCT CCGTCGTCCG	120
CCAGNNGAGA GAGGGATTCC CGGGNCGAAC GTTTTCTACC TCCACTCTCG TCTGCTGGAG	180
CGTGCTGCAC GTGTTAANCC GGAATACGTT GAAGCCTTCA CCAAAGGNAG ATGGGAAAGG	240
GGAAACC CGG TTCTNTGNAC CGCACTGCCG ATTATCCGAG ACTCAGGCGG GTGACGTTTC	300
TGCGTTCGTT TCCGACCAAC GTAAATCTTC CATTANCGAT GGTTTCAGANC TTNCTGGGAA	360
ANCAAAC TGT TTCAAGGCCG TTATTTTCGTC CTGNGGTTTA ACCCGGTTAT TTTCCGTATN	420
CCGTGTTTGG TGGGTGCAAG NAAAGNCCCA GGTTTCATGGA AAAAAATGTT CCGNGGGTAT	480
TCCGTA	486

(2) INFORMATION FOR SEQ ID NO:1356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1356:

GGCANAGGGA TACACTCCCT TGATGGAAGC TGCCCGGGAA GGACATGAAG AAATGGTGGC	60
ACTACTCTTA GCACAAGGAG CAAATATAAA TCCCCAGACA GAAGAACTC AAGAACTCC	120
TCTTACTTTG GCTTGCTGTG GAGGATTTCC TGGAAGTTGC AGACTTTCTT ATTAAGGCAG	180
GGGCTGATAT AGANCTTGGC TGCTCCACAC CTCTGNATGG AGGCATCTCA GGAGGGACAC	240
CTGGGAATTG GTTAAATATT TCCTGGCTTC TGGCGCTAAA TGTGCCATGG TNACAACAGC	300
AACAGGGGGA CACAGCCTTN AACCTATGCT TGTGNAAAAT GGGACATACG GATGTTGCAG	360
ATGTTTTACT TCAAGCAGGG GTTGNTTTTA GACAAGCAGG NGGGNCATGA AGACTATTTT	420
GGAGGGCNAG ATCCGGCCAG NTCAGTG	447

(2) INFORMATION FOR SEQ ID NO:1357:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 359 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1357:

GGCACGAGCT CAACTCAGCA GGCAAGATGG ACAAATGAG GTTATTGAAC ATCCTAATGC	60
AGTTGNGAAA ATGTTGTAAT CATCCATATC TCTTTGAATG GAGCAGAACC TGGTCCACCT	120
TATACAACAG ATATGNCATC TAGTAACCAA CAGTGGGCAA AATGGTGGTT TTAGACAAGC	180
TGCTCCCTAA GTTAAAAGAA CAAGGTTTAC GAGTACTNAA TCTTNAGTGC AAATGACAAG	240
GGTATTGGGA CATTTTGGAA GGTTATTGGC ATGTGGGNGA AATTNTGAGT ACTGCCAGGT	300
TGGGATGGTT CAGACANCCC ATGATGNNGA GNCAAGACTC CTTCAATGCC TTACAATGG	359

(2) INFORMATION FOR SEQ ID NO:1358:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 101 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1358:

AAATCCCTGN CCAGAACCAC CATTGTAAAC ACGGCAAGTT TGGCAAGTTG GGNTGNNGGAA	60
CAACACCCCC ATGTGGCGTT TNCCCAGGAC CCCACCANTT G	101

(2) INFORMATION FOR SEQ ID NO:1359:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 104 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1359:

ACGTGAAAGC ACCGTAAAGC CGCTGCCNCC NCGCCGTTGG AATTTCCCTG AGGGGCAGGN	60
TACATCAAGG GCATCGTNAA GNACATCATC CAGAACCCGG GCCG	104

(2) INFORMATION FOR SEQ ID NO:1360:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 359 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1360:

AGCGCGGCCG GCCGGGNGCT TCGTGGCGGG GCTTGGNAAG GTGCGGCCCT ACTCCGTCTA	60
CCTCTTCAGC TTCTCCATGT TCTTNAACGG CCTCGCGGAC CTGGCGGGCT CTACGGCGGG	120
CAACTACGGC GGCCTCGTGG TCTTCTGCAT CTTCTTTGGC ATCTCCTACG GCATGGTGGG	180
GGCCCTGCAG TTCGAGGTGC TCATGGCCAT CGTGGGCACC CACAAGTTCT CCAGTGCCAT	240
TGGGCTGGTG CTGCTGATGG AGGCGGTGGG CCGTGNTNCG TCGGGCCCCC TTTCGGNAGG	300
TAA AATTCCT TGGATGCAAC CCAAGTTTTA CANGTAAGTN TTTCAATCTT GGCGGGGGG	359

(2) INFORMATION FOR SEQ ID NO:1361:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1361:

GGCAGAGCCC NNNGGGCAAG AAGTGGCACG NGGAGCACTT TATTTGTCCC AANTGTAAGT	60
AGCCATTC	68

(2) INFORMATION FOR SEQ ID NO:1362:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 301 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1362:

TGCANAGGTC CAGGGCCCTA GCTGTGACCG CTGTGCCCCC AACTNCTGGA ACCTCACCAG	60
TGGCCATGGT TGCCAGCCTT GTGCCTGCCA CCAAGCCGG GCCAGAGGCC ATCCTGCAAC	120
GAAGTTCACA GGGCAGTGCC ACTGCGGTGC CCGGCTTTTG GAGGGNGGAC TTGTTCTGAA	180
GTGCCAAGAA GCTCCACTGG GGAGACCCTG GGTTCAGTG CCATGCCTGT GAATTGTGAA	240
CTCTGGTGGG AATTAGGATA ACACCTTCAG TNTGNAACCG NTTTCACAGG TTCAATGNCN	300
A	301

(2) INFORMATION FOR SEQ ID NO:1363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1363:

GGCACAGCTT GCCTGCCCTG TGTCGTAAAA TGGGGGTCCC TTACTAACAT TATCAAGGNN 60  
GNAGGCANGA CTGGGACGGC TAGTCANNAG GAAGACCTGG CACCACTGTC G 111

(2) INFORMATION FOR SEQ ID NO:1364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1364:

GGCACGAGGT TTTTTTTTTT TTTTTTTTTT TNAAAAAAAA NAANCCCTTT TTTNAANG 58

(2) INFORMATION FOR SEQ ID NO:1365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1365:

NAGCTTGCTG ATGTAAACAA CATTGGA AAA TACAGATCTG CAGGAGCATG TACAGCTGCA 60  
GCATTCCTGA AGAATTCGT AACTNATCCT AAGTGGGCAC ATTTAGACAT AGCAGGCGTG 120  
AATGACCAAC AAAGAATGAA AGTTCCTAT CTACGGAAAG GCCATGANTG GGAAGGCCCA 180  
CAAGGACTCT NATTGAGTTC TACTTCGTT TCAGTCCAAG ACAATGCTTA GTTCCGATTA 240  
CTCCAAAATG TCTTCACTCT GTNTTAAATT GGNCA GTTGA CTTAAAGGTT TTTGATTAA 300  
TGGGTTGGAA ATTTTTTTTAA CGGGGGCCAA GGGTTGGTTT TTTAAAAATT TGGGGCCCCC 360  
ATGAAATTGG TTGCCCCGAT TTTTTTTTN CCATTTNCCC CCCGGTTTTT TAANGGNAAN 420  
GTTAATTC 428

(2) INFORMATION FOR SEQ ID NO:1366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1366:

GGACTTTTGC CGTCAGNTGA AAAGTGTGAT TATTACTTTA GTGTGGATGC AGATNTTGT	60
TTGACAAATC CAAGGACTTT AAAAATTTTN ATTGANCAAA ACAGAAAGAT CATTGCTCCT	120
CTTGTAATC GTCATGGAAA GCTGTGGTCC AATTTCTGGG GAGCATTGAG TCCTGATGGT	180
TACTATGCAC GATCTGAAGA TTATGTGGNT ATTGTTCAAG GGAATAGAGT AGGAGTATGG	240
GAATGTGCCC ATGTTATGGG CTNAATGTGT ACTTGAATTG ANNGGAAAGA CACTNCGNTT	300
CAGAGGTGA	309

(2) INFORMATION FOR SEQ ID NO:1367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1367:

TGACCGANAA NGGACAAGTC GTGTCCCCCG TGTGCCGTCA GACTANGGAC CCGGGTGCAG	60
AATCGGCANA GGTCCGGGTT CCTGNTCAAC AGTGCTTGGA CGGACCCGCG TCGTCCCCAC	120
CCCGGCCGCC GCCATAGCAG CTCCGNACCT CTTCACCGAC CCTCGGCTGC CCAAGCCCCG	180
NGCGTCCAGG NCGCGANNAC CGCGCGCGCG CTCTCTTAGT CGCGCATGAC GCCGCGCCAC	240
CTCGCAGTGC GCAGAACTAC CACCAGACTC ANAGGCGCAT CACCGCAGAT CAACCTNGAG	300
TCTACGNTCT ACGTTACTGT CATGTNTACT ACTTAACGGA TGATGTGCTT GAGACTTGCA	360
ATANTTCTCA CATCTATGAG AGAGGACATC TAGAACTGTG AGTNAGACCA CGAGTGNCGA	420
TCTCTTCAGN TACAGAACAG CTGTATGCTG GAGGGGGTGA TGATGAGTTG ATAATTGAAA	480
ATGTATNANC ANTATGACTG AAAC	504

(2) INFORMATION FOR SEQ ID NO:1368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1368:

CCNAGGTCAT CTTGAATTNG ATGCGCTACA NGCAGACGGT TGGNCATCTG GTCNTGGGC	60
TGCATCATGG CGGAGATGTT CACAGGCAAG ACGCTGTTCA AGGGGCAGTG AANCACCTGN	120
AACCAGGTGN AAGGT	135

(2) INFORMATION FOR SEQ ID NO:1369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1369:

TAAAGCTCNT CACAGTTTTA CAGCAGAGAC CAGTNATGAC TTATCATTCA ANAGGGGNGA	60
CCGGATCCAA ATTCTGGAAC GTCTGGATTC TAACTGGTGC AGGGGCAGAC TGCAGGTACA	120
GGGAGGGGAT CTTCCCAGCA GTGTTTGTGA AGGCCCTGCC CAGCTGAGGC AAAAAGTATG	180
TTGGCCATAG TTACCGAAGG GNTTGAAAGG CCAAAGCCTT ATATGAATTT CCGAGGGGNG	240
ANTGANGATG GAACTTTTCC TTTCAAGGGC TTGGGGGNTG	280

(2) INFORMATION FOR SEQ ID NO:1370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1370:

AGGGATGANT TGTTTACCTC TAAAATCTTT AAAGTGGAGC TGCAGAACGT NCCTCGCCAC	60
GCNAGCTTCA GCAACGTCCG GCGCTTCCTG GGCCGCTTTG GTCTGCAGCC CCACAAAACC	120
AAACTCTTTG GGGCAACCAC CCTGTGNCCT TTTTGAACAT TCCGCAGCGC TGCAGAGAAG	180
GGACAAGGCC CTGCGNCGTT TTGCATGGTG CCCTCTGGAA AGGCNGCCCA CTCAGTGTGC	240
GCCTGGCCCG GCCCAAGGCG GACCCCATGG CCAGGNGGAG GCGACAGGNG GGTGAAAAGT	300
NAAGCCACCA GTAACACGAG TGNGACGACG TGGGTGAACC CTTCTTGGG NCA	353

(2) INFORMATION FOR SEQ ID NO:1371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1371:

AGCGGCGCGT GCCCAGCAAN TTNCAGCGCC CGCGGCTCGT GAAGCAATAT GTTCTTCGTT	60
AAGGATGTGC TCAAGCTGAT GGCGAATTTC CTCGANATCC AGCGCCTTGA GATGAAATTN	120
CAGACAGCGT GACAAAATCN TCACCGGCAA TTTCTNTGGA TCGGTCGTCTG CCAGCAGAAA	180
CTTAACGTGC TCCGGCGGCT CTTCAAGGGT TTTTAACAGT GCCGTAAAG CTGTGGCGCG	240
GACACATGAT GCACTTCGTC GATNCAGATA AACTTTGAAA CGACCACGCG CCGGAGCGTA	300
ACTGGGACGT TTATCCAGCA GGTTCGCGGG TTTCTTTCAA CTTTGGTGCG CGAGGCGGCG	360
TCGATTTTCA ATCCAGATCG ACAAAGCGGC CCCTGCTTCG TTTTCACGAC ATTATTCGNA	420
CAAGTCGNAA GNGTCGNGGG TNAATGCCCG TTTT	454

(2) INFORMATION FOR SEQ ID NO:1372:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 466 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1372:

CCCAAGGNGC TCCAGGTNTG GTTGCAGGAN TACCGCCNCG ATAGTGGAGA GGAGGCCGTA	60
ACCCTTGNAAG AAGACTTGGA AGCTTAATTT ATCAGGACAA CAGGTCCCAG GTCAAGTNCA	120
TGGACCTNAA ATGCTCGNAA GGGGGATGGT GCCTCTGGAT CCATTTTCAGG AGTCCTCNAG	180
CTTTAACCTT CATCACGAAG GCCACCCAGT CCCACTTCAA ACATTTCGTTT CGGAAAACCC	240
CGCCTTTTAA CAGTNCACNA GCTCTTGCTT GCTTGCCCCAC ATNCCTGCAC CCCNGCATGA	300
AGGGTANTTC CCAGAGAACC AGGCGATGGG CATTGCCANT ATTTACACAGC GGATTTCCCA	360
GGCATGGTGG AAGATCGAGG ACNGGCTGTT NTCCTCANTC TGGAGGAATG GGGATTNAAG	420
ANTTGGGTTC GGAGGNATTT TCATAGGGGN CAACAGGCAG AGATTA	466

(2) INFORMATION FOR SEQ ID NO:1373:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 500 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1373:

AAAAAGAAAG ACTCACATTT ACAAGAGGCA GATNTCCAAG TAGAGCAGAA CCGGCAACAC	60
TTCTATNANC TGTCTCTCGA GTATGTNTGT AAGCNGCAGG AAATCCAAGA AAGAAAGAAG	120
TTTNANTTTG TGGAACCTAT GCNGTCATTT TTNAGGGGA TGTTTACCTT CTATCATCAG	180
GGCCATGAAC TTGCCAAGAA CTTCAATCAC TACAAAATGG AACTACAGAT CAACATTCAG	240
AATACACGGA ATCGATTTGA AGGAACAAGG TCAGAAGTGG AAGAGCTCAT GANCAAAATC	300
CAGNCAGTTC CCAAGGNCCA CAAACGAGCA AGTCAGTTTA CAGCCGAGTT ACCTGTTTGT	360
GCCAGGAAAA AGGCCTGCTC CNTTTGGTTC CATTGGGTTC AANCATTTTT GCCNGTTTTTC	420
GAAAGCAGCA AGGNAGTTCC ANCTGTTCCC CTTTtaggca CCGTTTGGT GGGGAATTNG	480
GGGNCGGNGA GGTGTTCTTT	500

(2) INFORMATION FOR SEQ ID NO:1374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1374:

NTACGTCGCT CCNACCTNCT GGCTGNCTAG GGGGAACTCT CCCCCAGCGA AAAGGACATC	60
AAGAAGATCT TGGACAGNTG GGTATCGAGG CGGACGACGA CCGGNTCAAC AAGGTTATCA	120
GTNANTGAAT GGAAAACNTG AAGAGTCNTG CCAGGTTTGG CANCTTGNN A TTTACCTCTG	180
GTGGGGTGTA GCGTNTNGCT GCCCCGGTCTG CAGCCTGTGT GGTNTTCCCT GCTGCAGANA	240
GGAGAGNAAG TGAGAGAGGA GGAGTCTGAA GGTCACTGTG ACNNGGATTG GCNTTTGATT	300
ANNTCTGTCC CTGCAATAAA GCTTTTACAC TCTCAAAAAA AAAAAAAAAA T	351

(2) INFORMATION FOR SEQ ID NO:1375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1375:

GGCAAACGAC GTGGGCAGCG TGGATGGAGA AGTCGTCATC GCACACGGTG CCCCANTGGC	60
CATCATAGTA CACCTCCACC CGGCCCTCGC TGTGCTTCCT CTTCTGCCCA GCCAGGCGCA	120

NTNAATATCT TGGCCACGTT GGCGGGTNTC TNGGAGCTGG TGAATACTNA GGAAGCCGGT	180
TGCTGGAAAT NACTCGGGGT AAATGGGNGC CAGCTGTAAA TACTGTGCCA GGTCAGGGG	240
GGACAGGNGG GCCAGCATT GCCAGGCANT TGCAGAGGTG GGGAGCACAG AGGCCTTTTC	300
CATCCCTGTT TTTCGGGCTG ATGATTCCCA CGNAANGGNC CCTGCGCATT GAAAGGGGGN	360
ACAAGGCGGG GGTACAGAA GCANCAGGGG TTTTTTT	397

(2) INFORMATION FOR SEQ ID NO:1376:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 283 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1376:

CANCAAAAC TAAAACTGNN GGTCCAGATC AAACAGAAAT GANCTATTGA GGGCTTGCGA	60
GCNCACAGTG GAGTATGTGG TTAGTGTCTA TGCCTCAGAA TCCAAGCGGN GAGAAGTNAG	120
NCTCTGGTTC AGAACTGNNG TAAACCAACA TTGAATNGGN CTAAAAGGN ATTGGNATTT	180
CACTGATGTG GGATGTGGGT TTNCATTNAA AATTGCTTTG GGAAAGNCCA CAGGGGCAAG	240
TTTTCCAGGT TCAGGGTGAC TTATTTGAGC CCTNNGGGTT GGG	283

(2) INFORMATION FOR SEQ ID NO:1377:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 186 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1377:

GCCANCCAG NTTCCGNAA CNTGCCAGGA GCTCAAGGTA AGCCATCAAG AGCCTGCAGT	60
GGNTGGCGGG CGGTCACCTT CACGGGGGAG GCCCTGCAGT ACAGGGGGAA CCAGNTGTTG	120
NCGNCCCAGC CCGAACAACC GTNTCGCCCT GGTCATCATT GACGGGCGTT CAGACANTCA	180
GAGGGG	186

(2) INFORMATION FOR SEQ ID NO:1378:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 316 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1378:

CTNCCGGATT CGGCGTGGTC AGCAGCCGAA AAGAATTTCC CCGCTTATNC GNACCTTCCA	60
TAATAAGCAA GCNATCTNCT GGCTGAAAAA AGCTGCCCTA CAAGGCCATA CTTTGNCTTC	120
CAACGCCCTT GGCTGGNACA CTGGATCGTG GAGAAGCCCC CATTATGAA AGANGCGGTT	180
GTTTGGTATC GAATAGCCGC GGAGAGCGGA ATGTNTTATG CGCCAAAATA ATCTTGGGTG	240
GATGTACANA ATGGCAACGG AGTCGCAAAG ACTNTGCGCT GGCTTTTNTT GGTNCAAACA	300
GTNGCTTACA GGCCTT	316

(2) INFORMATION FOR SEQ ID NO:1379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1379:

TGTNNCAGGG AACTTGCTAC TACCAGGCAC CATGNCCTAC CAATATCCAG CACTGACCCC	60
GGAAGCAGAA GAAGGAGCTG TNTGGGNATC GGTCAACCGA TCGTGGGACA CCTGGGCAAG	120
GGACATCCTG GCTAGCAGAT NNANTNCCAC TGGGAAGCAT TGCCAAGCGG CTGCAGTCCA	180
TTGGTNACCG AGAACACCGT TGGTGAACCG G	211

(2) INFORMATION FOR SEQ ID NO:1380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1380:

GGCAGANANA CCTTGGCACC CGNNATCAAC TGGTTGCTTT TNNTCAACAC CATCTTCTAC	60
CCCGTGGAGA TCAGTNAATC CAAGCCTATT GTGGTCTATG ACAAGGNAAT ACCTGAAGC	120
AGATCTCCAC TCTCATCAAC ACCACCGACA GATGCCTGCN CAACAACCTAC ATNATCTGGA	180
AACCTGGTGC GGAAAACAAG CTCCTTCCTT GAACCAGNGC TTTCAGGACG CCGATGTGAA	240
AGTTCATGGG AAGTTNATGT ACGGGNCCAA GAAGACCTGT TTTCTCGCT GGGAATTTNG	300
CNTTGGTGAT CACAGTAAAC ANCCTGGG	328

(2) INFORMATION FOR SEQ ID NO:1381:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 314 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1381:

GGCAGAGCCC TGGTCCGCAT CTNCTNTGGC CGCCACCCGA TGCTGTTCAG TTACCAGCGC	60
TCCCTGCCAC GCCAGCCCGT GCCCTCTGTG CAGGACACCG TGCGCAAGTA CCTGGAGTCG	120
GTCCGGCCCCA TCCTNTCCAA CGNAGGACTT CGAACTGGGA CCGGGGTCTG GGCGCAGGAA	180
TTCCTGAGGC TGCAGGCGTC GCTGCTGCAG TGGTACCTGC GGGCTNCAAG TCCTGGGTGG	240
GGCGTCCAAT TATGGTCCAG TAACTGGTTG GNAGGGAATT TTTGTNACCT GNGGATTCCC	300
GGAAATTCCG NTTG	314

(2) INFORMATION FOR SEQ ID NO:1382:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 488 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1382:

GGCAGGAGCN AGCCTCAGCC TTCCCTGGCC AAGAGCTCAT GCTTTCCTTG CTCTCCCCAG	60
GGTCCTGCTG GTCCCCCGCG TCCTGTCGGC CCTGTTGGCG CCCGTGGCCC CGCCGTAAAG	120
TACCCTGCTG TNTCCCCCAT GCCTTCANAA CTCTACAGAT GCAGACAGTG CCCCCTCGA	180
TGCCAATGGA AACTTCCGCC TGAAAGTTTG TCCCTTTNTC TCTTCTAGGG GACCCCAAGG	240
NCCCCGTGGT GACAAGGGTG AGACAGGCGA ACAGGGCGGA CAAAGGCATA AAGGTCACC	300
TTGGGTTCCTT TGGGCCTCCA GGGTNCCCCT TGNNCCTCCT GTAAGTTATG GTTCAGNCCT	360
TNCCCAGTCC CCTGNTGTTG TGTGGGTTAG NAAGGGGGAG TTTGGNCTNA ATTTTCCCTT	420
TGGGTNGTTN ATTNTTTCCT TTCCTNATGG GGATTGGGGG TNTNAAGATT TNTGGGGNAT	480
TTCCAAGT	488

(2) INFORMATION FOR SEQ ID NO:1383:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 347 base pairs  
 (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1383:

GGCACAGCAG GGTTCACACC GGTGAAAGCC CTNACGTGTG TGGTGA	60
CTGT TGGTGA	
TCAGCCGAAG CTCCAACCTT ATTCAGCATA AGAGGGTTCA CACTGGTGAA AAGCCATATG	120
AGTGCCAGCN ACTGTGGGAA GTTCTTNAGC CAGCGTTCCA ACCTCATTCA TCATAAGAGG	180
GTTTCATACGG GCAGAAGTGC CCATGAGTGC AGTGAATGTG GGAAATCTTT CAACTGCAAC	240
TNNGAGCCTA ATTAAACAT TGGAGAGTTC ACACTGGAGA AAGACCTTAC AAGTGTAANA	300
NATGTGGGGA AATTTTTTAG NCCACATTGT NCAGNCTTCA TTCCAAC	347

(2) INFORMATION FOR SEQ ID NO:1384:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 337 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1384:

AGCAACGGCG ATCATTGTAA CTTCAATTCT GGTGCCAATT CTNACCTCTA TCTGGNCACG	60
TAAAGTCAAA GCCAGAGCAG CGAAAAATCG AAATTTTAGG TACGGTGAAA TAAACCTGCT	120
TCCTTAATCC CCACNGTCGG ATGANCTAAC GTTCGTCCGG TTTGCTATTG AGTTCCTGCC	180
TGGAATACTT ACCGAGAAAA ACAGCACGNC TGAACATTAA AATAAAATNT GGGTACTAAA	240
TGGGGGAAAT TTTCTGCGTG GGAGAGGGAA ACAGATGNCG ATTATTCCGN TTGATTGTNT	300
NACACAGGAC AAGGTTTCCG GGATTTTCC CGGANGG	337

(2) INFORMATION FOR SEQ ID NO:1385:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 242 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1385:

GAGGATAAAA AGTACATATA CAGTTCATAC AATAATCTTA TGTATGTANA ACCCCGTTAC	60
GATGTCGGCG ACGGGGCCCA TCAGTAACTA TTACGTGGAC TCGCTCATCT CTNACGACAA	120
TGAAGACCTC CTAGCGTCCA GGTTCCTGGC CACCGGGGCT CATCCCGCCG CCGNCAGACC	180

CAGCGGTTTG GTGCCGGNCT NTAGCGATTT TCCGTTCTTG TGAGCTTCGG GNCCAAGCCG 240  
GN 242

(2) INFORMATION FOR SEQ ID NO:1386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1386:

GGGGACCCCC AGGAGGTGAC CCTGCAGCTC TTCACAGATG GAATCACAAA TAAACTTATT 60  
GGCTGTTACG TGGGAAACAC CATGGAGGAT GTAGTCCTGG TGAGAATTTA TGGCAATAAG 120  
ACTGANTTAT TAGTCGATCG AGAATGAGGA AGTAAAAGAG TTTTCGAGTG TTGCAGGCTC 180  
ATGGGTGTGC CACCACAAC NTACTGTTAC CTTCAATAAT GGACTATGNC TNATGGATTT 240  
TATACAGGGA GGAAGCACTG GGATCCAAAG CCATGTTCTG GCAACCCCAG CCATTTTTC 300  
GGGCTAANTA GCTTCGTTCA GTTTGNTTAA AAATCCCATG NCTTATTTCC ATGGCACCAC 360  
CAATTGGGCT GGGTTTCCCC CAAATTNTAA TTCTTTTGGG NTTAAAGATT GGGGGNAAGG 420  
TTATTTTNTT TT 432

(2) INFORMATION FOR SEQ ID NO:1387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1387:

TCCTCCTGGC CATNATCTTC CTGCTGGGGA AGATCTGGAA GGTNCAAGTG CTGCAGGGCA 60  
TCTTTGGGAN GAGCCAGNTC CTGTTTGCNC TCGTTTTCAG CAC 103

(2) INFORMATION FOR SEQ ID NO:1388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1388:



ATGGCTGTGC CACCCACGTN TGCCGATTTT NGCAAATTTG CCAGGGAATN TTTTCACCAA	60
GGGCTATGGT TTTNGTTTAA TAAAGCTTNA TTTGGAAAAC AAAA	104

(2) INFORMATION FOR SEQ ID NO:1389:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 306 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1389:

TGAGGGACTT NACCCAATNA ACTACCTGGG CATTANNACC AACATTCAAG GCCAGGTGCC	60
TNACGTCCCA GCAAATTTAA CAGTCCACAT CTCTCCCTAC AAGGAGCTGT ACCACTACTC	120
CAACTCCACT GTAACCTCTA CAAGTNCCNG TAGACTACTC TNTAACTTTT GGTGCAATCA	180
ACCAAACATG GTGCTACCGC ATCCACCAGA ACATCACTTA CCAGGTGTGC AGGTACGNCC	240
CCAGACACCC GTCCTTCCNC ACCACCCAGN AGNTTGAACG TGGACCGGGT TTTTTCCTT	300
TGTNAT	306

(2) INFORMATION FOR SEQ ID NO:1390:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 466 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1390:

GGCAGAGNCT TGGAAGAATT TATTTAGATA TGCTTAATGT ATACAAGTNC CTCAGTGAAA	60
ATATTTCTNC AGCTATCCAA GCTAATGGTG AAATGGTTAC AAAGCAACCA TTGATTAGAA	120
GTATGCNAAC TGTAAAAAGG GAAACTTTAA AGTTAATATC TGGTTGGGTG AGCCGNTCCA	180
ATGAATCCAC AGATGGTCGC TGAAAATTTT GTTCCCCCTC TGTGGATGC AGTTCTCATT	240
GNTTATCAGA GAAATGTCCC AGCTGCTAGA GAACCAGAAG TGCTTAGTAC TATGGCCATA	300
ATTGTGCAAC AAGTTTAGGG GGACATATTA CCAGCTGAAA TACCTCAAAT ATTTGATGCT	360
GTTTTTGAAA TGGCACCTTG GATTATGGTA AATAAGGACT TGNAGGATTT TCCCGNACCT	420
GGACGGACTT TTCCTTACTA CTCNCGGTGT TCAATTNNCC TTGTTT	466

(2) INFORMATION FOR SEQ ID NO:1391:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1391:

GGCAGAGAGA NGCTGCGTCC CGGAGTAATC TGAAGCGGGT NACGCTGNAG CTNGGGGGGG	60
ANGAACCCCTT GC	72

(2) INFORMATION FOR SEQ ID NO:1392:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 312 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1392:

AANAAACCAT CTGGTTCANG TTCCTAATTG GGCCAGCAAG TAAGGATGGC CAGGCCTCTG	60
GAGCAGGCGG TACTGCNATC NTTTGCACCT TCCAGGTAAT ACGCAGGTGC TGTGGGGACA	120
AATACAAGCN CTGCCAGGCG GACTCAAGGA GCTGCTGCAG AAGGAGCTGG CCACCTGGNA	180
CCCCGANNAA TTTTCGGGAA ATNTAACTAC AACAAATTCC ATGANTNTTC CTGGGACACC	240
ANCAAGGACT GCAAGGTGGG ACTTTTTTGG GAGTATGTGC GCTCACTTGC TCTGNTCGCN	300
TTTTCTACTG CC	312

(2) INFORMATION FOR SEQ ID NO:1393:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 309 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1393:

AAACNTNTN TTNTCCTGTA AACAGTGGCC AGCCCCCAA CTATGAAAAT GCTCAAGGAG	60
GAGCACGAGG TGGCTGTGCC TGGGGGCGCC CCANAACCCT GCTCCCCGA NGTCCACNGT	120
NAATCCANAT CCGCAACGAA GACCTCCNTG CNCCGACCAT NTGGTNTGGT CCCTNTTCAA	180
CANCCTCTTC ATGNAANCCC TGCTGCCTGG GNTTCATAGC ATTCGCCTTA NTCCGTGAAA	240
GTTTTAGGGA CAGGGAAGAT GGTGGGGGA CGTNAACCGG GGGNCCCAAG NCTTATGGTC	300
TTCCAACCG	309

(2) INFORMATION FOR SEQ ID NO:1394:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 341 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1394:

TTTATGCTGA AGTATTATCG ACGAATGCAA TTATCATTGA AAAAAACAT AATATATAAG	60
TNATTATCTC TAAAATCATT GATGATTTCA GAGTGTAAGG TTTCAATGAA TGANGTTTAA	120
AGGATGTTAG CATGTTTTAC CTTTATAATG ATGATAACTT TTCCAAAAC TCTTGACTGT	180
NGAGGTTAAT TAAATTTNCT CTTGGAGCCC TACATACCAT CTGGATTCTT CCCATACCCA	240
CCAATTAANT CCCGGATCGG TTGGTCCATA AAACCGTGGA TATTGGGTCT NTCCAGTGGC	300
CGCCGTTAAA ATGGGNTTAA CCCCCTATNN CACCGGACAC T	341

(2) INFORMATION FOR SEQ ID NO:1395:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 203 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1395:

AGCCACATGC NCTACGNTTA NNANGCCTAC GCATACCTNC AATATATTGA NTCTGCAGGA	60
CTTTGTAGNC CGGNTAAGGN GTTAACGCCG ATACAGGCAT TAACAAAGCG NATTTGTCAG	120
CAATCTAAGT AACGTCGCAA TCANTTTTCT TNAATCCCAC ATCATTTGCA NTTCCATTAN	180
TTCTCAAACA TCCATGCCCA ACG	203

(2) INFORMATION FOR SEQ ID NO:1396:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 429 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1396:

TAGTNAGGGT CAGGTGCAGA TGGCGATGAN CGGCGGCATC TANAATGAAA GCAATGCCCC	60
GCTCGGTTTG TACATNGAAA ACGGTCAGCA GAAGGTGGCG TTAAATCTCG CTTTCAGGTGA	120

AGGGAAATTN NTTTATCCGT CCTGGCGGCG TGTTTTAATG TCGCGGGAGA ATAAAGTCGG	180
CATCGTTCGT CTGGTATGCC TTCAAAACCA GTNAAAGNGA TTCATTTTGC GGTGCAGTCC	240
AGGGCCAATN TTGATGGAAA ACGGTGTAAT TAATCCGCGT NTTTCATCCCA ACGTCGCCTN	300
AAGCAAATTT CGTGAACGGT GTTGGGGTTA ATAAAACCTG GGGAACGCCN TGTTTTTTTT	360
TGNGCCCGCA GGCANCAAAT TTTTAATGGA TTTTGTCCCN GTTATGNCCC AGGGGAAACT	420
TAACCTTTG	429

(2) INFORMATION FOR SEQ ID NO:1397:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 314 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1397:

NAGCTTTTNG TATTTTAAAT ATNAGGTACA TAAGAGTTT AATTTGTTCC TTTTTTAAAA	60
TAACCTTTNAA AATTATTATA TGGTAACCTT CTTTATTATG AATACTTGNA AAATGTAGGC	120
ACACAAATAA CCTTTTTGAA TTTATATCCT GTAATGTATA TTTCCCCAGT CTTTNNACTT	180
TACTCCAGTC CACTAGGAAA TCAGTGGTTG GTTGTTTACC TCTCTTGAAA TGTCTTTTTG	240
TATTGTGGTC TCCACCGTGC CATTTCNATA ATGGCATATT TNTNTTTGNG CCTAGCCATG	300
TTTAGNGGTG TTTG	314

(2) INFORMATION FOR SEQ ID NO:1398:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 208 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1398:

TCCATCATAG TCAACTGCTT GGGANGAGAA AGCCAAANGA NTGCAATGTT GTGAAAGATT	60
CCANTTNATG CCAGTAAACC TAATCCAAAT GAATGTGGAG TTTGAATAAA TCTGTATTTG	120
GATATGATTG GAATCATCCA TCCCTGTACT CATCCTGAGG ACAAACCAGC ACCAAAAANT	180
GNGGNTGNNA ATGAATGGTT GCAATTTT	208

(2) INFORMATION FOR SEQ ID NO:1399:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1399:

TGANTATTCA NCGTGNGAAA GAAGANTTGG AACAAAGGGA AGCTGAACTC CAGAAAGTCC	60
GGAAGGCTGA GGAAGAGAAAG GCTGCCCCAG GNAAGCAAAG GNGAGAGAGA AGGAGCGTAT	120
CTTACAGGAA CATGANCAAT TCAAAAAGAA AACTNTCCGA GAANCNTTTG GNGCAGATCA	180
AGAAAACAGA ACTGGGTGCC AAANCTTTCA AAGGTATTGA ATATTGAAGA CCTTNAGGNA	240
TTGGTTTCCA GTTTTTTCCT GGGTTAANCA GGTTGANCAC TGGGGAAAG	289

(2) INFORMATION FOR SEQ ID NO:1400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1400:

GGCACGAGCA TGGCTTTTAA TGAAGAAGGA CAGGCAACAG AAACAGACAC AAAANTCAGA	60
GTGTGCACCC GGGCCTACCA TCTGCTTGTN AAAAACTGG GCTTTAATNC AAATGACATN	120
ATTTTTNACC CTAATATCCT AACCATTGGG ACTGGAATGG AGGAACACAA CTTGTATGCC	180
ATTAATTTTA TCCATGCAAC AAAAGTCATT AAAGAAACAT TACCTGGGNG CCAGANTAAG	240
GTGGAGGGTN TTTCCAACCT GTCCTTCTCC TTTNCCGGGG ATTGGAAGGC CTTCNGGGAA	300
GGCATTGCTT GGGGTTTTCC CTTTACCCTT GCATTCAAGT NTTGGCTTGG CCTTGGGGGT	360
TNTTNATTNC TGGGAAACCC CCCCCTGGNA TTGGGG	396

(2) INFORMATION FOR SEQ ID NO:1401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1401:

GGCACAGGNT TTTTTTTTTT TTTTTTTTTT TTTTTTTTNG GGNTTTTTTT TTTTNTN	56
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(2) INFORMATION FOR SEQ ID NO:1402:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1402:

CAAAGGCGGA GGACCCGTGG CCCACGAAGC TCATCTTTNA ACTNTCCCCG CNTTCTCCCG	60
CCTTGAANTT GTGAACCCTA GGCCCTTTGG GCGGACCTNT NAACCCAGCT AGCCAGATCC	120
CGGACCCAAA CCATGTTCCC TGTGAAAGGT GAAAAGTGA GGAATCAGA GCTGGAGATG	180
GCCAAAGCCC GGTAACCAAC TGGTTGCTGT TTTGCAGTNT CTGCTTGGAG GANGAGTCAC	240
ATGGNACAGG GAGCGTNTGG TTGAGGGAAG CTGGGGAAAA CACCCTCAGG ACACCCACAA	300
TAAGGNACTG TTTCCATCGC AGGCCACTGG GNAAAAAGGG CCATCTTNCC CGTTTTTCCC	360
CCACCAAGGG GAGGAAGAA GAAGNGGGG NGATTGGTTG	400

(2) INFORMATION FOR SEQ ID NO:1403:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 245 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1403:

TATATTGTAG CTCATCANGG GNAATNGGNA CTGTTCAAAA NGGATTGCCC CACAAGTGTT	60
ACCATGGGCA AACTGGAAG AGTCTACAAT GTTACCCAGC ATGCTGTTGG NCNNGGTTGT	120
TATNCAAACA NGTTTANGGG GCAAGATTCT TTCCAAGAGT NTTTAATGTG CGTATTTTAG	180
CACATTTGGC ACTCNAAGTG TCCGCGATAG CTTTCNGAAA AGTGTTNAAG GGNAATGAA	240
TTCAG	245

(2) INFORMATION FOR SEQ ID NO:1404:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 340 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1404:

GGCAGAGTGG TCATCGAGTT CTCCAGCCGC CCCGGCCAGC ACGAGCTGAT GGAGCCCGAG	60
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GTGAAGCTCN TCGGCAACAT TCATGGCAAC GAGGTGGCGG GCCGGGAGAT GCTCATCTAC	120
CTAGCCCAGT ACCTGTGCCT CTNAGTACCT GCTTGGTAAC CCCC GCATCC AGCGCCTGCT	180
CCAACACCAC CCGCATCCAC CTGNTGCCCT CCATGAACCC TGACGGCTAT GAAGGTGGNC	240
AGCTGCCGAG GGTGCGCGG TTACAACGGG TGGGACGGAG CGGGAAGGTN AGTAACGTGN	300
CAAAACCTGG GTNTCTNGAA CCGAAATTTT CCCGGGACNT	340

(2) INFORMATION FOR SEQ ID NO:1405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1405:

AATCGCAGAG CTTGTNACAT TTTGGAATGC TGTAATGGGC TGGCCCAGGA ATGTNATCGG	60
CTCCATCGGA CAAGCCTTTA AGCTCCGGTT TAAGCAATAT TTACAGTGTC CTACCAAGAT	120
TCCCGCTCTC CATGAATCGA NTGCAGAGTC TGGATGAGCC ATGGNACGGT AAGAGGAGGG	180
AGATGGCTCA GAACCACCCA TTA CTTACAA CAGCATCCCA AGCAAGATGC CTCCTCCCAG	240
GGGGCTTTTC TTGGATACTT AGGACTGAAA CCCAGACCCC ATGGTTCCTG AACACAGCCC	300
AGTTTTGCAG GGAAAAGAGG CAGATTTTTT ACCAGGGAAG ACATTTGGGG GACATTTTGG	360
CGANANTGGG CAGCAAACAN CTTTAAGGGC AAGGTNCCCG GANAT	405

(2) INFORMATION FOR SEQ ID NO:1406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1406:

GGCAGAGCCC AATTCTTCGA AGGTCTGGAA TGTATACTGT AGCCATTGCT TTTTGTGGCT	60
CTNGTAACAA CAAAGCAATT CGAGGACTGN TAGATGTTGC TGTAAGTAAT GTTAATGATG	120
ATGTCAGGAG GGCAGCAGTA GAATCACTTG GGTTCATTCT ATTCAGAACC CCTGAACAGT	180
GCCCAAGTGT TGTCTCTTTG TTGTCAGAGA GTTACAACCC TCATNTGCGC TATGGAGCTG	240
CAATGGCCTT NGGGATATGC TGTGCTGGTA CAGNAAACAA GGAAGCCATT AATTTGCTAG	300
AACCANTGNA CAAACGACCC CGTGGAAC TA CGTGAAGGTC AAGGGGCACT TCTTAGGCTT	360

NCAGTNCCTTC ATCCATGTTT CCAGGCAGAC TNGNAATCCA CTTGTTCCAA AGGTNGAT

418

(2) INFORMATION FOR SEQ ID NO:1407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1407:

GGCAGAGGAA GATTGACGTG GGGGAAGCTG AACCACGGAC TGTGTGATNC GGCCTGGTAC	60
ATTCGTGCCC AAGGAGGAAC TGCAGGACAG GCTGGTAGTG GTGCTGTGCA ACCTGAAACC	120
CCAGAAGATG AGAGGAGTCG AGTCCCAAGG CATGCTTCTG TGTGCTTCTA TAGAAGGGNT	180
AAACCGCCAG TGANACCTCT GGACCCTCCG GCAGGCTTCT GCTTCCTGGT GGAGCACGTG	240
TTTNTGAAAG GGCTATGNAA AAGGGCCAAC CAGATGGAGG GAGCTCAAGC CCAAGAAGAA	300
AGTCTTTTCGA GGAAGTTTGC CAGGCTGGAC TTTCAAATTT TCTGAAGGGA GTTGCATCGC	360
CCAGTTGGGN AGGCAAACCA ATTTTCATGGA CCAGTTGGGT TNCCNTTNCC GTAAATCGTT	420
GAAAGGGGGG NACATTAGTT TGCCAGCCCG CNTTTTCCCC TTTTTCAC CTNGGGTCAT	480
NTGTGTNTTT TCNTTTGTTC	500

(2) INFORMATION FOR SEQ ID NO:1408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1408:

TACTATCCGG AACTGGCTGC GCTGAATGTN GNAANCTTTA AAACCGACAA ACCACAGCCG	60
GTTAACGCGC TGCTGAAGAN CCGAAAAACG CAACCTGTCG CTGTTACAGG CACGCTTGAG	120
CCCAGGNCCT GNGCGGCGAG NAAN	144

(2) INFORMATION FOR SEQ ID NO:1409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1409:

GGCACGAGGC GGGGCTACAA CTACGCCACC TGCCTGGAAG GAGCCCTGAA AATTAAAGAG	60
ATAACCTACA TGCACTCAGA AGGCATCCTG GCTGGGGAGC TGAAGCACGG GNCCCTGGCA	120
CTGATTGACA AGCAGATGCC CGTCATCATG GTCATTATGA AGGATCCTTG CTTCGCCAAA	180
TGCCAGAACG CCCTGCAGCA AGTCACGGCC CGCCAGGNTC GCCCCATTAT ACTGTGCTCC	240
AAGGACGATA CTGAAAGTTC CAAGTTTTGC GTATAAAGGN CAATCGGAGC TGCCCCACAC	300
TGTGGGACTT GCCTTCCAGG GGNATTCCTT GAGGCGTGGA TTCCGTTGGC AGTTGCTGTT	360
CCTTNCACCT GGGCTGTTCT TCCGAGGGAT ATGACGTTGA CTTTCCCCAG AAATTTGGCC	420
AATTTTAA ANTN TGGGAT TAGGNTNAGA CCGTNAAAAG GCCATTAACC ACTTT	475

(2) INFORMATION FOR SEQ ID NO:1410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1410:

ATGGGAGTGG ACATCCGCCA TAACAAGGAC CGAAAGTTCG GCCGCAAGGN GCCCAAGAGC	60
CAGGNTATCT ACCTGAAGGC TGTTGGTCAA GTTATACAGG TTTNTGGCCA GAAGTAACCA	120
ACTCCACATT CAACCAGGTT GTNTTGAAGA GGTGTGTTAT GAAGTGGCAC CAACCGGCCG	180
CCTCTTTCCC TTTCCCGGAT GAATACGGNA AGNATGGAAG CTTTCCTGGG CCGGGGAAAA	240
CAAAGACGGG CCGTGGGTTN TGGGGGGACC ATAAACTGAA TGATTTGCGG GGTTCAGGA	300
AGGGTTACCC AACTTTAAG TTATGTGNCA CTGNCGTNA ACCCAACGGG GNCCC	355

(2) INFORMATION FOR SEQ ID NO:1411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1411:

ATGATAATAG TGTTGATACA GCCACGCAA ACCGCGACCA GACAGATAAT TTAAATGCA	60
GCCATGCTGA CCACAGCCGC AGCGNCGTGA ACGGGAAAAT CCAACCCCAT CATGGTTAAC	120
GCATCAACCG GCAGACGCAT ATGGNCAAAC TCGCCGGTAA ATGTAGCTTT TACCGGTAAT	180

CGGTTTGCCG TTGAAAAATC AGCCCGCCGC CAACACCGGT GCCGAGANTC AACCCCATCA	240
CCAGTGGGAT ATTGGAGTAA AATTTTCATCA TCCCAGGNTT CTGNAAGGGG CAAAACAGTT	300
GGCATCGTTT ATTCAAGGCG TACATCGGGG TTCAAGAACG TCGGTTTCAGT TCGGCAGGNN	360
GCGGTTTTTAC NTTGTCNAGG GGGGGAACCA TGGGNGGCTT ACAGGGTTAC CCTCTTTTGG	420
TTT	423

(2) INFORMATION FOR SEQ ID NO:1412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1412:

GGCAGAGCNA GNCCGGAGTG TCAGNGNATG ATGCGGTTNA TGCTATTATT CAGCCGGCAG	60
GGGAAAACTG CGGCTGCAAA AATGGTACCT GGCCACTTCG GACAAGGGAA CGGAAGAAGA	120
TGGTNCGCGG NCTCCATGCA GGTGTCTCTG GCTCGAAAGC CCAAGAATGT GCAGCTTCCT	180
GGAGTGGAGG GNACCTCAAA GTTGTCTATT AAGAGATATG CCAGCCTCTA ACTTNTGCTG	240
CGCCATTCTGA GGGCCAAGAC AATGNAGCTT CATCACACTG GAGCTGTATT CCACCGATAC	300
GTGGAGCTCT TTAGGACAAA TACTTTGGGC AGTNTGTGCC GAAGCTGGAC ATCATCTTTC	360
AACTTTNNAG GAAGNCTNA TTTTCATCCG GGATGAGTTT TTTGATTGGG GGGGGGNTTT	420
CCAGGACAAC TTCCAGAAGA GTGTGCTGAA GCCATTCTGAG CAAGGTGANC NACTTGNANA	480
GGG	483

(2) INFORMATION FOR SEQ ID NO:1413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1413:

AGCCCCCTAG ACAGGTTAAA ANGTTATCTN TGGCAATCAA NGGCAGTTTG GATGAAGCCA	60
AGGNTCTTTN CAAACCTCCA AAGGACTCCC AAGAATGACG AGAGTNAACT CAAATGCCGN	120
GGAGGAGCAG ACTACGANGC GCCCGGAGAA CCCACACTGG GGGTTCATTT GGNCGNCAAA	180
CG	182

(2) INFORMATION FOR SEQ ID NO:1414:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 283 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1414:

GGCANAGGGN TCAACTACCT CACTGTAATT GGCTACCCAA ATGCTGAGTT CAAATCTTGG	60
TGGCCGGCCA CTGCTCATAT CATAGGTAAG GACATTCTCA AATTCCATGC CATCTATTGG	120
CCTGGCCTTC CTGTTAGGGG NCCGGTCATN AGCCCGNGCA CAGCNCATCT NTNGGCCATT	180
ACCCACTGGA CAGTCTGTGG CCAAAGTTG TTCCAAGAGC TTGGAGCAAC GTGGTNGNNT	240
GCCGAGGACT TNGCCTTTAA CCGCTATACC GTGGTATGGG NTT	283

(2) INFORMATION FOR SEQ ID NO:1415:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 393 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1415:

GGCAGAGTNT CGATGCCACT NTCAACAAGG CCCTGGCAGA AAGATTCCAC ATCTCAAAGT	60
TTCCTACGTT GAAGTATTTT AAGAATGGAG AGAAATACGC ATGCCTGTGC CTCAGGTACA	120
AAGAAGAAGT TTCTCGAGTG GATGCAAAAC CCTGAGGCCC CCCC GCCCCC AGAGCCCACG	180
TGGGTAAGAG CAGCAGNACA AGCGTGTTGC ACCTGGTGGG GGACAACTTC CGGGGGGACC	240
CTNGAAGAAG AAGGAAACAC ACTTGTTTCA TGTTCTTACG NCCTTGGTGC CCACACTGTA	300
AGAAGGTTCA TTNCCGATT TTA CTGTTAN NGTTGATGCC TTTCAAAGAT GGACCGAAAG	360
NTTGNCTGTT GCCGTTGTTT GATTTTTTAA AGG	393

(2) INFORMATION FOR SEQ ID NO:1416:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 117 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1416:

TCCCNNTGGG ACAAACACTGT TGGTTCAATT AAGGGTTGTT TTTTCANGAG GNTCCTTGGT	60
TCTTTAAAAG GCAAGGTCCC GNNGGGGAAG GGTCCAAGGT TCAAGTTTGT NAAGGGG	117

(2) INFORMATION FOR SEQ ID NO:1417:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 277 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1417:

GGCANAGGGA AGAAGGAAAC CCAAGGTTGT GGTATGCTGC TTTACTGTCT TTCACAAGCG	60
CCTTTNATAT CCTGTCAATC ATCTGTGTCG GGCTGCTCTA TACATATTAC ACCAAACCAG	120
ATGGCTGCAC AGGAAAACAA GTTCTTCATC AGTATTGAAC CTGATCCTTT GCGTTGTGGC	180
TTCTATTATG ATCGATCCAC CCAAAAATTC CAGGGAACAC CAGCCTTCGN TTCCGGCCTC	240
TTGNCAGTTC CTTCCCTNCA ATNCAACCCC TNCTGAC	277

(2) INFORMATION FOR SEQ ID NO:1418:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 477 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1418:

GGNACGAGCT GGTGGCTGGC AAGATCGTGG AGATGGAGGA TGTGGGTTTA CTCTTTGCNC	60
GCCTTGGAAG GTACATTCTG TGCTGCCTGC TGGGTCACGC CATCCATGGG CTCCTGGTAC	120
TGCNNGTCAT CTACTTCCTC TTCACCCGCA NAAACCCCTA CCGCTTCCTG TGGGGCATCG	180
TGGACGCCGC TGGCCACTGC CTTTGGGAAC CTCTTCCAGT TCCGCCACGC TGCCGCTGAT	240
GATGAAGTGC GTGGAGGAGA ATTAATGGCG TTGGCCAAGG CACATTCAGC CGTTTTTCATC	300
CTGGCNCATC GGNNGCCACC GTNCAACATG GGACGGTGGC CGACGGTTCT TTCCAGTGCG	360
TGGGCCGCAA TGTTTCATTG CACAGTTCAG CCAGCATTC TTGGANTTCG TNAAAGATCA	420
TCACCANCTG GTCAGGGCAC AGGTCCANGT TGGGGGCAAN GGCATCCTG CTGGAGG	477

(2) INFORMATION FOR SEQ ID NO:1419:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 349 base pairs
  - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1419:

TCAGCAATCA GACTGTCGAC ATTCCAGAAA ATGTCGCATT GACTCTGAAG GGACGCACAG	60
TTATCGTGAA AGGGCCCCAG AGGAACCCTG CGGAGGGNAC TTCAATCACA TCAATGTAGN	120
AACTCAGCCT TCTTGGNAAA GGAAAAAAA GAGGCTCCGG GTTGACAAAT GGTGGGGTTA	180
ACAGNAAAGG GAACTGGNCT ACCGTTCCGG GACTTATTTG TGAGTNCATG TTACAGGAAC	240
ATGGATTCAA AGGGGGTGTT TNACCACTTG GGGGGCTTTT CCGGTTTAAC CAAAGGNNTT	300
GNAGGGGTNC TTGGTGGTTA TTGGGCTCCC AAATTTTTC CCCCCAAA	349

(2) INFORMATION FOR SEQ ID NO:1420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1420:

CAAGNTCNC GGCAAGNGT TTTCCANACC CTGGTTGCTT CAAGGACACA TTAGAACTCA	60
CACGGGGGAG AAGCCTTTTT TTTGCCCTCA CTGCAACAGC NGCATTTGAC AGACAGGTGA	120
ANTCTGAAGG NGTCATCTGA CAGACCCATT NTATTGTGAA NGAAATACCA	170

(2) INFORMATION FOR SEQ ID NO:1421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1421:

GGCAGAGCGA GAGCATGCCC TTNTGGCTTA CACTGGGT GTNAAACAAC TGAATTGTCG	60
GTGTTAACAA AATGGATTCC ACTGAGCCAC CCTTTTTTTT TTNTTNGTNT GTT	113

(2) INFORMATION FOR SEQ ID NO:1422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1422:

GGCANAGCAG CCACGGATCT NCGGGTGGAG GCATNAATGC TAACATGAGG GGTGTATTTC	60
TACATGTTTT NGCAGATACA CTTGGCAGCA TTGGGN	96

(2) INFORMATION FOR SEQ ID NO:1423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1423:

GGCAGGAGCC CAATTNTTCG AAGGTCTGGA ATGTATACTG TAGCCATTGC TTATTGTGGC	60
TCTGGTAACA ACAAAGCAAT TCGACGNCTG ATNANATGTT GCTGTANGTG AATGTTAATG	120
AATGATGTCA GGAGGGCAGC AGTAGNAATC ACTTGGGTTC ATTCTATTCA GAAACCCCTG	180
AACAGTGCCC AAGTGTTGTC TCTTTGTTGT CAGAGAGTTA CAACCCTCAT GTGGCGCTTA	240
GGGNGCTTGC AATGGCCTTT GGGGATATGC TGTGCTTGGT ACNGTAAACA AGGGAAGNCC	300
ATTGAATTTT GNTAAGAACC CCANT	325

(2) INFORMATION FOR SEQ ID NO:1424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1424:

AACAAGACGG AATTGGAACG GGGTTNTGNG CTACTATGGT NCCACTCCGN AGTGTGTGGG	60
GATGCTAGGA AACCCACCC	79

(2) INFORMATION FOR SEQ ID NO:1425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1425:

CNCATGAANC GCTTCGAGGG GNTCACGGTG CTAAAGGNT GCGCCGTGGA NCCGGGACTG	60
GGAACGTGGG CAGTCAGGGT GCTAGCTGCT TCTGGAGGTG AGCGAGCGGG TCGAAACCT	120
TGACCCGGCC TACTTNTNCC CGGAACGNCC CTGCTTCTTT CCTTNACCCA NCT	173

(2) INFORMATION FOR SEQ ID NO:1426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1426:

GGCANAGCAA GANCTCACCT CAAAGAGAAG CCCTTTGACT GCAGTCAGTG TGGAAATGCA	60
TTCCGGACCC TCTCGGCCCT GAAAATCCAC ATGCGAGTNC AACTGGCGA GAGGCCTTAC	120
AAGTNTGATC AGTGCGGGAA GGCTTACGGC CGNNGCTGCC ACCTCATCGC ACACAAGAGA	180
ACGCACACCG GAGAGAGGCC CTACGAGTGT CACGACTGTG GGGAAAGCTT TCCAGCACCC	240
CTCCACCTC AAAGAGCACG TNAGGAATCA CACGNGGGGA GAAGNCCTTA CGNNT	295

(2) INFORMATION FOR SEQ ID NO:1427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1427:

CCGATCGATC AGCTGGCGAC CGATTCTAAC TACCTGGAAG TTTGTNACAT CCTGCTGAAT	60
GGTGAAAAAC CGACTCAGGA ACAGTATGAC GAATTTAAAA CTACGGTGAC CCGTCATACC	120
ATGATCCACG AGCAGATTAC CCGTGTGTTC CCATGCTTTC CGTCGCGAAC TCGCATCCAA	180
TGGCAGTCAT GTGTGGTATT ACCGGCGCGC TGGCGGCGTT CTATCACGAC TCGCTGGATG	240
TTAACAATCC TCGTCACCGT GNAAATTGCC GCGTTCCGCC TGCTGTGCGAA AATGCCGACC	300
ATGGCCGCGA TGTGTTTACA AGTTATTNCC ATGGTTCAGC CATTTGGTTT NACCCGGGGN	360
AACGATCTTT TCNTANG	377

(2) INFORMATION FOR SEQ ID NO:1428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1428:

GACCAGCCCC TNCCGGGNGT CCTCTTATCC NTGAATTGGT GGCCTGTTTC NTTCCAACCT	60
NTTGACCCAG GACAACGGCA TTTTACCATT TTCAAACCTG AGGCCCTGGA CCANTTNTTA	120
CTTCAAACCC ATGAATGCAA GGAGTTCCGG TTTGAAGCCA TCCTACACAG AATGAATNGA	180
GNTGCAN	187

(2) INFORMATION FOR SEQ ID NO:1429:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 438 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1429:

GGCAGAGCTC GTCCANGANA GNATTNTNCC CCATGGGGAA GAACTNACAC TGCGTCCGGT	60
TTGTNCCCCA GGAGATGGGC GTGCACAGGT NCAGCGTCAA GTACCGTGGG CAGCANTTCA	120
CCGGNCAGCC CCTTCCAGTT CACCGTGGGG CCACTTGGTG AAAGGAGGCG CCCACAAGGT	180
GCGGGCAGGA GGCCTGGCCT GGNAGAGAGG AGAAGCGGGA GTCCCCAGCT GANTTCAGCA	240
TTTGGGACCC GGGGAAGCAG GCGCTGGAGG CCTCTCCATC GCTGTTGAGG GCCCCATTAA	300
GGCCGAGATT TACATTCGAT GACCNTAAAA ATGGGTTCGT GCGGTGTTAT CTTATATTGC	360
CCAAGAGNCT GGTAATTAGG AGTGTTCCNC AATTTCATG TTGNGCACNT CCGGAAGCCT	420
ACNGGTGCNG TTNTGAAC	438

(2) INFORMATION FOR SEQ ID NO:1430:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 359 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1430:

GGTACAGTAA TCATGGACTC CCGTCACCCG GATACCCTGC TGGCGGCACG TTCTGGTAGT	60
CCGCTGGTGA TTGCNTGGG GATGGGCGAA AACTTTATCG CTTCTAACCA GCTGGCGCTG	120
TTGCCGGTGA ACCCGTCGCT TTATCTTCCT TGNAAGAGGG TCGATATTGC GGAAATNACT	180



CGCCGTTCCG TAAACATCTT CGATAAAACT GGC GCGGAAG TAAACGTNC AGGATATTCG	240
AATCCAATTC TGCAATTATG ACGCGGGGGA ATAANGGGCA TTTTACCGTC ACTACATGGC	300
AGGAAAGGGA TCTTACGAAA CANACCGAAC GGGANTCANA AAACNACCTT TACNCGGAN	359

(2) INFORMATION FOR SEQ ID NO:1431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1431:

CCCCCGCCCG TGAATGCCGA AATGGTTGCC GATGTGCGCG TACTGGGGGC CATTNGCGTG	60
GTCGAAACCA CTNCATCCGG TGAATATGGC GCGCTGCAA AAATTCTTTG TCGAACAGGG	120
TGTCTGGATC CGGCCTTTTG GCAAACGTAT TTACCTGAAT GCCGCCCTAT ATTATTCTCC	180
CGCAACAGTT GCAGCGTCTN ACCGCAGCGG TTAAACCGGC GTTACCAGGA TGAAACATTT	240
TTTTGCCAAT AAACGAGAAG TCCGCGTGAG GGTTCCTGGC TACACTTTCT GCAAACAAGA	300
AAGGAGGGTT CATGGAAANT CATCAGTAAA CGGTCTGCGC GTTGGGGNTT AAATTGCCCCG	360
CANTCGTCAT GTCTTTTAAC GGGCATGGGG TTACNGATGG GGGTTAATAT TTTCANCNGA	420
TTTGGGGTGG GGNTGATGTT CNCGNNGGGA CGAAAAGTT TTTTGTACAC CTGTTACGNC	480
CC	482

(2) INFORMATION FOR SEQ ID NO:1432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1432:

CAACGGATGA AACCAAACCT GGTGTGCGGT CCGGTACAAA TNTGCTGGCA TAAATTCGCC	60
CGCNACTGGG AATGTGGAGC TCGTGAAAT CCCTATGNCG CCCCAGTCAG TTGTTTATGG	120
ACCCGAAACG CATGATTGAA AGCCTGTGAA CGAAAACACC ATCGGCGTGG TGCCGACTTT	180
NGGCGTGACC TACACCGGTA AACTTATGAA GTTCCCACAA CCGCTGCACG GATGCGCTGG	240
GATAAATTCC AGGCCGACAC CGGTATCGAC ATCGACATGC ACATCGACGN TGCCAGGTGG	300
GCTTTCCTGG GCACCGTTNG TTCGCCCCGG ATTATTCGTC TGGGAATTNC GNCTGCCGNG	360

TGTGAAATCG NTCATGTTTC AGGCCTNAAT TCGGTTTGGT TCCTTGGGTT NGGTTGGGTT 420  
ATTGGGGTAA GANAAGCGTT NCCAGAATNG TTGTTNACGT 460

(2) INFORMATION FOR SEQ ID NO:1433:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 415 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1433:

AGCAGGGAGC AGCACTTTAT CGGGNTCGGT GNTTTCACCG TCAATGAACA ATTTTTTNCG 60  
GATTAAATAA GTTGATAGCA ATGGCGATGG TTTTACCCAG ATGACGACCG ACATACTCAA 120  
TTACTTCCGA CGCCAACTA TCGCCTTTNT TCGCGGCTTT GCAGATTAGT TTTGAATGGT 180  
GCAGTCGTCC AGCGGCAGGA NCTGCTGGTA GCCCTGCTTT TAACAGGTTC AACACCCGTT 240  
GTTCCAATGG CAGCGTTGGC AGCGATATTT TTCCAGGCAG CCAAGTTGCC GCAATGGCAG 300  
CGTTTCACCC AGCGGTTTCG ACCTGAATTA TGGGCCATTT TCACCGACGT TGCCCTTGNG 360  
GGCCAATAAA AATGCGCCCN TTAGGGGNT NATNCCGGGG CCCGGGTNNC CCATT 415

(2) INFORMATION FOR SEQ ID NO:1434:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 469 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1434:

TTCTGGGCAA AACCATGACC CGGAACAGAT TGATTTGATT GATTTACTAG TGCAGTTGTG 60  
GCGTGGCNAG ATGACAATCA TCATTTCCGT CATTGTGGCT ATTGGCCTGG CTATTGGGAT 120  
ATTTGGCAGT GGCGGAGGNG AAATGGGACG TCAACAGCAA TTATCACTCA GCCCCGACGTG 180  
GGGCAAATTG CTGGGCTATA ACAATGCCAT GAATGTTAAT CTATGGTCAG GCTGCACCGA 240  
NAAGTTATCG GNTTTTCCAG GANGTCGTTN AATTGGTCGG TTTTCAGTTC TGCCNNNCTC 300  
TGGCATTNAG CAGAAAACGC TTGGGATAAT TCAGGGNAGG GANCGNGGAA AANNTTTACC 360  
CNTGGGAAAC CTTGCTGTTT TAGGAANCCA GGCAATTTTA CCCTTGATC TTGTTTTCTT 420  
AATGNTNNGG GGCAAACTN TCAGAGGGGG GGCACAATT TGATAGTTT 469

(2) INFORMATION FOR SEQ ID NO:1435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1435:

GTGAAGGGCT GAAAAATCGC TACGGCGCGC TGATGGNNGC CATTTNCGGC GTGCACTACA	60
NTTCTCTCTT GCCAATGGCA TNACTGGCAA GCAAGTGCGG TGNTATCTCG GNCGCTGATG	120
CCAAANAGAA AATTTCTGCG GGCTATTTCC GCGTTATCCG CAATNACTAT CGTTTCGGTT	180
GGGN	184

(2) INFORMATION FOR SEQ ID NO:1436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1436:

TAACCCGTCT NACCTTGAGA TTGTAAGCCC GGTAGTTATC GGTTCNTTTC GTGCCCCTTT	60
GGACAGACTT GAATGAGCCG AGCAGCAACA AAGTGCTGCC CAATCACCAT CCACGGTGAC	120
GCCGCAGTGA ACCGGGCAGG GCGTGGTTCA GGAAACCCTG AACATGTCGA AAGCGCGTGG	180
TTATGAAAGT TGGCGGTANG TAGTATTCGT NNATCAACAA CCAGGTGGT TTTCACCACC	240
TCTAAATCCG CTGGATGCCC GTTCTACGCC GTACTGTACT GATNTTCGGT AAAGATGGTT	300
TCAGGCCCCG ATTTTTCAC GTTTAACGCG GACGATNCGG AAGCCGTTNG CCTTTNTGAA	360
CCCGTTTGGG GGTTCGTTTT NCGTAACAAC TTTTAAAGGN GA	402

(2) INFORMATION FOR SEQ ID NO:1437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1437:

GGCGGGCGTA TTAAGACCAC GNTCAAGGCC AGCTGTNAAG GCATCGGCAG AGTTTTCCTG	60
CGGCGGCAAA CCTGNGNCAT TCAATGAGTG ATTTAACAGT AAATAATGTA ATTCACCGGT	120

CATCACGGTG CGNAAAATCG TTGAATTTGC TGGCTNTCGG NCTGCACCCA TTTGCAATGG	180
GTTCCGGGCA TGNCATAAAG AGAGGAAGGA GCCAGNGCTC GCGCGCCGNT TCAATTGTGT	240
TTCTTCCGNC GGGNGTTCAC ATTGTGGTTT ATCGTCATGA GAGACACATT AATCCGGGGA	300
TTAATCCCAG ATTATTGTNC GCCAANTNGA CGNTTAATTT GTTTCGGCCA TTAGGACGGG	360
NAAAACAGGG CCAGG	375

(2) INFORMATION FOR SEQ ID NO:1438:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 330 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1438:

TCAGAGGCAA GTTCAGACCG TGTTGTTTTT TTTTCACGGA TCCNGCCCTN NCTTCCCGNA	60
AAGAAGACAG CTTGGGTCG CGATTGTGGG GCTTNGAAGA GTCCAGCAGT GGGCAATTTT	120
TAGGAATTTG GGAATCGAGT GCATTTNCTG ACATTTGAGT ACAGTACCCA GGGGTTCTTG	180
GAGAAGAACC TGGTTCCCAG AGGAGCTTGA CTGACCATAA AAATGAGTAC TGCAGATGCA	240
CTTGATGATG GNAAACACAT TTAAAATATT AGTTGGCAAC CAGGTNATTN CATCTTGGNT	300
TTTATGGGGG GAAAGGTTGC AGTCAGNGGG	330

(2) INFORMATION FOR SEQ ID NO:1439:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 464 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1439:

GCATGANGAA TGTNCAGCTC GTCGATTTN TGGGGTTCCG CGCGGCCAG ACTCCAGCTC	60
AACGCTTTCT CTTTNATCTC TTCATAGAGC GCCANACGGC GTTTTTCGCT CAGCTTTTTG	120
GGAATCATTC AGCCCGGCAA TCGGGCGCGC CCGGGTCAAG GATCACCGCA GCGGTGACGA	180
ACCGGCCCAA CTGAACGGAC CCGCNTCCGA TTTCATCCAC ACCCGGCAAC CAGCTGNGTG	240
TGCGGGATNA AACAAATTCG GTGCATTGTG NTNAATNCCA GNAACGGTTT GTGCCACCTG	300
GTNCATCGGA CATTGACAGC GGNTTTGCTA GATGGNAGTT NCACGGNAAG GTTTTCGTNN	360
CANCGCGTGG TTGGTTTTNC CNGTTAGGNC AACAGTGTTT AACAGTGACC GCAGCCAGTT	420

TTTtagggTT CACATTTTtn CTGGCANTAA TTATTtGGGA TTAA

464

(2) INFORMATION FOR SEQ ID NO:1440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1440:

ATACGTCCGG TGGAGAAGGA GATATGGCAC AGCACTAAAG AGGCCACCAT CACCACCATT	60
TCTGGCGCAC CAAGTGCAAA CTGCAATTCG TTACCCGTCA TAAAGGCAAT TAGCGTGACG	120
ACAGGTNACG GTGAAGCGAA AATGGTTGCT AACACTGGAA CCAAAGAACA GATTCATCGC	180
GCGCTGAAAC CTGGTTGTTC AACACTGCTT TTNAATGCAC CTGAAACCTT CCGGCGACAG	240
ATTCAACAGT GCCACCAGGN AAGCCAGTTA AAGGCGACCA GGGGTCATTT CATGCTGTTC	300
GAGGCAATGT CTTCCCAGCG AGCTTGCGGT TNCATTTTTG GTTCACCGNA ATTAACGGGN	360
AATTCAGNTG GGNTAATTCA AACC	384

(2) INFORMATION FOR SEQ ID NO:1441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1441:

GANTACCAAT GGTACCGACC AGCATAGAAG CCATAAAGGT TGACCACTCA ATATTCAACC	60
CGCTGGTCAT CAAGATCATT CGGGAACCAT GACCTATCGA GCCAAGCAGC GCACACCAGC	120
NTTAATTTCC GCTCTGTAAA ACGTTCATCA TGCCTTTGAA TTTGCCCCTG ACAACGCGCT	180
NAAGGCTNCA TACTGGTATT GCAGGCTGTT ATCGGCAAAC TGGGTGCGTT CGCGAATACC	240
ATAATACGGA CGGTATTNAC CGTCCAAGNC GAAAGGCTGG TNCCGGGAAT NACGGTNTTT	300
GNCAGTTCCT GCGGGTTAGG NAGGGCGTTC ANGCCCTGAC GCCCGGGNAA TGTGTTTGA	360
CGTTTGGAGG GTNCATCGTN CAGTGNCAAC CCACCATTGG TTTGNATACC CCGTCCCAC	420
GTTTGNCATG NACNTTTTTT TNAAGTTTCA CTGGGGCAAA ATCGGTTATT CGNGGGGCCT	480
GN	482

(2) INFORMATION FOR SEQ ID NO:1442:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 321 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1442:

AACTCCGTGC NTGGCGACCG CAGCCCGGTT GTAGATATCA NCTTCCCGGA AATCGAGAAG	60
TTTGACCGTN TACCGGAACC GCGCGCCGAA GGCCGGACCG CTTTTTTTTTC CATCATGGAA	120
GGCTGCAATA AATATTGCAC CTACTGCNTG GTGCCTTACA CCCGTGGTGA AGAGGTAAGC	180
CGTCCGTCCG ACGGATATTC TGTTTGAGAA TTGCCCAGCT TGC GGCTNCA GGGCGTGCNT	240
GAAAGTCCAA CCTGCTCGGT CAGAACGTGA AACNCCTGGN GTGGGTGGAA AATAACGACG	300
GGCACCACCG GTTNCGTTTT G	321

(2) INFORMATION FOR SEQ ID NO:1443:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 361 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1443:

TTTCTGCATC CCCTGCGGGA AGCCTGCTGC CATGACAGCC TGAGCGTGAA TGCGCGGNTA	60
TCAATGCCGA CAATTCACGN CCGTATCACC CCAACAAGCG CAGATGTTTA AATATCATCA	120
GCTCGCGGTG GACAACAATT GGC ACTCCCG TAGACTGNCC CTCATTGCCA TCAATCCGGC	180
TATCAGGGGC GCATGGCGAT CCACGNAAAT GGATGGTGGT GACGCCGNA ATTAACGGGN	240
CCGCTAATTG CATGAAAAAT GTGGATGNAA CAAGCACTGG GAGGCGAACT TAGTACCGGN	300
CAACAACACA AGGNCCTTCA ATCAAAAATG GGCCTGCAAA AAGTGATNAG CGGTGTACAC	360
N	361

(2) INFORMATION FOR SEQ ID NO:1444:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 480 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1444:

TTATAACGGC GCGCTGGTAC AGAAGGCCGC TGATGGTAGC ACCGTGGCGC AAACGTCTCT	60
CAGCTATGAC GACTATCGTT TCCTGGAAAA ACTCTCTCGC GAGTCGGTTC TCATTTTCNAC	120
GGCCTGGACC GCACCACGCT GTACACCGCC AACCGTGAAT ATCAGCTACT ACACGGTGCA	180
TGAATCCTTC GTTGCCACCA TTCCGCTGGT GTTCTGCGAG GGAGNAAAAT GGACCCCAAT	240
ACCCAGTTCC TGAAAGTGAA TGATGATTGA TGAACCCGCC ATCCTCGGAC CAGGCTTATT	300
CGCGCGTTAT TTCCGCAGAA GTTGNAAGA GGAAATATTA CCGTGCTTGN AAAAGTGGCG	360
NCNGTAATTT CCTCGGAATT CCTCGGTTAA ACGGGGTAA ACAAAGGTTA CGGGGGGTNG	420
AAAATCATTG GGCCNACGTN TTAAGTTTTT NAAACCGGAG GGAATTCATG GGGGNTTGG	480
	480

(2) INFORMATION FOR SEQ ID NO:1445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1445:

GGCACGAGTA ACTCTNTCTT TTCCTGATAA CATGGCCAGC AAGAAAGTAA TTACAGTGTT	60
TGGAGCAACA GGGGAAGCTG GTGGCAGACT CCGCCAAGCA CCTGGGTCTG AAGCACGTGG	120
TGTACAGCGG CCTGGAGAAC GTCAAGCGAA CTGACGGATG GCAAGCTGGA GGTGCCGCAC	180
TTTGAACAGC AAGGGCGAGG TGGAGGAGTA CTTCTGGTCC ATTGGCATCC CCATGAACCA	240
GTGTCCGCNT GGCGGCCTNA CTTTGAAAAA CTTTCTCGN GGNGTGGCGG CCCGTGAAAA	300
GCCTCTGAAT GGNG	314

(2) INFORMATION FOR SEQ ID NO:1446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1446:

TAATGCNCAC GGAAGTGGAA GGGAATTTTA AATGATTCCA CCCTGCTGGC GGATCTCAAT	60
AGCCCATTGC CAGAAGGCTC CGTGCGTAAC TGGAATCCTG CCGGTCGTCG CGGNNTAGTG	120
AATTCTGGTC ACTAAAGAAG CGCATTGCCT TGGCGATTG TTGATGAAAG CCAATTAACG	180

GCGGCCTGGA TGTCGAAATC GCGGCAGTTA ATTGGTTAAC CACGATAATT TACGTTCTCT	240
GGTTGAGCGT TTTGAATAAT TCCGTTTGAG CCTGGTAAGC NCATGNAAGG GTTTAACCCG	300
NAAAGGNGCA CGNTTCAAAA GATGGGGGG	329

(2) INFORMATION FOR SEQ ID NO:1447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1447:

ACTAATGGCA CCTGCAGATG ACCGTGGGCT GGATTTTCAG TAAGTCTCTG GGGGTTGATG	60
AATCCACCGT GGCAATCGTT GTTATGGCAA CCATGCTGCT GCTGGGTATC GTTACCTGGG	120
AAGACGTGGT TAGAAATAAA GGCGGCTGGG AATACCTTAA TCTGGTACGG CGGTATTATC	180
GGCTTAAGCT CTTATTATC GAAAGTTAAA ATTNCTTCGA ATGGGTTAGC TGAAGTCTTT	240
AAAAATAAAC CTGGGCATTT TGTGGGTCCA CGGGTAACGT TGNGTGTCTT CGTTAATTAT	300
TTNCCTCAG GATTGTTTCGT GGCCTTAATT TCCTTNGNT TTCCCGTTAG GTG	353

(2) INFORMATION FOR SEQ ID NO:1448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1448:

GGCANGAGGG NAGACAGAAA ACAGGTCTTG NTTCCCAAN TGGCATTGGA CTTTCTGAT	60
ATTACTGCCA ACTCTTTTAC TGTGCACTGN GATTGCTNCT CGAGCCACCA TCANT	115

(2) INFORMATION FOR SEQ ID NO:1449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1449:

GGCAGAGGGN AGAATGGAGA GGGGGCTGCC GCTCCTCTCC CCCGTGCTCG CCCTCGTCCT	60
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CGCCCCGGCC GGCNCTTTTC GCAACGATAA ATGTGGCGAT ACTATAAAAA TTGAAAGCCC	120
CGGGTACTTN ACATCTCCTG GTTATCCTCA TTCTTATCAC CCAAGTGAAA AATGCGGATG	180
GGCTGATTTTC AGGGTTCCGG ACCCCATACC AGNGNATTAT GATCAAANTT NAAACCTTCA	240
ATTTGGATTT TGGAGGGACA AANGAC	266

(2) INFORMATION FOR SEQ ID NO:1450:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 390 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1450:

GGCANAGGCA AAGATCCCTG AGGATGTGTC TGGTCTCGTT TCTCTTGAGG TTCTTATCTT	60
ATCAAACAAT CTTCTAAAGA AGCTTCCCCA TGGTCTTGGA AACCTTAGGA AGTTAAGAGN	120
AGTTGGGATC TAGAAGAGAA CAAATTGGGA ATCCTTGNCC AAATGNAAAT TGNCATATCT	180
TAAGGNTTTA CAGAAATTAG TCTTGACAAA CAACCAGTTG ACCACTCTTC CCAGAGGCAT	240
TGGTCACCTT ACTAATCTGC ACACATCTGG GGCCTTGAG AGAACCTGAC TTGACTGCAC	300
CTTTCCTGNA GGAAATTGGT AACTGCGGAG GAACCTTGGA GGNACTGTAT TTGNANTGAC	360
AAACCCCAAC CGGCATAGGC NTTCCCTTTT	390

(2) INFORMATION FOR SEQ ID NO:1451:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 313 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1451:

GCGAAGCTGC CTGCAACCTG GAACCGGGNA GCGGCACAGG AGACGGTGCG GCTGCTGGGC	60
GGGCCAGNGA AGCAAGGNGG GGCCGCCCCG AGGGAAACCA TGCTGCCTTC CAGGCTGACG	120
TNTCTAAGGC CAGGGCCGCC CAGTGCCTGC TGGAAACAAG TNCCAGGCCT GCTTTTTTTCG	180
CCCACCATCT GTGCGTTGTN TCCTGTGCGG GGCATCACCC AGGATGAGTT TTCTGCTGCA	240
ATTTGTTTGA GGATGACTGG GANCAANTCA TNAGCTGTNN AACCTCAAGG GGCACCTTTC	300
CTAGTCACTC AGG	313

(2) INFORMATION FOR SEQ ID NO:1452:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 180 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1452:

GTCGTCGCCT TTAATCAGAC GGGTATTAAA ATCATCGGCA AAGCAGCTAT TAAAAATTTT	60
AATCAACTGC TCGTANTGGT GTGTACTGTT CATTAGTTCA TCCCCAACCA NTGGGGGNTC	120
TCCTGTCCGT GGTGTGCGTA ANTTAATTTG GCACTGCATC ACCGTNCGAG ACGNTTAACA	180

(2) INFORMATION FOR SEQ ID NO:1453:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 489 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1453:

AACCTGGCCT CANTTTGATT CACCCGCTTC AGGTGTTCTGA GGTGAACAG CAGGATAATG	60
AAATGNTGGT CTATGCTGCC CCCCCTGAAT GTGCGTGAAA CGTACCTGGG CAGCTTGATA	120
CGCCTTTATT TACGTTGCGC TTTTCTCCC CACAGGTAAG GTATTGTCGG TGTGCGGATT	180
GAGCATTTTC AGGGGGCGCT GAATAACGGT CCTCATTATC CGCTCAATAT TTTGCAGGAC	240
GTGTAAGGTC ACAATCGAAA ACACAGAACG TTATGCTGAG TTAAAAAAGT GGGCAACTTA	300
AAGCGNCGCG TNTTCAGCAA AAGGTGGAGT TTCTGGGTCA CTGGGATTTT TCTGAGGCAA	360
CGGNGNGNCG TTATTAACCG GTTAGTTCAG TGGAAAATTA ATTGGGTAC GTGCAGGACA	420
NGANTAATTC ACGCAATTAT ATGTTNAGG CGGTTGATCT TGGGGTTGGG GAACAGTTTA	480
GGGTCNNGG	489

(2) INFORMATION FOR SEQ ID NO:1454:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 325 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1454:

TATCAATGCC GAGAATATCC AGCCACTGCT GCACCANTTT TTGCTGGCGA ATCCGAAACG	60
GCCTGATAAA TGGCCAATCG GAATCAAAAT GAGNCCAGTA AAGGAATGCA CATTNACGGN	120
ACGGTAAGNT NGNAGCCCGG TNAATGCCAG ATGGCAAAC AACTTGCTGN ACGTGAACCG	180
NATNATGNCT TTTTGAATAT CCCAGAATGG GTTTNCGCCC GCTGCCGNGA ACGTTCGTTC	240
CGAAAAAGGC GGTGCAAATC GTTTGCTGTT AACCTTGCGG GATGGATNGT CATTAACCAG	300
GGTTNATTA AGTGNGTTTT NCCGG	325

(2) INFORMATION FOR SEQ ID NO:1455:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 238 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1455:

AACCATTTCG ATATCTCTCT GCGGATGTTT ACCCATGTGG GCGCGGCGGC ACCGGGTAAT	60
CCTACCGCTA TCGATACCCA CTGGATTGTTG CAGGAGGGTG ATTGTGCCTT GACCCAAAAT	120
CCGCTGGAGA TTA AAAACGG AAAAATTGCC GTTCCTGATG CGCCCGGTNC TGGGGTGGNA	180
GCTGGNACTG GGGAACAGGT NNCAAAAGGC ACATGAGGCC TATAAACGT CTGCCTGG	238

(2) INFORMATION FOR SEQ ID NO:1456:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 414 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1456:

GGCACGAGCC TTCATTGCCT CATGTAAGAC AACCTCACCA AATACAAGAA AACAGTGTCC	60
AGCCACCTT TGACACAGTT TTTNCTTGAT TGTGGAGGAC TAGCTCGAAC AGATAAGAAA	120
CCTGCCATTT GTAAAAGTTA TCTCAAATA ATGACAGANC TGTGGCATAA AAGCAGGCCA	180
GGATCTGTTG TGCTACTAC TCTGTTTCAA GGAATTAAAA CTGTAAATCC AACATTTTCG	240
GGGTATTCTC AGCAGGATGC TCAAGAATTC CTTCGGTGTT TAATGGATTT GCTTCATGAA	300
GGATTTGAAA GAGCAAGTCA TGGAAGTAGG AGGAAGGTCC GGNAAACCAT AACCCCTTNT	360
GGGGGGCCAT TGGGAGGGNG GGNCAAGGGC NATCCGGTTT TTGGGTTTTT CAGG	414

(2) INFORMATION FOR SEQ ID NO:1457:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 384 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1457:

GGCACGAGGA CATATTGATC CCTCTCTNAG ACTCATCTGG GATTGGGCTT TCCTTGGAAG	60
CTCTTACGTG ATGTGGGAAA TNACAACACA GGTGTCACAC TACTACTTGG CACAGCTCAC	120
TAGTGTGAGG CAGTGGAAAA CTAATGATGA TACAATTGAT TTTAATTATA CTGTTCTACT	180
TCATGAATTA TCAACACAGG AAATAATTCC CTGTCGCATT CACTTGGTCT GGTACCCTGG	240
CAAACCTCTT AAAGTGAAGT ACCACTGTCA AGAGCTACAG ACACCAGAAG AAGCCTNCGG	300
GAAACTTGAA GGAAGGATCT NCNTGTAGTT ACCCAACAGA GCTTTAGTAA TTTTTTAAAA	360
AGGAAAAANT GATNCTTTTT TCCG	384

(2) INFORMATION FOR SEQ ID NO:1458:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 468 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1458:

CTGCTGCCCC TNAGGGGCCA AGCCAACANA GGCTGCTACG GGATCCCAGG GATGNCCGGC	60
CTGCCCCGGG CACCAGGGAA GGATGGGTAC GACGGACTGC CGGGGCCCAA GGGGGAGCCA	120
GGAATCCCAG CCATTCCCGG GATCCGAGGA CCCAAAGGGC AGAAGGGAGA ACCCGGCTTA	180
CCCGGCCATC CTGGGAAAAA TGGCCCCATG GGNACCCCTT GGNTNTTTAA GGGGTGCCCCG	240
GCCCCATGGG CATCCTTGGA GAGCCAGGTN AGGAGGGCAG NTACAAAGCN GAANTTTCCA	300
GTTAAGTTTT TCACGGGTCA NTNGGCAGAC CCCAACCAGC CCCTTGNAAC CNAAAAGCTT	360
NTTANNTTTA AAGGGGGGTT CTTAACAAAC CCGAAGGGGT TTTTNNACA AGGGCAATTG	420
GNAATTTTAA CTTGAAAANT NCCCGGTTTT AATATTTTTT TTTTACCA	468

(2) INFORMATION FOR SEQ ID NO:1459:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 415 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1459:

GGCANAGCCA GCATCAGGCT TCCAGAGTTT GCAATTCCGA CTATTAGAAA ACAAGATAGG	60
TGTTCTTCAG AACATGAGAG TCCCTTATAA CAGAAGACAT TATCGTGAAT AACTTCAAAG	120
GAGAAGAAAA TGAAGTCTA CTTAAATCTG AGCCAGGAAA AGACACTTCT GGAAATTAGT	180
GGAGGCATGG CTGGAAAGAA CTCCAGGTTT AGAGCCACAT GGATTTAAGT TCTGGGGAAA	240
GCTTGAAAAA AATATCACCA GAGGCCTGGA AAGAGGAATT CCNTAAGGTT TCAGGCTAAA	300
GAAGAGTCTG ANGAAAAGGG GGAACAGTGG CTGAATTTCG GANGCAAAAG AGGTGCTATG	360
TCCNTATTTG TTGAGAAACG TCCTGAACCA TTCCCTTNGT NAAGGTTAAA NACGG	415

(2) INFORMATION FOR SEQ ID NO:1460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1460:

GGCAGGAGCT CGGCTACATT CACCTGCTAT GCTTGTNACT CCACCCTGCT CTAATGCCGC	60
TTTCTCTGCA GGCTCTTCTT GGTCCCCAA GCTAAGTGGC TCTTGCCCTT GTGTACCTGC	120
ATTGCAGTTT TATGATACTT CTCATGTCGT GTCTGTGCTT TCCTACCATG CATTATTATT	180
CACGTGCTTG TCTCATCTCT TCTGCCAAAT TCTAAGCATC TGGATGGCTG GGTTTAAGTT	240
GCATCTCTGT GTCCTTCAGA CCATATGCCA TAGTGCCTTG TGCCTCACGG TGACTTGTAT	300
TTTGCAGAAG CTTAACAGAT ATTAAGTGG ATATCCAATT ATAAAAGAGT CATNAAATAG	360
ATGGTATTTT ATGGTTAACA ATATTTAAAT GTAGGAAGTT TATTCAGTTC CTGCGNAAAA	420
TCAACTCTCA AATTCCAGTT TTGTTTTTCT TTGAAAGTGT CTGAAAAACT NG	472

(2) INFORMATION FOR SEQ ID NO:1461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1461:

GGCAGGAGGT TTCTTATATG CACACAGCAT GCCTCTGCAA TGCCATCATT GCTTTGCTGA	60
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AAGTTCCCCT TTCTTTCCAG AGATATTTTT TCCAGAACT ACAGTCTACC AGCATCAAGC	120
TTGCTCTGTC ACCATCGCCC CGGAATCCTG CAGAGCCCAT TGCTGTCCAG AATAACCAGC	180
AGCTGGCGCT AAAGGTAGAG GGAGTGGTTC AGCACGGGAT CTAAACCAGG ACTCTTCCGC	240
AAAATTCACT CTGTCTGTCT TGAATGTTTT CTTCCACACT GCAGAGTAAA ATCTGGGACA	300
AGACTTACAA GGTTACCCCA TTTGACAAAC ATGGACCCAA TGNGGTTGGA GCAAAGGGTT	360
TGAACNCCN AATGGTTATT TTCAGTACTC NATTTCTGTT GGAACCTTTG GTTATCCTTG	420
GGACCACACA CCTTTCAGTG GGATNTTTTT TTGAAAGATG NCCATGGTTT GGTTTTGGAG	480
GCTTGAG	487

(2) INFORMATION FOR SEQ ID NO:1462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1462:

GTTCGGCGTT TTGCGTCGCT GTGNCCTTCC ACCATCGNAA TCATCCGATC CAGAAATNTC	60
TCGCCGGGGT TAACGCTACA CTCAATCACC AGCCAGTNAG AAAGNAATAC GCGTGCCTTC	120
GGTGAACGGA GGCAAANATN CGCCGCCGGG ATTCACGGAT CACCGGTGAC CNATNTCCCC	180
GGTGATGGTC GNTTTGCATA CGACCGANGC ACCCCCTTCA ATAAACTTNA CCATCGCAGG	240
GGG	243

(2) INFORMATION FOR SEQ ID NO:1463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1463:

GGCANAGCCG CAGGACCCCA TCCTGTTCTC GGGGACCCTG CGGATGAAAC CTGGACCCCT	60
TCGGCAGCTA CTCAAAGGAG GACATTTGGT GGGCTTTGGA AGCTGTCCCA CCTGGCACAC	120
GTTTGTANGG TCCCAGCCGG CAGCCTGGGA CTTCCAGTGC TCAAAGGGCG GGGAGAATCT	180
NAGCGTGGGN CANAGGCAGC TCGTNTGCCT GGGCCCGAGC CCTGCTCCGC AAGACCCGCA	240
TCCTGGTTTT AAAACGAGGC CACAGCTGCC ATCGAACCTG GGNGACTGAN AACCTTCATT	300

CCAGGGTTAC CATCCGGNAC CCAATTTGAA TACCTGNANT GTTCCTGACC NTGGAAAACG	360
GNTTTAACAT TTTCNNGGATT ACANCAGGTN CTGGTTCCTG GACAAGGAGT AGTAGTTGAT	420
TTAATTNTCC AGCCAACTTC NTGCAGTAGN GGCATTTTTT AGGGATGGCC AAAATNTTGG	480
ATTTGTC	487

(2) INFORMATION FOR SEQ ID NO:1464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1464:

CCTGTGTACA NAGGATTGCT NCCNCTACGC TATGTGGGAC ATTGNCCATC CCATGCAACA	60
ACAAGGGAAG CTCNATCAGT GGGTTTGAAT GTGGTGGCAT GCTGGGCTCG GGAAAGTTCT	120
GCGCATGCGG TGGGCACCAT TTTTCCCCGT TGAGACACCN CATGGGAAGG GTTNATGTCC	180
TNGTCCTCGT NACTTCNGAC AAGAG	205

(2) INFORMATION FOR SEQ ID NO:1465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1465:

GGCAGAGGAT TTGAGTGGCA TATAACCAAA GGCGGAAATA TTGGGGCTAA GTGGACTATT	60
GACCTGAAAA GTGGTTCTGG AAAAGTGTAC CAAGGCCCTG CAAAAGGTGC TGCTGATACA	120
ACAATCATAC TTTCAGATGG AAGATTTTCAT GGAGGTGGTC CTGGGGCAAG CTTGACCCTC	180
AGAAGGCATT CTTTAGTGGC AGGCTGAAGG CAGTAGGGGA ACATCATGCT GAGCCGAAAA	240
CTTCAGATGA TTCTTTAAAG ACTTACGGNC AAGCTTCTGG AAGGGGCACA CTNACACTTT	300
TTANTGAAAA ATGGGANTCC TTAAATAAC TCTCTTTCAC CCCAANTANG GTTTGGNTTA	360
TTCTGGCAAA AGTGATTTAG GANCTTAGGT TGCAGGGGAA ATTGGTTTTA ACTTTTTNCA	420
GTTTTTC	426

(2) INFORMATION FOR SEQ ID NO:1466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1466:

GGCAGAGCTT TTTCCANAAT TTAAAATTGT AATAGAAACA GAAGATGAGA TTATGCCTGA	60
GGTTGTGGAA AAGGAAGATT ACTCAAAGAT TATAGGGAGC ATGGGGATAT AATGGGAAAG	120
CAACACTCCA GTGGTGCAGA TGCTCACAGT CTTATGGAGG AGCCCAAATG AATATCTGGG	180
GAAGTTAAAG TCCATATGAA TGNACTGATA AAGAGTACAA TACAGGTGCC ATGGGGANCA	240
CGTGNGCATT CACTGGAAGA CTGCCTGGNA GGGGGCCGCG CGTGTTTTCCT ATGGCCTATT	300
ACGGTTAANC CTGGTNACAT AATGGAAAAT GCTTATNCTT TAGGTGGAAA GGNGAGCCTN	360
GAGTTTAGCC GGTTCAGGG T	381

(2) INFORMATION FOR SEQ ID NO:1467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1467:

GGAACGACCT TAATNAAAGC NATTNAGGCT TATGGAATGA NGCCACATNA AATATTCAAG	60
GCAAATAACC TTTTANGAA TTGGAAAACA TGNCCCAGGT TCAAACACT CTGGTGGCTC	120
TGGACAGGTC TGGCTNAAAN CAAAAGGTTT CCATACANCC ATTGACATTG GGGTTAAGTT	180
TGCGGANAAC CAANCAAGAG GTTTTGATG	209

(2) INFORMATION FOR SEQ ID NO:1468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1468:

GGCANAGCTC GAGTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTAN NCCCCCN	57
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(2) INFORMATION FOR SEQ ID NO:1469:

(i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1469:

AGATGCAACT ACCATCACAG AATGTNTTCA TACCTNNNGT AAAAGCTGCA TCGTAAGACA	60
TTTTTACTAC AGCAACAGAT GTCCAAAATG CAATATAGTA GTACATCAGA CACAACCTCT	120
TTATAACATA AGGTTGGACC GACAGTTACA AGACATAGTG TACAAATTAG TGATCAATCT	180
AGAGGAAAGA GAAAAAAGC AAATGGCATG GATTTCTATA AAGGNAAGAG GTCTAGNNGT	240
ACCTNAAACC TGCTGTTCCA CACNC	265

(2) INFORMATION FOR SEQ ID NO:1470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1470:

AAAGGNTTGA ACCGTGCCTC ANAGGCAGTA NAAGCCCCAT GGTGGTGGTG CTGNGTGGNA	60
GTATGGAGCC GGCCTTTGAA AAGAGGTGAA CCTCCTGTTC CCTAAAAAAT TTCCGGGAAA	120
GNCCCAATNA AAGATGGTGA AATAGTTGTT TTTAAAAGTT GANGGGNCGG GN	172

(2) INFORMATION FOR SEQ ID NO:1471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1471:

NATGTTTAAAG ANCACTCGTN AAAGTGCNTT CAGGCCATCA AGGGTATGCA TATAGAGAAA	60
GCCACGAGTA TTCTGANAGA TGTGCACTTT ACGGAAACAG TGTGTACCNT TCCGACGTTA	120
CATGGTGGNG TTGGCNGTGT GCGNGGTCAG G	151

(2) INFORMATION FOR SEQ ID NO:1472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1472:

GGCANAGGNC AAAANATACT AGAATTNATA GTGGAGAGAA ACCTTACAAG TGTAATGNGT	60
GCAGCAAGNC CTTCCGTCTA AGGTCATACC TTGCAAGCNA TCGCAGNGTT CATAGTGGTG	120
AGAAAACCTT ACAAGNGTAA TGAGTGCAGC AAGGNCCTT	159

(2) INFORMATION FOR SEQ ID NO:1473:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1473:

GGCANAGGGG ANGCCAACTT CANTNTATCC TCAATNCATG GAGACATNCC CANAAAGNGC	60
GGGNGTCCAT CATGAAGGAG NTCCGGTTTCG GGCGCCACCN GGTGCCTTAT TTCTGACAGA	120
TNNTCTGGGC CAGGGGGTTG GATGNCCCTC AGGTGTCCCT CATCATTA	168

(2) INFORMATION FOR SEQ ID NO:1474:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 374 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1474:

GGCAGAGACG GNCACGAGAA GACTTAAAGG TAAAGCGTAT TACCCCTCGT AACTTGGCAA	60
CTTGCTATTC GTGGAGATGA AGAATTGGAT TCTCTCATCA AGGGCTACAA TTGCCTGGTG	120
GTGGTGTGTCAT TCCACACATC CACAAATCTC TGAATTGGGA AAGGAAAGGA CAACAGGAAG	180
ACTGTCTGAA AGGGTGCCTG GNATTCCCTT GTTAATCTCN AGGNACTGTT AAATNACTCT	240
GAGCAGNTGG TCCCAGTGTT GGTGATTCCC AGTGGA CTGT GATGNTCTGT GAAAAAACC	300
ACAATTTTTG CCCTTTTTTG GGTTAATTGC TGTTTTNAGG CCAAGTTTGG GGAAGNTTTA	360
AATTAGNNTT TTCC	374

(2) INFORMATION FOR SEQ ID NO:1475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1475:

TGCCAGTATT TGANCATTAC CATGAAGGAA CTAGCAGTTA TGAAGTACT GGTTTAGCCA	60
GAGGTGGGGA ACAGTTGGCT AAATTAAAGA GGAATTATGC CAAAGCAGTG GAACTNACTG	120
GTGGNAACTN AGCTTCTCTG CCAGACTTCT TTTGTTACTT TGGATGAAGC TATTAAGATG	180
AACCAACAGG CGTGTGAAAT GCCATTGNAN CATGTGCATC ATCCCCGGG ATTGANCGTA	240
CTCTTGCTTA TATCATCCAC AGTAGCTGGG ATGGAGGAGA GAGNN	285

(2) INFORMATION FOR SEQ ID NO:1476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1476:

GGCAGAGATG GGCAGTGGTG CTGGATTAA NGTTGATGCC ACTAAAGATC CTTGGGAAAA	60
CCAACTACAG AATGTNCTCT TAATGTNACA AAGGAGCTTC CCCAACTNAT AAATGCCCCA	120
TTTNCAGTG GGATCCCCAA AGGAATGTCT ATTTTGGCC ACTCCATGGG AGGTCATGGA	180
GCTCTNAATC TGTGCCTTTG AAAAAATCCT GGGAAAATTA CAAATCTGTG TNAGCATTTN	240
NTCCCAATTT GGNAACCCTG GTAATTCTGT CCCTGGGGCA AAAAAGNCTT TGGTGGAT	298

(2) INFORMATION FOR SEQ ID NO:1477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1477:

GGCAGAGNCA CCAGCCTCTN ACGGAGGCAT CTTAATGTNA ACCTACCTAC CATTGCCCTG	60
TGTACACAGA TTCTCCTCTG CGCCTATGTG GACATTGCCA TCCCATGCAA CAACAAGGGA	120
AGCTCACTCA GTGGGTTTGA ATGTGGTGGA TGCTGGCTCG GGAAAGTTCT GCGCATGNTT	180
GGGCACCATT TCCCGTGAAA CACCCATGGG AAGGTCATGC CTGGATCCTG TACTTCTACA	240

GAGNATCCTG AAGAGGATTG AAAAAGGAAG AGGCAGGCTG CTGCTGNAGG AAGGCAGTGA	300
CCCAAGGAGG GAATTTTTC A GGGGTGAATG GACTGCTTCC CGTTTCCTGA GTTTCAATGG	360
TTAATTTAGG CTTGNGTTNN CANATTTGGT TTN	393

(2) INFORMATION FOR SEQ ID NO:1478:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 88 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1478:

GGCANAGCTA TGGGTCGTGG AACAAAAGTT AATCCTACAC CTAAANANG ACCAAACTAA	60
GTACTTGGAG GAACGAGNNA TAAAGGTG	88

(2) INFORMATION FOR SEQ ID NO:1479:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 72 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1479:

GGAAGAGTNT CTACTGTGGG CAAGTNTTTA AGANGTCCCC CATGCGGTAA AAGANCTTNG	60
GAATCTGGCT GC	72

(2) INFORMATION FOR SEQ ID NO:1480:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 249 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1480:

CTCCGTGNCA CTTTATGAGC GCATGAATCA GTCTCTCTCC CTGCTCTACA ACGTGCCTNN	60
CAGTGGCCGA GGAGATTCAG GATGAAGTTG AATGAGGTNC TTCAAAAAGA GGCAAACTG	120
ATTNCAAATG ACGTCTTGGC CAACATGATT AGTGAACCAA GGAATCAGTT ACGGAAACGA	180
TGCTCTGCAT GCCATTCTTT NAACCGAAAC GAAAACCACC GTGGGNGGNT TCCTTTCCCG	240
TNGNAATGG	249

(2) INFORMATION FOR SEQ ID NO:1481:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 364 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1481:

GGCAGAGGNT GAATCTCCTA TAATGATGGA AGAAGAGGTT CTCTTGTCTT AGATAGATNA	60
GAGCCTTCTC CAAGAGCAAT GTCAAAACTT GGGCTGTCAT CTTTGAGCTG TTTACCAAAA	120
TACAGACCAT TATTGAAGAA AAACAAATTA TCTATTTTGT TTTCCCCCAT CTAATATGAT	180
AGTGCCCCCA ACCAGGTTGT AGCATTGCCT TTATAAAGAG ACTCACTCAC TCTTAGTTTT	240
TAAGGAACTG GGAAATTTCC CATCCTCAGA TCCCTTAAAG GATGAAGAGT TGGCTGTACA	300
CTTAGCGGAC TTGCCTCNTG GTATGCAAGG GANTACTGGT TTGAAGGTCN GTTTTGNNCG	360
TGTC	364

(2) INFORMATION FOR SEQ ID NO:1482:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 398 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1482:

GGCANAGGGA CAGACCAAAG TATCCTGGAA TCAAATTTGA AGAACTCTTT CCAGATTGGA	60
TATTGGCATC ANAATCTAAG CGAGACAAAA TAAAAACAAG TCAAGCCAGA GAATCTGTTA	120
TCAAAAATGT TAGTGAATTG NATCCTGNAC AAGCGGATCT CTGTAGACGA ANGCTCTGCG	180
TGCACCCATA CATCACTGTT TGGTATGACC CCGCCGAAGC AGAAGCCCCA CCACCTTCAA	240
ATTTATGAAT GCCCAGTTGG GAAGAAAGAG AACATGGCAA TTGAAGATTG GGAAAGAGCT	300
AATTTTACAA NGAAGTCCTG GGTGTGGGAA GGAAAGGAAG CAAGGANTGG TGTTTGTA	360
AGGATCNAGC CTTCCGATTG CCAGCAGTNA GTTGNC	398

(2) INFORMATION FOR SEQ ID NO:1483:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 259 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1483:

GGCANAGTNA GGAATGGAGA AGCCAGAGAT TATTGATGAG CTGCTGAATA TAGAGAAAAA	60
TCCCCAAAAG CCTCAATATA GTATGGCTGT AGAATTCCT CTAGTCTTAT ATGAACTGTG	120
ANTTTGAAAA TGTGCAAGTG GATCTATGAA CCAGGAGGCT CAGGAGTTCA ATATTACCCA	180
CCTACAACAA CTGTGGGTCT TAATCATGCT GTNCAAAACT GCACATGGTT TGTATTAGG	240
TATNNGTAAC NTGAGTTNT	259

(2) INFORMATION FOR SEQ ID NO:1484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1484:

GGCAGAGGAG TTTTTTTTTT TTTTTTTTTT TTTTTTNNAT TNTNAAANTT TT	52
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(2) INFORMATION FOR SEQ ID NO:1485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1485:

ATCCTAACTC CAACCCACCA TGTNACAAGA CAATGGATGA GGATATTGTG AATTCAGCAG	60
GACGATGAGA TCCGCTTAAA GATTGTGGGG ACCCGTGTGG ACAAGAATGA NNATTTTTGC	120
TAATTGGCTC CCTGAATGGA CGATTACTTG GGGCTTGTA GCTGAGCCTG GTGGCCTCCT	180
ACCNTTGGTC CTA CTCTAGG AAGTGTGATT GTAACNCTTA TCATGTTGTC CAGAGGTCCA	240
GTTTGGCTGC TGTGTGGAG GCAAGGNAGG CAACTCATNC CAGAAGGCAT CTGGGTGCTT	300
CTGTAGCTT AA ACTAATTG CCTCCTCATN TTTCAAGTAT GTGGTCTTA AGTATTAAAA	360
AGTNCCTNGG TTTCTCCAAA AAAAAANAAA AN	392

(2) INFORMATION FOR SEQ ID NO:1486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1486:

GGCANAGGGA GACCCAGGTT GCTAGGACTC TTTCTTGGC TTGATGAAGC AAGAGGCCAT	60
GTCAGGGATC CATGAGGCCA GGAAGGAGGG CAGCCCACAG GAACCTCTGC AATAACCTAG	120
GTGAGCTTGG NAAGCAGCTC CTTCCCCAGC CTCACGTTCA GATGAGCTCT CCTCCCTGAG	180
TGATACCTCG ATCAGATCAC AATTCTCAGC AGACTCAGCA AAGCCATGTC CAGCCTCCTG	240
GCCCACAGAA ACCACAAGAT AATAACTGTA TGTGTTTAG GACCTTAAAG CTCNTAGTCA	300
TCCATTCCAC AGCAATAGAT ANTACTGGAT AAAAGGAGGT TAGGAAAGAA ATTTNTTTAG	360
GTTAGGTTAG AGTGAAAGAG TCCCTCAGCC AGAGTTTCCC TTTTAAACAC AAAGCAGNCC	420
CNGGNAAAAC ATTTCTNGTT TTAACAAGGG GC	452

(2) INFORMATION FOR SEQ ID NO:1487:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 502 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1487:

GGCAGGAGAG ATCAATGACT TTTGCCGTTT TCAGTGCCCT CCAATTAAGT TTATCAGTGC	60
AGATGTACAT GGAATTTGGT CAAGGTTATT TTGTGATTTT GGTGATGAAT TTGAAGTTTT	120
AGATACAACA GGAGAAGAAC CAAAAGAAAT TTTCATTTCA AACATAACGC AAGCAAATCC	180
TGGCATTGTT ACTTGCNTTG AAAATCATCC TCACAACTG GAGACAGGAC AATTCCTAAC	240
ATTTTCGAGAA TTAATGGGAT GACAGGTTTA AATGGATCTT TGACAACAAT TAACGGTGAT	300
NTCGCCATTT TNCTTTTAGT ATTGGTGGAC ACCACAGAAN TGGNAACCTN TTTGACNGGN	360
GGCCTAGGNG TGCCAGTTNA GGANTCCTAA AACANTTTTT TTGGATTCAN GGNGGGGNGC	420
TTTAAACNT CCAAGTGCCC TTTGTGGGT TTTNGNCAAC NGGCGGGCA CCTTGGGGGT	480
TTACACAGT TTGTTTGNCC TG	502

(2) INFORMATION FOR SEQ ID NO:1488:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 222 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1488:

GGCANAGGAA AGATGGTGTT ACTGCAAGNA TGCTACTCGT GAGGTGNAAT TCGTGAAC TG	60
ATACCAGTTC TGTCATTGAT GCACAATGTT CAATCCTTGT GGGTATTCGA TGAATGGATG	120
AAATCGGATG GAACTTATTG GACTATTCAA CATCACTNCA GACCAGANTT TCTTATGTTA	180
GNTTGGACAA CTTAGTCAGC CTCTATGATG NCNGTCAGAA GT	222

(2) INFORMATION FOR SEQ ID NO:1489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1489:

GGCACGAGGT NTCCCTGTTG CCCTTGGTCT CGGGGNCGCT GTCGGCGCTG AGGCTGCAGC	60
TATCATGGTG AACTTACTTC ANATTNTGCG GGACCACTGG GTTCANGTTC TTGTCCCTAT	120
GGGNTTTGTC ATTGGATGTT ATTTAGACAG AAAGAGTGTA TGAACGGGCT AACTGCCTTC	180
CGGAACAAGT AGTATGTTCA TNTAAAAGGG AATTGCAACC CAGTGAAGAA GTTGATCTGG	240
TAAGTTAAAG ACTAGCTNAG NATTATCGAA TGTTACATT TNNAAGTTC TGTGGAGAAN	300
GAAAAACATG AAG	313

(2) INFORMATION FOR SEQ ID NO:1490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1490:

GTTGTANGNA ANGTAATCA AAAANTTGA AGCTGTACAC AGCAAGACGT TAAGTTACAT	60
GTTCCAAAAG ATTTATGTNA TCAGTTTGGC TGACCCCGT CTCCCCCTGC GNCTGGNTGA	120
TGCTGTNCGG CCTGAGGCAG AGGGAGANG	149

(2) INFORMATION FOR SEQ ID NO:1491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid



(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1491:

AGTAACATGA TAGANAGTTG GTCGATTACA TTGCNATACT GCTTAGTFTN AACTGGTTTA	60
TTTTAATTGT AGCAGAAATG ANCNAAAAA AAATATGGGT TTAANANTCA CACACATGAA	120
AGTNCCATTT TGTAACCTCAN CNAAAGNTAA ANCATTCTTN ATCAAAAGGC TTCTNGCTTG	180
GTGTCAGGTT GTCACATGTG ACCNCTGTGN CAATGCGAAG CATNACTTCT TCAGTGCCAC	240
AANGTCATGT TTAACCTTGG GAAAGNGGN TGCTACAGTG GTTTCCAAAG TTCCGTGTTG	300
TGGGCCNNGG AATTTTCCCT TAGTCTTGCT TG	332

(2) INFORMATION FOR SEQ ID NO:1492:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 298 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1492:

AACAGTGCCT CCNAATNAAA TCTAACGANA GCTTCCCAA TCGTTTAAAC GTGGATATCG	60
GCANANGGTT TTCCTAGACT GTGGAGCCAT GGCTGAGCCA AANCCTGAAA ATTNACTGGG	120
TCACTCCCAT TGGGAAATAA GNTAACTNTG GAAACCCTTT NAAATAATTN CAAGCTAAGT	180
NGCGAGGGTA CCTTGGGAAA TATCTAAGCA TACAATTTGA NGA CTCAGGA AGGTACACAT	240
GTNTTGCCCA GANTGTCCAG GGGCAGNCAT CGGGGTGGCC ACCATTNAGG TTTACGGG	298

(2) INFORMATION FOR SEQ ID NO:1493:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 130 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1493:

TNATTATCCA AATGTNAACC ATGCCAAGGT GAAATTCCAA GGNAAAGGAA GTTGGTGTTT	60
ATAANGCTCT GAAGATGACA GCTGGCTCAA GGGANGATTT TTTNACGACT GACCAGCGCG	120
TGGCGCTCNT	130

(2) INFORMATION FOR SEQ ID NO:1494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1494:

CTTCAAAAAA TAACTGATTT NCAGAACCAA CTCAAGCAAC AGGAGGAAGA CTTTAGAAAA	60
CAGCTGGTAA GATGAAGAAG GAAGAAAAGC TGAAAAAGAA AATACAACAG CAGAATTAAC	120
TGNNAGAAAT TTAACAAGTG GCGTCTCCTC TATGAAAGAN CTATATAATA AANCAAAACC	180
TTTTCAGCTA CAACTAGATG CTTTGTNAAG TAGNAAANCA GGCATTGTT GGAATG	236

(2) INFORMATION FOR SEQ ID NO:1495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1495:

GGCANAGCGG CACGAGGTG GACCGACAGT TACAAGACAT AGTGTAACAA TTAGTGATCA	60
ATCTAGAGGA AAGAGAAAAA AAGCAAATGC ATGATTTCTA TAAAGAAAGA GGTCTAGAAG	120
TACCTAAACC TGCTGTTCCA CAGNCAGTGC CCTTCAAGCA AAGGNAAGAT CTAAAAAAGT	180
CCTAGAAATC AGTGTTTCGT ATTCCACCTG AACTTGGATA TGTCTTTATT ACTGGGAGTT	240
CCATTGGTGC TAAATGAAAG GCACGGGNAC ATTTTAAAGC CATTGGGAAA AGAAAGTTTG	300
TTCCGAGTTT TCAGGAGGAA GCAACTATTG GGACCATGTT GGAAAATTTC CTCAGANGAA	360
AATGGGGTCT TGATCCCNCT TGTNCCAGTA GGTTTAATCC GTGGTGATCA CTGTTGGGGC	420
CGTNTCAACT CTTAGGGNAT TC	442

(2) INFORMATION FOR SEQ ID NO:1496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1496:

GGCANGAGAA GGTACTGCAA CATTTNAATG GGACGGCAAT AGCAAATGCA GTTGNTAAAG	60
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ANCTTGCTGA GACTATAAAA TGTCGTACAT TATTTNCAAC TCACTACCAT TCATTAGTAG	120
AAGATTATTC TCAAAATGTT GNTGTGCGCC TAGGAACATA TGGCATGCAT GGTAGAAAAT	180
GAAATGTGAA AGACCCCAGC CAGGAGACTA TTACGTTCTT CTATGAAATT CATTAAGGGA	240
GCTTGTCCTA AAAGCTATGG CTTTAATGCA GCAAGGCTTG CTAATCTCCC AGAGGAAAGTT	300
ATTCCAAAAG GGNCATAGAA AGCAAGGNAT TTGNGGNAGT TGANTCCGTC CCTC	354

(2) INFORMATION FOR SEQ ID NO:1497:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 349 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1497:

TNATGTNCTT TCTGCATGGT TATATACTAC TAGTNNTTTT ATCAAAACTN CTAAAATTTA	60
AATTACGTGG TAAAAGATCT GTAAAAGGCT GCATAAATGT TAAGTTGGCA CATAAGACA	120
ATTGTAGAAG TTGAAAAAAT GATTGCAATA TTTCAATGNT TATNCCCACT CAACATACTG	180
NCTTCTAAAG CTTCCCTTTT TTTGTTCCAA AGGCATGNTC CTTGAAAGGT NATGTTTAAG	240
TTAATGGNTG TAATGCCAGG GTTCCCTACA CTGTGATTN GGGCGCATGT GCNGTGGGCC	300
CTCTGTGCCC CTAGANTATA TGCCACACAG GGGGNCAAGT TNAAAAGCT	349

(2) INFORMATION FOR SEQ ID NO:1498:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 487 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1498:

GGCACGAGCT GTCTGGAATT TAGCCAAGTN AACAATCCCC TCATATCCAG GCTTTATNAT	60
CTATATAGCT TCCAGGTCAT CCCTGNCCTG GGAGAGGTCA TCGCTGGAGA CTGNAAGTCC	120
TATCAGTACC TTGTAGAGAG TATCCGAAGG TTTCCGTCTC AGGAAGNAGT TCAAGGACAT	180
GATAGAAGAT GCAGGCTTTC ACAAGGTGAC TTACGAAAGT NTAACATCAG GCATTGTGGC	240
CATTCATTCT GGCTTCAAAC TTTAATTCCT TTCCTATCAT GGAGCATGAN CCAGTCATAT	300
CCTGTTTGAA AGCCTGGAAC TTNAAGGNTA ATCTGGGCAA TGAAGACAGC AGCAGAGCAT	360
CTCCCTCTTT AAGGATACGT GGCCTTGGNA CTCATGTTTG AATCGGACAG TCTCAAAGTG	420

GGGAGGACAA TTCTTGTCAC TTTTACAG GTTCTTTT GGGTTGTTT CAGTCCCATT 480  
TCCCAAG 487

(2) INFORMATION FOR SEQ ID NO:1499:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 276 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1499:

TCNNCAANNT NGAACGATGC AGGGTCCAGC TGGGCGGATC TGATCAACTA GGCAACATCA 60  
TGTTCCGGAT ATGAGTTCAT CAACAAGTTG ACTGGAGAAG ATGTATTTGN GAATCACCGT 120  
TCCTCTAATT ACAAGTACAA CTGGNGCAAA GNTGGGGAAA GTCTGCTGGC AACGCTGTTT 180  
GGCTAAACAG AGATAAGACA TCTCCATTG AATTGTATCA ATTCTTTGTC ANGCAACCGG 240  
ACGTTTCANT GGNAAGGTAC CTGANGNTGT TCATTT 276

(2) INFORMATION FOR SEQ ID NO:1500:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 72 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1500:

GGNGGCGTTC AGCTGCTTCA AGATGANGGT GAACATNTCT TTCCCAGCCA CTGGTTGCCA 60  
GAAACTCNTT GA 72

(2) INFORMATION FOR SEQ ID NO:1501:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 291 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1501:

AAAATNTCCC AACTNATGAT ATCCACATGA NGCAAGTTGA TCTGGAGANT GTATGGCTTC 60  
ATTTTATCCG GGAGTTCATT GCACCANTTA CACTGAAGGT NTTTGCAGGC TATTATACGA 120  
NGGGNTTTC ACTACTGAAT TTTGTAGTAA AATACTCCCC TNANCGACAG CNTTCTCTTN 180

GTCTCATCA TGATGCTTCT ACATTTTACC ATAAACATTG GCACTTAATA ACGTGGGGAN	240
AAGACTTTCC AGGGGAGNTG GTTGCAAATT TNNAAGGGNT CCAATTTGCC C	291

(2) INFORMATION FOR SEQ ID NO:1502:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 477 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1502:

TGGAAATACT TGTTATTGC ATGATCCAAT GGCTTACTGG CCATCTTCCT TGGGAGGATA	60
ATTTGAAAGA TCCTAAATAT GTTAGAGATT CCAAATTAG ATACAGAGAA AATATTGCAA	120
GTTTGATGGA CAAATGTTTT CCTGAGAAAA ACAACCAGG TGAAATTGCC AAATACATGG	180
AAACAGTGAA ATTACTAGAC TAACTGAAA AACCTCTTTA TGAAAATTTA CGTGACATTC	240
TTTTGCAAGG ACTAAAAGCT ATAGGAAGTA AGGATGATGG CCANTTGGAC CTCAGTGTG	300
TGGAGAATGG AGGTTTGAAA GCAAAAACAT TANCAAGGAN GCGNAAGTAA GNATTGNTGA	360
AAGCAAGGAN CNCGTGTTTG AAGTTACGGN TTGTCCAACN CACCGTCCGN GGTGGGCCCTT	420
CCGACCCNTT TCAGGACCCG AAGGGGTCCC GAGTATTCGG TGCTGTGACC CGTTTCC	477

(2) INFORMATION FOR SEQ ID NO:1503:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 250 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1503:

GGCAGGAGCA AAGGCGAGGA GTCCAACAGC TCAGCCANCA AGTGTCTGCT GAAGGTGGCT	60
GGTTACGCTG NGCTNCTNGA GCAGTATCAG AAGGCCATTG ACATNTACGA NCAGGTGGGG	120
NCCANTGCCA TGGNACAGCC CCCTTCCTCA AGTACAGCGC CAAAGACTAC TTTCTTTCAA	180
GGCGGCCCTC TGCCACTTCT GGCATCGNCA TGGCTCAGCG TGCAAGNTGG CTGGTCCAAA	240
AGNATNNAGG	250

(2) INFORMATION FOR SEQ ID NO:1504:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 248 base pairs
  - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1504:

GGCACAGAGA AGATTCCTTC ATGAGTGTAG AAGTTGGACT GATTTCTAAA GTNCCTTTCT	60
ATTTTAAGAN TCTNTTCTGC ACAGTTATGA GCTACACATA ATGCACTGAA TCTGTCCCT	120
TGNATAGTTT CTGCATAGGC TTTGGTTGTG CCACAAGTGT GCCTGGCAGT GAAATGAACC	180
TGGTCTAAAC TCTGGCATTG GTCCTAGGGN CTGNAACTGT TNCAGGAATN TGNGCTAATC	240
CTNGNGGG	248

(2) INFORMATION FOR SEQ ID NO:1505:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 373 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1505:

ANACAGCCAC ACCCGTNACG GTGCATTAGG GACAATGGCA GTCGGTGAGG GCGGCGGTGA	60
GTTGGTAAAA CAGCTGCTTA ATGACACCTG GGATATCGAC TATCCGGGCG TGGTTGCGGT	120
GCATCTAACC GGAAAACCTG CGCCGTATGT GGGGCCACAG GATGTNGCGC TGGCTATCAT	180
TGGCGCGGTG TTCAAAAACG GTTACGTCAA AAACAAAGTC ATGGAGTTCG TTGGACCGGG	240
CGTTAGGGCG CTTCTCTTAC CGATTTCCGT AACAGCNTTG ACGTGATGAC CACTTGAAAC	300
GGACCTGTTT AAGTTCTGTT TGGCAAACCG TTGAAGNAGT NCCATAACTG GTTGGGGGTT	360
TNAACGTTNG GGG	373

(2) INFORMATION FOR SEQ ID NO:1506:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 395 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1506:

GGCANAGTCC AGAAGCTACG CTTTGAAAT CTATGACATA GACAACAAGA CGCCAGACCT	60
GAGGGATGAT GACTTCCTAG GGGGTGCTGA GTGTTCCCTA GGACAGATTG TTTCCAGCCA	120
GGTACTGACT CTCCCCTTGA ATGCTGAAGC CTGGGAAAAC CTGCTGGGCG GGGGACCATC	180

ACGGTCTCAG CTCAGGGAAT TAAAGGACAA TCGTGTAGTA ACCATGGAGG TAGAGGCCAG	240
AAACCTAGAT AAGAAAGGAC TTCCTGGGNA AAATCAGATC CATTTTNTGG AGTTCTTTCC	300
GCCATGGTGA TGGGGNAATG GGCACNGGGT GTTACAGTTC TAAGGGTNCA NTCAAGGACC	360
AACCTGGAAC CCTTACATGG GAAGTTTTTT TTNAA	395

(2) INFORMATION FOR SEQ ID NO:1507:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 182 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1507:

CAAACAGCCC AACAATTTC AACTGCGAA CCGCCAGACT TATTGGCGTA CGCAGTCTG	60
TGTGCTTTCA CAGCATCAAG ACGTAGGGCN TGCCCTCGCCA TGAACACGC GGTGCCAGC	120
CGTAGTATNA TCGTCCAATG ATCGTCGACC CGTACCNATN CGNCTCTTGG TGTGGGGTGT	180
GT	182

(2) INFORMATION FOR SEQ ID NO:1508:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 484 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1508:

GGCAGAGTNT TGGGGCATTG CCGGCGGGCC CACCCGGA CT CACGCAGCCC ACTCTGTGTC	60
CCCCGGCAGT ACCCTGGCTA AAGCCGGGNC CGGAGCCTNC TGCCCCCTCTC ATGCCCGCAG	120
CCAGCCTGGG CTGTGCAACA TGTTACAAGG ACTCACACCA CCCGGNCAAG AACTGCTCAC	180
TACGGCTCCC TGCCCCAGAA GTTCACACGG NCCGGACCCA AGATGAAAAC CCCGTAGTCC	240
CACTTTCTTT CAAGAACATT GTGAACGCCT NGCACACCAC CCCC GTTCGC AGGGGAAAGG	300
GNGAGAGGGA CTGTTCCNTG AGCAGATTTT AGCTNNGGGG GCCGAGCAGA GNAACCCAGG	360
NTTTTGGGTT ACGGAGGCAG AGCGTCCGA TTTTAAATCG GTTCACAAGG GGTTTCAAGG	420
GATTCGTTGC CCAGGGAAGT TTTCCAAATT TTTTAAGTTG GGAGNAGAGN TAGTTGGTTT	480
TGGT	484

(2) INFORMATION FOR SEQ ID NO:1509:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 172 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1509:

GGCANAGNCT GCATCCTACA GAGCCATGGA TGGNGGCAAG TGTTTGCAAT GGGAAGTGTG	60
TGTGTTTGGG NTCATGAAAC ACAGACACTG GTGGAAGACA TTTGAAGTGT GTGATCTTCC	120
TGTTTCGTAG CTNCAAAGTT TGGTTGNCAA AGGGAAGNAT TTTTTNGTGT TG	172

(2) INFORMATION FOR SEQ ID NO:1510:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 352 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1510:

GGCANAGGCA TCAATGTTAT AGCGTGTGTC AGTCCTTCAT GACTTTCTGT GGATGAATAA	60
TATTCCATTG CATGGATATA CAGCAGTTCG TTTANCCATT CAGCAATTGA TGGATATTTG	120
GGCCTGTTTT CACATTTTGG CTATTATGAA ATCCANTTTT TTAAAGAGAA GATAGNAAAC	180
CTGGATTTTT GAAATCTAGT GTTTAAATGT TGGCTGTGNA ATTTTAAAAA TTNAAGAATA	240
TGTTTGAGC TAATTAAAAA GCTATCTGGG GATGGGCACA GGNNGCTTGG TTGACTGCCC	300
ATTGGTCCAT CTCTTTGCCA CTTGGGGNCA GCCTGGGGAC CCTTTNTNGG TT	352

(2) INFORMATION FOR SEQ ID NO:1511:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 436 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1511:

GGCANAGNCA AGACTGGTCA CCCTCGGTTC TTCAACCAGC TCTTNTCTGG GTTGGATCCC	60
CATGCTCTGG NCGGGNGCAT TATCACTGAG AAGCCTCAAC ACCAGCCAGT ACACATATGN	120
AAATCGCCCC CGTGTGTTGTG CTCATGGAAG AGGAGGTGCT GAGGAACTG CGGGCCCTGG	180
TGGGCTGGNA GCTCTNGGGA CGGAATCTTC TGCCCTGGTG GCTCCATCTC CAACATGTAT	240



GCTGTNAAAT CTGGCCCGCT ATCAGGCTTA CCNGGGATTG CAAGCAGAGG GGNCTCCGNA	300
CAATGCCGCC CCTGGCCCTT ATTTACATC GAAGGAGGTT GGGAAGAGGC ACAGGNCCAA	360
CCCTGGGTTC NTGATTTTAA TTTCCAGCCN GTTAAGTAGA GACCTTCCAG TTTTGTTCCT	420
GGCCTTNNTA ACATTC	436

(2) INFORMATION FOR SEQ ID NO:1512:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 158 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1512:

GGCANATNGG GACTTCCCGT GCNCTCTGGC TGAGGGGTGT TGCTGCCTTT GGTAGCTGGC	60
CCTGGTGTTT CAAGTACCAC CCTTAGGGTG GAAGTGGTAG CTTTTTTAAA GANTGTNNCC	120
CAAAACTACA GTTNCCTGTC ACTCACTTAC ACAGTATT	158

(2) INFORMATION FOR SEQ ID NO:1513:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 308 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1513:

GGCAGCAGCT TCACTAAGGT GGGATGGATA GCAGGTCTN AGGCACAACC AGTAATGGAG	60
AGACAAANCC AGTGATCCA GTCATGGAAA AGAAGGAGGA AGATGGCACC CTGGAAGCGG	120
GGGCACTGGT ANCANCAAGN TGGAGTTTNT CCTGTNAGTG GCTGGGGAGA TCATTGGCTT	180
AGGCAACGTC TGGNGGTTTC CCNATCTTTG CTAACAAAAN TGGGGGAGGT GAGTTGAGAG	240
CCCTTTTGCC CACCCNACCC ACTCCTGGAA GGGGNTTACT TCCATCTCCC TGCATTTACG	300
NNCCCTTT	308

(2) INFORMATION FOR SEQ ID NO:1514:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 372 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1514:

GGNAGAGGGG ACACAAAGGT CGGNAGGCAG CACACAGAGG GACCTACGGG CCAGCTGTNC	60
CTTCCCCCAA NTCAAGAATC CCCGGAAGNC CCGGNGGCTG NCAGCAGGAG AGANCCATGA	120
AAGTAAGCTG AATGGTGGTG CCTGNGTCTG AATTGCCTGC AGCCTGGGCC AGAGGAGCAG	180
AATGAANTTG GTGCATGGCG GACCCTGNGA NCAAGACATC TTNACCCCTN ACCAAGCTGC	240
CCTCTNACAC CTGGGGCCAC TTGCTCTGTG GTGGGGTCCT TATTCCATCC ACTGTGGGTC	300
CTNANAGNTG CCCACTGCAA AAAACCGTTT TTCCAGGTCT TCCTGGGGGA GGGNTTAACC	360
TTGGNGCAAA GG	372

(2) INFORMATION FOR SEQ ID NO:1515:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 135 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1515:

TGCTGAAATT AAAGAAATNT NGCAATGATT TAAAAACGG AGNTGTGACA GTAAGGAGGC	60
CTGACCCCAT TAACTGGTCA TTGAAGTATA AAACCTCTGN ATTTTANGNC TNCGGGTTTT	120
ATGACAGTGG CAATG	135

(2) INFORMATION FOR SEQ ID NO:1516:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 159 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1516:

AATTCGGCAN AGGNNAGCCA TGNCTGGCGA TGGTGGCAGC GGCTGTNACC TTGGAGGTTG	60
CTGCAGGCCC GTGGCTTTCC ACAAATTTT GCACCCAGCC TGGGCCTANG AGCGAGGACT	120
TGTTCCCAGG GCGACTGCTC GTNATTCNCG CANGNCTGT	159

(2) INFORMATION FOR SEQ ID NO:1517:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 63 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1517:

AGCCCCGCAT CTTCCACCT CGNCGCCGCC GNAGCTCCCC GCGCTCGTGC CACCGNCGCC	60
GGT	63

(2) INFORMATION FOR SEQ ID NO:1518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1518:

TATTATGGAA AACTGTTGCG GGGCATATGG AAAACTGTTG CGGGGCATGT GGTAGAGACC	60
ACCCAGATGA GGCCCTCCAA GACCTTGTTG TCTAGGGTGA TTTATTCCCT TTATTTAGAG	120
ACCCAGGCAA TTGAATTCAT TTCTTTTTGT GNATGATAGG CTTTGGCTG TTAGACCAGA	180
CCAGACGCTG TGTTACTCTA TGAGATGAAT AATAGTGGAG AACTATATAA CTTAACTATT	240
TTGACTTTTT ACCTTGCTT CCAGGAAGCA TAGAGTGCAA TCTCGNTTAC TGCAATTTNC	300
AATGAATTGA CACATAGCCT AGGTTTTTGG TACAACCACC TTTG	344

(2) INFORMATION FOR SEQ ID NO:1519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1519:

GGCAGGAGCA TGTTTCCTGT TTTGTGTGTG TAGTCTGTGG AATGNCCATT CGGATGAATG	60
TTTTTCACTT GGAGGATGGT GAACCCTACT GTGAGACTGA TTATTATGCC CTCTTTGGTA	120
CTATATGCCA TGGNTGTGNA ATTTCCCATATA GAAGCTGGTG ACATGTTTCCT GGAAGCTCTG	180
GGCTACACCT GGGCATGTGA CTTGCTTTGT ATGCTCCAGT GTGTTGTGAA AGTTTGGNAA	240
GGTCAGACCT TTTTCTCCAA GAAGGACAAG CCCCTGTGTT ANGAAACATG CT	292

(2) INFORMATION FOR SEQ ID NO:1520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1520:

GGCAGAGGG NGCACCCNGG TAGGGGGNCG GCTGAGCCGG CAGTGCGGTA CCCTCGCGGG	60
GAAGTGC GCCGACACCA TGTCTCAGGA AGGTGTGGAG CTGGAGAAGA GCGTCCGGCG	120
CCTCCGGGAG AAGTTTCATG GGAAGGTATC CTCCAAGAAG GCGGGGGCTC TGATGNGGAA	180
ATTCNGCT	188

(2) INFORMATION FOR SEQ ID NO:1521:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 359 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1521:

GGCAGAGCTC ATGATGACGT TTGCTTTTCC TCCCGACTCA AAATTACCT TTTGGGGTCT	60
TACCCTGGTT GTAGNGCTG GNTTTTCCTG GGGATTAAGG CCTAANTCTT CCTACNCNTC	120
GCACTGCCTT GCACTGCCCC CCATATGTTC CCAGGGTAGC TCTCCAGCTG GANCCTTGCT	180
GATGCCATGT CCCAGAAACA CCTCCAGATC AACCAGACGT TTGAGGAGCT GCGAACTGGT	240
CACGCAGACA CAGAGNAATG AGTTTAAAAA AGCTGCAGCA GACTTCAGGA GTTACTTTCA	300
TGCATCCAGT TACCAGGNAG AGCCTNGAGG GATTCCAAGC TCAGTTTTGG GCCCGTTGG	359

(2) INFORMATION FOR SEQ ID NO:1522:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 198 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1522:

GGNANAGGCA ACCCCTTG TN TCGTGTGGAT GGGGCGCTNG CCGGCGCTGT GAACCTNAAC	60
CTGCAGNCCG ACTGCAAGNN TGCCCTGGAA GTCCTGGCAC GACATCCGCC GAGACAAC TG	120
CTCTGGCCAG AAGCCTCTGC TTCTGCTGGG AGCACANCCA GCTCCNAGCA CAACCTGTNT	180
GNCCTTCCTN GAGGTTCA	198

(2) INFORMATION FOR SEQ ID NO:1523:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 483 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1523:

TTGCCATCGC GAATGGGGCC CAGTGGCCTA ACGCCCCGGC GGCGCTTNGG TAAAACCGAC	60
ACCACGGCAC TCTGTCGGCC AGGTTGCAGG TTCCCATTTT TCCGTGGAAG CAGTGGCGAG	120
AATTGCCGTT TTTNAGGTTG GTCATCAGCT TGTCGAAGAA ATACACACCA GAGAAAAAGC	180
GTAAATTCTG TTCCGACCGT GCAGTTNACC GTAGAGCGAA AATTTTGCG CCATATAAGC	240
CGAGAATGCT GGCGCGCTTT ACCGGNAACT TNTCTTTCCA GATCCATCCC CAGCACCAGC	300
GCCTGGTCCG GAAAGTTCGG CACCAGCAAA CCGTACATNC ANTTTAAAGG TGGTCGATTT	360
TNACCCGGGC CTTTGGGGCC CCAGNAAACC AAAAATTTTC CCCAAGTTTN AAGGGCAAAT	420
TTGACGTGAT CCGTTGGGNG GCAAAATNCC CCAATTTTTT TGGTCAATTT TTNGGTTTGG	480
GTT	483

(2) INFORMATION FOR SEQ ID NO:1524:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 399 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1524:

AAAACAATCC CTTCTATCAA TTATATCGGC TATCTTGAAG CCAATGAGTT GTTAACTGGC	60
AAGACAGATG TGCTGGTTTG TNACGGCTTT ACAGGAAATN TCACATTAAA GACGATGGAA	120
GGTGTTGTCA GGTATGTTCC TTTCTCTGCC TGAAATCTCA GNGTGAAGGG AAAAAACGGT	180
CGTGGTGGCT ACTGTTATTA AAGCGTTGGC TACAAAAGAG CCTGACGAGG CGATTNCAGT	240
CACCTCAACC CCGACAGTT ATAACGGCGC CTGTNTGTTT AGGGTTNCGC GGCACGGTGA	300
TTAAAAAGTT CATGGGTGTC AGCCAATTCA GCGAGNTTTT TGCGGTTCGC GATTNGAACA	360
GGCATGNCAG GCGGTGCAGC GACCAAGTTN CNTCAGCGG	399

(2) INFORMATION FOR SEQ ID NO:1525:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 200 base pairs  
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1525:

CACCNCCTAA AAAACTCGCT GGATCTNNAT CTGGAAATGT NCCCGGCCCA GGTGNCAGCT 60  
TCCTCCNCCT CCAAGCNAGG NTTNANTTCC ACCTGGGAAA TCTGGCCANA GAAAGGTGCT 120  
TGAAAATCCT TCCNGCACAT GCCAAACCCT AGAACCCGGG GANAGCACGG GGGNGGTGGG 180  
ATTACCTGGT GCAGCANACT 200

(2) INFORMATION FOR SEQ ID NO:1526:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 146 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1526:

GGCAGAGTGA ACAGCCCCCG NCGGCGCANA CGAGCCCGGA CCACACCCGG TNCCGGAGGT 60  
TCCCACAGCA AAGACAGGCA CCGGAAGGAG ACGGACCGGG AAGCGTAGGG GCAGCGNCAG 120  
CAGGTAAGGN ACAGCCGNCA CCGNCG 146

(2) INFORMATION FOR SEQ ID NO:1527:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 347 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1527:

GGCAGAGNCA ACGCCACTCC TTCTAAGTCT TCATCGATCA ATGACATTTN ATCCATGTCC 60  
ACTGAGCAGA CGCTGGCCTC AAACACAGAC AGCAGTCTTA ATGCCTCGAA CGGGNACCCC 120  
TTGAAAGGCT GTCGAATGGA TAGGTTAGGA AATAGCAAAC CTGTNNAGCA TTGAAGGGAA 180  
CTCTGNACCT GCCGTGGGGC CTGAAATGCT TGGGAGTTGA TGGGAACCAA ATAGAAAAAC 240  
TCCATGTTCC TGGCATGTAA AGAAACACAA TGNCTTGGNC CTNTTTCAAA CCGGTGGGGT 300  
TTGCNCTGCT TTAGATGGTT AAAAATGGGG GGCAGGANTA TGTTTTG 347

(2) INFORMATION FOR SEQ ID NO:1528:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1528:

GGCAGNGCAG CTATGCTAAT TTGCAAACAG GTTCTGGAGT NCTTAAAGAT AGTTTNTCTG	60
GTGGAATGCA GTTGCTTCCA GATCCTNTAT ATTCTCTTCC TACNNATAAT ACTTACCTTT	120
TAACAATAAC TTNCACTGAT AATGGGCAGA ATTTTCTTGG CTGGNAAAGG ATGGCTGTTT	180
ATATGAAAGT AGCCTACCAG GCTGTAAGCA GGGTGGTTTA GCCAAAGATG TAGGGAAAAT	240
AAACCACTCA AAGAGCTTCA CTTTCTTTNC CTTGGTNCCT TCCTTGGCTA CCAATTTAC	300
GTTTCTTCAG AAGGATGNAT NCCNTATTTT TT	332

(2) INFORMATION FOR SEQ ID NO:1529:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 348 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1529:

GGCACGAGGG AAAATCGCAA TACTATATTA TGTTTGGNCC CGATATTTGT GGATTTNATA	60
TCAAGAAAGT NCATGTTATT TTACATTTCA AGAATAAGTA TCACGAAAAC AAGAACTGN	120
ATCAGGTGTA AGGTTGGATG GCTTCACACA CCTGTACAC TCTAATTTTN AAGACCAGAT	180
CTTTCTTATG ATGTGNAAAA TTGATGGTCA GTGCAATTGG AATCCGGCAG CATAGAGTTA	240
CGGACTGGGA ACTTAAACAT CACTCCAAGA GGGAAACGTC CCCCAGNCAG ATTCGAAGGA	300
TTGGGCAACA GGAAGTAAAG GNNCAACAAA GCCCCAGGGA CTTGGGGC	348

(2) INFORMATION FOR SEQ ID NO:1530:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 366 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1530:

GGCACGAGCT CGTNCGNTGC AAAACCACTC CCACCAAGTG AACGCTTGGA ACAGGAACTC	60
TTTTCTGGAG GCAACACTGG GATTAATTTT NAGAAATACG ATGACATTCC AGTTGAGGCA	120

ACAGGCAACA ACTGTNCCTC CACATATTGA AAGTTTCAGT GATGTTGAGA TGGGAGAAAT	180
TATCATGGGA AACATTGAGC TTACTCGTTA TACTCGCCCA ACTCCAGTGC CAAAAGCATG	240
CTNATTGCCT ATTATNCAAA GAGAAAAGAG ACTTGATGGC TTGTGCCCCA AACAGGGTTC	300
TGGTAAAAAC TGCCAGGNAT TTTTNTTGCC CNTCTTGAGT NCAGATTTAT NCAGATGGTC	360
CAGGCG	366

(2) INFORMATION FOR SEQ ID NO:1531:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 408 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1531:

GGCACGAGGC TTGGCGGGGT GGATAATATC CTGGTCAAAA TNACTGACCC ACATCANTAA	60
TGTCGTTCCCT CCAAAGATGC CGTGGGTCAA ATATCTGTNC ATGTGGACAT CACTGCCACC	120
CCAGGAACGG GAGATCATAA AAGTCACTGT AAAAAGTGAA TTGCTATTAA TGACCTAAAC	180
TGGCAGACCA CAGCAATGTT CCGCCCCTTT NTGGAAGTTT GTATACTGGG ACCCAACCTT	240
GGAGACAAGA AGAGAAAACA AGGCACAAAA ACAAAAAGCA ACACATGGTC ACCAAAGTTA	300
CAATGNAACT TTGCAGTTCC TTTTGCGGAA AGGAAATTCG GCCAGGGTTT ATGAAATTGC	360
TCTGTCCGTT AAGGGTTATG TTTTGCCANG NAGTTCGNTT NTNGGATG	408

(2) INFORMATION FOR SEQ ID NO:1532:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 52 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1532:

GGCACGAGGT TTTTTTTTTT TTTTTTTTNG GAAAAAANAA NCTTTNAAAA NT	52
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(2) INFORMATION FOR SEQ ID NO:1533:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 301 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1533:

GGCACGAGCC CGACCGTNAA TGTGTGTNTN CTCTTCCCCA GTNCTGGCCA TTCAGGCCCG	60
AAAGCGGAGG CCGAAAAGAG AGAAACATCC GAAAAGCCG GAGCCTCAAC AGAAAGCTCC	120
TTTAGTTCCT CCTCCTCCAC CGCCACCACC ACCACCACCG CCACCTTTGC CAGACCCAC	180
ACCCCGGNG CCAGAGGNGG AGATCCTGGG GTCAGATGNT GAGGAGCAAG AGGACCCTGC	240
GGACTACTNG CAAGGNATTT ACAAGTTTTG TNACTATTTA TTGGAGNAAT TATTTTtagc	300
T	301

(2) INFORMATION FOR SEQ ID NO:1534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1534:

GGCACGAGGT TGGATGGTGC AGTGGCTGTA TTTNATGCCT CTCCTGGTGT AGAGGCCCAG	60
ANTCTCACAG TATGGAGGCA AGCTGATAAA CACAATATAC CTCGAATCTG TTTTAAAC	120
AAGATGGACA AAAGTGGAGC AAGCTTTAAG TATGCAGTTG AAAGCATCAG AGAGAAGTTA	180
AAGGCAAAGC CTTTGCTTTT ACAGTTACCA ATTGGTGAAG CAAAACCTT CAAAGGAGTG	240
GTGGATGTAG TAATTGAAAG AAAAAGTTCT TTTGGGAATT TGCCAATTCC AAATGGATGG	300
AAAAGACTTT GAGGAGAAGN CCCCTCTTTG GGAATGNATN GTTCCNGGAT TTGCTGAAGG	360
GGAACCACCT NAGGCAAGGG	380

(2) INFORMATION FOR SEQ ID NO:1535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1535:

GGCACGAGGT GAAGTTCAAA GATGTGGCTG GCTGTNAGGA GGCCAAGCTA GAGATCATGG	60
AATTTNTGAA TTTCTTGAAA AACCCAAAGC AGTATCAAGA CCTAGGAGCA AAAATCCCAA	120
AGGGTGCCAT TCTCACTGGT CCTCCAGGCA CTGGGNAAGA CGCTGCTAGC TAAGGCCACA	180
GCCGGAAG CCAATGTCCC CTTTCATCACC GTTAGTGGAT CTNAGTTTTT GGAGATGTTC	240

GTTGGTGTGG GCCCTGCTTA GAGTCCGAGA CTTATTTGCC CTTGCTCGGA AGGAATGCCC	300
CTTTGCATCC TCTTTCATCG GTGGAATTCG TGCGGTGGNG AAGGGAAGAG AGGAAGAGGC	360
AANTTTTTGG AGGGGCAAGA NTTTNGNCAG GGGGG	395

(2) INFORMATION FOR SEQ ID NO:1536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1536:

TGTTTTNAGT TTCTTTTTTT NCGTTTNATT TTTTNNAAT TGCATTTTAC AGTAGAAATG	60
CAGACCACTT TGGATAGCTA TGGCTCGATA CTTCTGGGTG CCCTCCTCCT AAGANATCCT	120
CTTCTTACAT TCCACTGANC AGAAAACCAT CCCTTCTACT GGCATGAACT TCTGCCCAAT	180
GAGGCATTTG CTGCAGCAAG AGCACAGAAA GCACTCTGTG GNATGCATGC CAGCTGAAAT	240
TGTTATAGGT CACCCGNTGC ACTTNCTGGG TCGATGGGCA TTGTGGGCNT CCTTGACACA	300
CCACAGGGTG ATTTNTTNCA AATAGC	326

(2) INFORMATION FOR SEQ ID NO:1537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1537:

GGCACGAGAA GCTTTCCCAC ACACATCACA CTCATAGGGC TTCTCTCTAC CGTGGATTTCG	60
CTGGTGTCCA ACAAGAGCTG AACTGTATCT GAAGGCCTTT CCACGCTTGT CACATTCATA	120
TAGTTTCTTT CCACTGTGGA TTTTCTGGTG ACAGAAGAGG CCCAAGCACT AGCTAAAGCT	180
TTTCCCTCAC TCACTACACT GCTATGGCTT CTNTTCAGTA TGAACCTCTGA TGTTGTCTCA	240
GATATGAACT CAGAGAGGAT TTCCCACAAT CATTACACTG GTATGGTTTC TTTTCCGTGT	300
GGAGTTTCTC TGGTGTCCAA ATAACATCTG AGGTNGTGGA TGGAAAGGAC TTTCCCACAC	360
TCACTTACAT TGGGAAAGGG TTTCTTCCTG TNGTGGGGTC CTTCAAATGN TGNNTAAGGT	420
TATGNACTGT AATAAAAGG	439

(2) INFORMATION FOR SEQ ID NO:1538:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 427 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1538:

GGCAGAGCAA AGAGGCATTT GGGCAGTCCT TCTCCATCCA CCGGAAGGTT GCTGAAGATG	60
GAGAGACTCG GGAGGAAACG CTTCTCCAGG AGTCAGCATC GAAGGAGGCT TACTATCTGG	120
GGAAGATCTT GGAGATGCAG AACGAGCTGA AACAGAGCCG GGCTGTGGTC ACTAATGTAC	180
AGGCAGAAAA CGAGAGGCTC ACCGCAGTCG TGCAGGATCT GAAGGAGAAC AATGAGATGG	240
TGGAGCTACA GAGAATACGG ATGAAGGATG AAATNCGCGG ANTATAAGTT CCGGGAGGCA	300
CGGCTCCTTT CAGGACTATT ACTTGAATTT GGGAGGANGA AATTTTCACC TTGCAGAAAC	360
TAGTGTTCCN CGTTTGNAGG CAGANCCAGT TGATTACGNG GGTTTAAAGC CTGGGTTTAG	420
CGCTTTT	427

(2) INFORMATION FOR SEQ ID NO:1539:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 489 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1539:

TTTTCNAGTT TCTTTTTTTN CGNTTAATTT TTTCNAAATT GCATTTNACA GTAGAAATGC	60
AGACCACTTT GGATAGCTAT GGCTCGATAC TTCTGGGTGC CTCCTCCTAA GACATCCTCT	120
TCTTACATTC CACTGAACAG AAAACCATCC CTTCTACTGG CATGAACTTC TGCCCAATGA	180
GGATTTNNTG CAGAAAGAGC ACAGAAAGCA CTCTGTGGAT GCATGCCAGN TGAAATTGTT	240
ATAGGTCACC CGCTGCACTT CTGGGTCGAT GGCATTGTGG CATCCTTGAC ACACCACAGC	300
GTGATTCTTC ACATAGCAGG GCTTGACAC GGGCTTGTTA TTGACCATCA CGTATATTCT	360
CCCCAGNTAG ANTGNTNTCA CAGTCAAAGC AGCAGAAGTG TTTCAGGTGC CATTCTGGTT	420
TTCTGCCTGG GTATACTCAT TGTNGATATC AGTTCGTCAC AGCCAGCACN CGGGGTTTTT	480
GGTGTCACA	489

(2) INFORMATION FOR SEQ ID NO:1540:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1540:

GGCANAGGNT TTCCTTGCCC GATTCCTTCA TGCTATATCT CATGAACCTC TGTAATCTTG	60
GGGGAGAGAC TATATTTAAT GATGACAAAC CTGTCACCAG TGTAGCAACA ACAGTGTGAG	120
GACAAAAGCA AATAAAAATT AAGNAAGCGT TCAAATTTAT ATTCAACAAG GAAGTCATTT	180
CAATCAACAA CTTCTGCTGC ATTATTTTTTC CAAGATGAAC CGATACACAA CCATGAGACA	240
GTTGGGGGAC GGCANTATGG GAGTGTGCTT ATGGGCAAGA GTAATGAATC CGGGGNGCTG	300
GTGGCCATCA AAAGGNTGAA GAGAAAGTTC TATTCTTGGG GTGATGGCAT GAACTTNNGG	360
GGAGTTTAAG TTTCTGNAGG AACTTTATTC NGGCCATGTT ATTTAAATNG AAAGANGTTT	420
TTCNNGGGAA ATGACCCTCT TTATTTTATA TTGGATTTTT GG	462

(2) INFORMATION FOR SEQ ID NO:1541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1541:

GGCACGAGCC GGACTCTTTT CCCTCTACTG AGATTCATCT GTGTGAAATA TGAGTTGGCG	60
AGGAAGATCG ACCTATCGGC CTAGACCAAG ACGCTACGTA GAGCCTCCTG AAATNATTGG	120
NCCTATGCGG CCCGAGCAGT TCAGTGATGA AGTGAACCA GCAACACCTG AAGAAGGGGA	180
ACCAGCAACT CAACGTCAGG ATCCTGCAGC TGCTCAGGAG GGAGAGGATG AGGGAGCATC	240
TNCAGGTCAA GGGCCGAAGC CTGAAGCTGA TAGCCAGGAA CAGGGTCACC CACAGACTGG	300
GTGTNAGTNT NAAGATGGTC CTGATGGGCA GGAGATGGAC CCGCCAAATC CAGAGGAGGT	360
GAAAACGNCT GAAGAAGGTG AAAAGCATTC ACAGTTTTAA AAGAAGNCAC GTTGNAATGA	420
TGCAGGTTGT TCTATGTTGG GAATTTGTTC CTTTNAATTT NTCCCATTAAG AGGTTTTACA	480
GCCTTTNTGC AAAG	494

(2) INFORMATION FOR SEQ ID NO:1542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1542:

GGCAGAGGNG ACTTGAGAG ACACCCTACC CCCCATTGC CGTTTGTTGA CGTGGCAACA	60
GGGTCCCTAG GTCAGGGATT AGGTACTGCA TGTGGAATGG CTTATACTGG CAAGTACCTT	120
GATANGGCCA GCTACCGGGT GTTCTGCCTT ATGGGNGATG GCGAATCCTC AGAAGGNTCT	180
GTNTGGGAGG CTTTGTCTTT TGCCTCCAC TACAATTGG ACAATCTCGT GGCGGTCTTC	240
GACGTGAACC GNTTGGGGAC AAAGTGGCCC TGCACCCCTT GTGGCATGGC GCAGACATCT	300
TACCAGAATT GCTGTGAAGC CTTTGGGTT GGAATAATTN ANTTANTGGA TGNCCATGA	360
NTGTTGGAGG CCTT	374

(2) INFORMATION FOR SEQ ID NO:1543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1543:

GGACGAGGTT TGCGGGACAG GCTCTACCA TCCTGGGAAG TACTGGACCA GTGCTTGTTT	60
TTGAAAAGAT TTTNTTCAA TTCTGCAAAG ACTATGCTCT TTCATACCTC TCCCTGCGAG	120
CTTGTATTGG ACTGTGGACC GCTTTCCTGT GTATTGTCCT TGTGGCAACT GATGCCAGTT	180
CCCTTGCTCTG CTACATTACC CGTTTCACTG AAGAAGCATT TGCCTCCCTA ATTTGCATTA	240
TTTTCATCTA TGAAGCAATA GAAAACTGA TTCACCTGGC AGAGACCTAC CCCATCCACA	300
TGCACAGCCA GCTGGACCAC CTTAGCCTCT ATTACTGCAG GTGTACTCTG CCAGAGAATC	360
CAAACANTCA CACCCTCCAG TACTGGAAGG ACCACAACAT CGTGACAGCA GAAGTCCACT	420
GGGTTAACNT GANTGTTTCT GTAAGTTTGG GNGTTGCCAG TTGTCNTAGG CNTGT	475

(2) INFORMATION FOR SEQ ID NO:1544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1544:

CTACCTGCCA ACTTTNCCCA TGGGCCTTCA ATTAGTACAT TGAATAGGA GTNCGGATGC	60
TGGGGCAAGG NAAAGAGAGC TANGAAGGGT CCTNCTGAGG TTTTCTCAA CAATGATGAA	120
GGCCTTATTA ACAAAAAGTT ACCCAAAGAA CTTCTGTAA GAATATTTNC CTTCTTGGAT	180
ATAGTAACTT TNTNCCGATG TGCACAGATT TCCAAGGCTT GGAACATCTT AGCCCTGGAT	240
GGAAGCAACT GGCAAAGAAT AGATCTTTTT AACTTTCAA CAGATGTAGA GGGTCGAGTG	300
GTGGAAAATA TCTCGTAGCT GATGCGGTGG ATTNCTGAG GTAGCTCAGN TTTNCTAAGG	360
CTTGCATTGN NTGTTGGG	378

(2) INFORMATION FOR SEQ ID NO:1545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1545:

GGCACAGGTG GATGGGCATC TNAGTGGTTG TCGTCTTTTT CTCTTCCTTT CACCTCTTTT	60
NAGGTTTTAT TGTGACTACT GCGATACATA CCTCACCCAT GGACTCTCCA TCTGTGAAGA	120
AAGACACACT GCAGGGGAAG GGAAACACAA AGAGGAATGT GCAAAGACTA TTNATNCAGA	180
AATGGGATGG GAAGAGCAGG CTTAGAGCC TGATTGGACA AAACAACGGC TGGCATTTC	240
ACAAGGGAAA GGTNACCTCC TGACTIONCAT TCTNCTGGTN CCTTCCTCCT GGCAAGGGGC	300
GGATGGTTAC CACCTTNC	318

(2) INFORMATION FOR SEQ ID NO:1546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1546:

AGGTGGAAAT GGCCCTAGAA GAATCATGGG AGCACAGTAA AGAAGTAAGT NAAGCCGAGC	60
CTNGGGGTGG TTCCTCGGGA GATTCAGGGC CCCCAGAAGA AAGTGGCCAG GAAATGATGG	120
TGGAAAAAGA GGAAATAAGA AAATCCAAAT CTGTGATCGN ACCCTCAGGT GCACCTAAGA	180
AAGAACACGT AAATGTAGTA TTCATTGGCC ATGTAGACGC TGGCANGTCA ACCATCGGAG	240
GNACAGATGA TGTTTTTGAA CTGGGAATGG TTGACANAAG GATCACTNNG	290

(2) INFORMATION FOR SEQ ID NO:1547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1547:

GGCAGGAGAG GAAGGCTCAC TCTGCTCCGT CTCCATCGAG AAGGCACTGC CTGAGNGACA	60
GAGGCTTATA CAAGTTTGTA GCCAAGATTG ACGCTGGCCA GGCGGAGTGC TCCTGCCAAG	120
TCACTGTGGA TGAATGCTCC AGCCAGTGAA GGAACACCAA GGCCCCAGAG ATGAAATCCC	180
GGAGNCCCAA GAGCTCTCTT CCTCCCGTGC TAGGAACTGA GAAGTGATGC GACTGTGAAA	240
AAAGAAACCT GCCCCCAAGA CACCTCCGAA GCAGCAATGC CCCCTTCAGA TCATCCAGTT	300
CCCTGAGGAC CAGAAGGTTA CGCGNCAGNG NAGTCAGTGG AGTTTTTTNG GCAAAGTGGA	360
CAGGGCATTG AGNCCATT	378

(2) INFORMATION FOR SEQ ID NO:1548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1548:

GGCANGAGGG AATCAACTCC TGAGCTTTCT GCAGAACCCA CACCAAAGC TCTNGNAAAC	60
AGTCCCAAGG AACCTGGTGT ACCTACANCT AAGNCTCCTG CAGCGACTAA ACCTGAAATG	120
AACTACANCA GCTAAAGACA AGACAACAGN ANGAGGACTT ACGTACTACA CCTGAANCTA	180
CAACTGCTGG CACCTAAGGT GNCAAAAGCG G	211

(2) INFORMATION FOR SEQ ID NO:1549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1549:

GGCAGGAGCA AGCCCTCCTT ACCATAGTAT GATGGGTGAT GATGAAGATG CGTGTAGGGA	60
---	----

CACCGAGACC ACTGAAGCCA TGGCGCCAGA CATCCTAGCC AAGAAATTAG CTGCTGCTGA	120
AGGCTTGGAG CCAAAGTACC GGATTCAGGG AACAAGAAAAG CAGTGGGAGA GGAGGATAGT	180
GAACCTCTCA CCTGAAGAAC GAGAAAAAAA GCGACAATTT GAAATGAGGA AGGAAGCTTC	240
ACTACAATGA AGGACTTCAA TATTCAAACT TAGCCAGACA ATTAATTTTC AAAAGACCTA	300
CATGNTGGTG GTTGAAGTTG NAGAAATGTT TAGAGANTGC AGATGGNGGA AAGCCTTGAA	360
TTACGGGAGG NTTCAATTCC AGGTCT	387

(2) INFORMATION FOR SEQ ID NO:1550:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 331 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1550:

GGCAGAGCT ACCCCAGCAG CACCAATGTG GAGACCGTCA ACGATGGTGN TGAGTCGGCC	60
ATGTTCAAGC AGCTGTTCCA GAAGTGGTCA GTAAAGGACC AGACCATGGG CCTGGGGAAA	120
ACGTTGAGCA TTGGTAAAAT TGCTAAAGTT TTCCAGGATA AATTTGNATG TGAATCTGCT	180
ACACACCAAG CCAGAGGTAG CTGCCCAGGG AAAGAATGGT CGATGGATGG CAACGGGAAA	240
AGTTGAGGTC TGGGAGGAAT TNGAGGAACC TGGGNGCTGG GTCCCTGTGG GAGTTATTCA	300
ATGGTNTGGG CTTTCTTTTN ATGGGNGGGA G	331

(2) INFORMATION FOR SEQ ID NO:1551:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 475 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1551:

GGCAGAGCAA CCCGGTGCCT AAACCTCTACA GATCTGTAAT TGAAGATGTA ATTGAAGGAG	60
TTCGGAATCT ATTTGCTGAA GAAGGTATAG AGGAACAAGT TTTAAAAGAC TTGAAGCAGC	120
TCTGGGAAAC CAAGGTTTTG CAGTCTAAAG CAACAGAAGA CTTCTTNAGA AATAGCATCC	180
AATCACCTCT GTTTACTCTT CAGTTGCCGC ACAGCTTGCA CCAAACATTG CAATCGTCAA	240
CAGCATCATT AGTTATTCCT GCTGGTAGGA ACTCTTCCCA AGTTTACCA CGGNGGAACT	300
GGGGCATTTC AAATTCCATG GCAAATTTAC NTTTTNCCCG GTTNTNCCCT TCCNGTACCC	360



GCAGGTNTTG NCCTTTCCGG CTGTTTTTGG GTCACTTTTT NAAGGGCAAT NTCCCATTTT 420  
GGGTGCCAGG GTTTTTGGGG GGGGCCGGGT TTTTTTNGGG TNCCATTGG GGNAG 475

(2) INFORMATION FOR SEQ ID NO:1552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1552:

GGCANAGGGA ATGCTTTTNA TCCAGTTGCC AAAGATTCCA GTTTATGTGG GCCGTTAAAG 60  
TACTTCTATA GAGGCCTTGT ACCTAATAGC AACTAATGGA ACCCCAGAAC TTCAGAATCC 120  
AGAGAACTT TCCCCAATGA TTTCGGGGAT TTCTTAAATC GATGTTTGGG AAATGGATGT 180  
GGAAAAAAGG GGTTCAGCCA AAGGAATTAT TACAGCATCC TTTCTGAAA CTGGCCAAAC 240  
CGTTATCTAG CTTGACACCA CTNNTNCATG GGCAGCTTAA AGNAAGCAAT GGAAGAGTTA 300  
ACCGTTNAAC ATCCACTG 318

(2) INFORMATION FOR SEQ ID NO:1553:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1553:

GGCAGGAGCN CGGTGGTACG CTCNAGGNCG CGAGCCNACC GAGCGGACGC CAGTGGATGA 60  
CCC CGGGCGG GGGAGGAGGN GATANCATCA GCAAATGCC AGACGTCAAG GAGAGTNTNC 120  
CCCCGAAATA TCCTGGCGAC TCAAAGGGCA GGTCTGTAA GCCCGAAACC TCAGGACCCC 180  
CCCAGGAAGA CAAGAGCGGC TCCGAGGACC CCCCTCCCTT TTTTCTGTC ACAGGTCTGA 240  
CAGAAACCGT TAATGAAGTT TCCAAGCTGA GCAACAAGAT TGGGATGAAT TGTGATTACT 300  
ACATGGGAAG AGAAGGTTTT ACCTCCAAGC AGTCTGGGAA GGCAAGGTTT AAGGAGACAG 360  
TGCACAATGC CTTTTTGGGG ACCATNTTAA AGGGCAANTN TCAGCAAATT CCCCTTGANT 420  
TCAGNTGTGC TCTTTGAACT TTTTGAAAGG AATTTTAAGG GGTTTTT 467

(2) INFORMATION FOR SEQ ID NO:1554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1554:

TCCTGAAACA CCACGGGNGC AGTTCAACCA AGGTCATTGA CTTTGGGTCC AGCTGTTTCG	60
AGTACCAGAA GCTCTACACA TATATCCAGT CTCGGTTCTA CAGAGCTCCA GAAATCATCT	120
TAGGAAGCCG CTACAGCACA CCAATTGACA TATGGNGTTT TGGCTGCATC CTTGCAGAAC	180
TTTTAACAGG ACAGCCTCTC TTCCCTGGAG AGGATGAAGG AGACCAGTTG GCCTGCATGA	240
TGGAGCTTCT AGGGATGCCA CCACCAAAAC TTCTGGAGCA ATCCAAACGT GCCAAGTACT	300
TTATTNAATT CCAAGGGCAT ACCCCGGTTA CTGGTCCTGT GNACTACCCA GGCAGNTAGG	360
GAGGGTTGTG NTTGTGGGGG GTCGNTCACG TAGGGGTAA AAAGCGGGGT NCCCCAGGCA	420
GCAAAGATTG GGGACAGCAT TGNAAGGGTG TGGTGGCTAT TTGTTTATAG GGTTTTTTGA	480
AAGGT	485

(2) INFORMATION FOR SEQ ID NO:1555:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 346 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1555:

AGCGGCACGA GGNCTCCTNT TGGCAGANTT GGCCAGTNTT CCCCAGTGAC AGCCTGGNTC	60
TTTGGATTCA AGCTGCCTGG TCAGACTGCA NGTTCATCTG TACAAAGAAG GAAGCAACAG	120
TGCCAGGTTT CAGCGTGCCT TCCAAGTTCC ACATTCTGTG TGGCAGACTC CCAACGCCAG	180
AGCAAAGGCA GGCCCCTGGC AGGGGGACTC TGNAGGAAAG TGGAACNCC AGGAGACACT	240
GCCTGNAAAT TGTTCCTAAA GTTCAAAGG AGCCAAACGG TGTNACGAGC TTCCCTCTTT	300
NGCCGTNCCC CTNTTNAAGA AGCCAGCCAT GGCCCTGAGT GATTGT	346

(2) INFORMATION FOR SEQ ID NO:1556:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 188 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1556:

GAGTCACTGG CATTACGAA CTCAGCTTAT GCAAAATNTC AGTCACAGGT AGTCCAGGTA	60
TGCAGAGAAG NNGAAGAAAA ATCTTAGATA CGTCATGGGC ATATGTCCGG GGAGAAGAGA	120
ACTTAGCNGG ACTGGCGGCC CCGTGGGAGN ACAGCCTTCA TCCTTNAGCA CCANTGGGGA	180
GCTGGNGG	188

(2) INFORMATION FOR SEQ ID NO:1557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1557:

GGCAGAGCTC ACCTCCAGTT CACATGTTAA AGTCCTCACC CCCAGCAAGA CAGTNTTGGA	60
GGTGGGGCCT TTGGGAAGGG GAGCAGGTTT AGAGAAGATC CTGGGGGACC CTCACGAATG	120
AGATGAGTGC CCTGATGGGN AAGAGACACC GGGAGCCTCC TCTCCAGGTA GTCACACACG	180
GGGACNGTGC ACATGAGCAA GAGGCTGCTG TGCCGTAAAG CTTGGGGGGT GGTCTTCCA	240
ACNGGTA ACT GGGNTGCTGT GGTACCTGG GAGGCTGTGT TTTCCCACT GNNCAGTAGC	300
TTGGGNGGA	309

(2) INFORMATION FOR SEQ ID NO:1558:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1558:

GGCACGAGCA ACAGACTCAA TAGAAAGACT CCCAGTGTAT AACAAAGCTG CCTGGAAGCA	60
TTACAACACC AACCACGAGG CTGACGACTG GTGCGTCCCC AGCAGAGAAC CCAAAGACAT	120
GACGACGTTT CGCAGTGCCT AGNACACACT TGGGAACATC GGNAAAATCC AAATGTGGCT	180
TTTGTATTAA ATTTGGAAGG CTTAACCTCT NCAAGCTCTT GAAGGTTATN AAGAGGGATT	240
GATTAGTGCC ATGGATTCCA GGTCTTGNAG ATTTAAAGGG CACGGAACGT NCCCTTCCCA	300
AGGTTACTGG CATTTTTTAA CAAGTTGGAA GNTTTGTGGG CAATTCTTNC ATTGNG	356

(2) INFORMATION FOR SEQ ID NO:1559:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 502 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1559:

GGCACGAGGG AAAGCACCCCT GAGAAGACAG GAAAGAAAGA ATGCAGCACT GGTTACCAGG	60
ATGAAAGCCC AGAGGCCAGA GGAATGCTTA AAACACATCA TTGTAGTGCT GGATCCAGTG	120
CTCTTACAGA TGGNAAGGTG GGGGCCAGCT CCTAGGAGCA CTGNAGACCA TGGAGTGCCG	180
CTGTGTGATT GAGGCGCAGC TGTGCCTTGC AGTGTCACTT GGAGGAGAAG GGCTGGGCCG	240
TCTGAGGACA GNGAGGACTG GGTGGAGGAG CCAACAGTAC TGGTGTGCT CCGGGCAGAG	300
GCATTTGTNT CCATGATCGA CAATGGAAAG CAAGGAAGNC TNGACAGCAT TATGAAAGGG	360
AAGGAAACGN TTCAGGGTTT TTAAGTGN CN TCACAGCAAA GNCAGCAAGG AAAGTTTTTT	420
CACTGGTGAT TNTGGTTCAG GGNAATGTTT CATTGTTTCAG ATTCTCCCCA GAAGGGGNAA	480
CAGGGGCAAT TAACCAGCCC AG	502

(2) INFORMATION FOR SEQ ID NO:1560:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 504 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1560:

GGCACGGCTC ACACCGGCCT GTCCTGAGCA AGGGTTTGCT GCTGCTCCTC TGGCTCTCCT	60
TTGCTGAGAC CTGNAGTCAC CGGTTGCGCT TTGATGTNCT CACTCGTCTT GGTGTGTTT	120
TCATAGCCCT TGGCAACTTG CTTCTGGGAT ATTCAGTTTC AGGGTGTTTA GGNGTTACGT	180
TATTGAAGAT AAGAGTTTCT TTTTCTGTAA CTTGTTCTAA TTTGGGTGGG TAATAAGAAC	240
AGAGGCCTTC AGAGAAGTAT TTAAGTCTGAC GTCTTTAAAG CTTTTTAAGG CCCACGGCCA	300
GATTTCTTTA ATACACTTTG GGCATCCTCT GTCTGTAAAA TTAGGGAATT GTATAATGTC	360
CTCGCTAACA TACTTTCAGG TTAACCTGTT TATGGTCTG ATGTATTTAC ATGAAATTTG	420
GGTAACACTA AATATAGTGA ATGTTTCTT ACAGACAGAA CCTCCACTCA ATACACCAGA	480
AAGCAGAGAG TATCTTGACAG NANT	504

(2) INFORMATION FOR SEQ ID NO:1561:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 340 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1561:

```
GGCANAGNAA AAAAAATTCA AGACCAAGAC CAAGAGCTGG CCACTGTGCT GTTGCAATCG      60
GCANTCGATT GTATTTTGG AGTGAAGAG ATGGCTACAA AAAAGCATGA ATAGTCAAGT      120
TTGCTGCANG NTCTTTGGTA TCTTGNTACT GNGANACCAC CGGNACCATC TCAAGTACAG      180
CTGATCAAAG CCACTACCAA CTCCTTTGAT GTCAAGTGGG ATGAAGTGTG TACAGTTGNG      240
GGCTATCTTT TGCAGTTGAG TACAGACTTG NCATACCAAG CTGGCATCAT CNAGATTTTT      300
TCAGCAGCAC CAATTNTGCA AGGAGTTCAG GNTGGGACCN                               340
```

(2) INFORMATION FOR SEQ ID NO:1562:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 307 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1562:

```
AAGAGAAAGG AGGCTCTCAG TAAATGACC CAAATCATCC ATGAGACAGA CCTGTTAATG      60
AACACCATGC TCATAGAAGA GCTGCANGAC TGGGAGCGGC GGCACAAATC GCCTGCATCG      120
GGGGTCCACT CCACAATGGG CTCGACCAGC TTCAGAACTG CTTTACACTA TTGGCAGAAA      180
GTCTTTTCCA ACTGAGAAGG CAATTGGAGA AACTAGAGGA GCAATCTTAC CAAAATGNAC      240
ATATGGAAGG TGATCCCATT CCAATGCAA GAACTCACAT NGTTAGNAAG AGTCACCTTC      300
TTGNTTN                               307
```

(2) INFORMATION FOR SEQ ID NO:1563:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 333 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1563:

```
GGCANANCTG CTTCGGGGCA TAGACAGCTT ATTCTNTGCC CCNATGGACT TCCGGGGNCT      60
```

CCCTGGGAAA CTACCACAAA GAGGAGAACC AGGAGCACCA GCTGGGGNAA CAACACCCTC	120
TCCAGCCACC TCCAGATCGA CAAGATGACC GACAACAAGA CAGGAGAGGT GCTGATCTCC	180
GAGAAATGTG GTGGCATCCA TTGCAACCAG CGGAGGGGGA GCTTCGAGGG TGATTTGAAA	240
GGTACCCAGG ATGGAGGAGA AGGAGGCCCT TGGTACCCAT TNCAGAAGN CCACGGGACA	300
GTTTTCCACA AAGAANTTCC NNCCCCGGTT TGG	333

(2) INFORMATION FOR SEQ ID NO:1564:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 319 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1564:

GGCAGAGGNA CCAGCGCGCC CCATTACCT TGGCTGTNGT NGTTNCACAT GACCCAGGCT	60
GGCCAGTNGT CAGGTTGCAC CGCCCTTTGG TTCCCAGCA TGCTGTTTTN TTTNAGCCTT	120
CTNTCCAACC TTAACCAAAT CGGCAGCAGC CACCTNGAAC CGNCCACACA TTCCTGGCCA	180
ATNAGCTCAG CTGTTTATTT ACCAAATGTT TTCACAACAA CTACAGCAGC AGCTTTCGGT	240
TAACAAAAAA GCAGGAAAAA TCCACAACAC CNNGTTGGGC AACCAANTAA ATCCAAGGGA	300
ACATNTGGNA AAACCTTTT	319

(2) INFORMATION FOR SEQ ID NO:1565:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 116 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1565:

ACGGAAACAA TCTGAAGGTG AAGAGAAGAC ATTAACAGGG GNCGTGTAAA ACCAGTCCTN	60
CCACGTAANT NNACCAAAGA AACAGCTGCC TTCTATTCCC AAAAATGCTT TGCCCA	116

(2) INFORMATION FOR SEQ ID NO:1566:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 379 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1566:

GCCCTGGAAG ACGATCCCNA GTTCAACGCA GGTGTGGGT CTNTNTTGAA CACAAATGGT	60
GAGGTTNAAA TGGATGCTAG TATCATGGAT GGAAANACC TGTCTGCAGT AGCAGTGTCC	120
GCAGTCCAGT GTATAGCAAA TCCCATTAAT CTTGCTCGGC TTGTNATGGA AAAGACACCT	180
CATTGCTTTC TGNACTGACC AAGGCGCAGC AGTTTTGCAG CAGCTAATGG GGGTTCAGA	240
GATTCCTGGA GAAAACTGG TGACAGAGNA GAAACAAAAA GCGCCTGGAA AAAAGAGGAG	300
GCATGAAAAA GGTGCTTCAG AAAACAGTT TGTTCANAA AACTTTGGGG AACCNATGGG	360
TGNTTGTNG TCTTGGGAN	379

(2) INFORMATION FOR SEQ ID NO:1567:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1567:

GGCAGGAGAG CCTCCTCAAC TGGAGGCGAG TTTNTTCCTT CACGGGGNCG GTTCCCCGCG	60
NCCCCGNACG NNCACCGAGC GGGGGCCATC CGGGAAGCTG ATGATCATCT TTGGAGGGGG	120
AAATAAGGGC ATCGCGGATG AAGCTGGCAC GTNTACAACA CGGCTACGAA TCANTGGTNT	180
CTGCCAGCTG TTAGAGGAGA TATCCCTCCA GGCTGTGNTG CCCATGGATT TGTCTGTGAA	240
TGGTACCAGG AATATTAGTA TTTGGGGGAA TGTTGAATA TGGGAGNTTA CAGCAATGGA	300
GTTTATATGA AGTTACCAAG CAAGTGCCTT GGTTATTGGG AAAAAAGTG AAACCCCAT	360
NCCCCCTNCN TTNTGGTTTT AACNCCCTTG TCC	393

(2) INFORMATION FOR SEQ ID NO:1568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1568:

GGCAGGAGGG AAGAAGCACA GTAATGANTT TAANATGACG TCATTCCTGT TAATCCAACA	60
CCTGCNACCT TTTTACTGT NTGANGCGGT ACAGCGGGGA TGAAGGGCTT CATGAACTCA	120
AAATACAGCA AAGCACAACG GAACACTGCC TTAAGANCTT TAACCTCACC GAATACCGTC	180

AGTACTGAGC CGAACCTTTC CATTCAAATC TACCAGCAGC TCTTGAAAAT TGCCGAGGGT 240  
GCGTTACAGC CGNTGATAGT TTNTTCCCAT GTTGGGAAAT NNGGGGCTTT CCNGG 295

(2) INFORMATION FOR SEQ ID NO:1569:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 308 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1569:

GGNACAGGTC GGCATTATTT AAATGAAATT GGACAGTATG ACAAGGATAT GGNTTTTNGG 60  
GGAAGAGAAA ATTTGGAAC TTNACTAAGG ATCTGGATGT TTGGAGGCCA ACTTTTATA 120  
ATCCCCTGCN CTCGAGTAGG ACATATCAGT AGGAANCAAA CTGGGAAANC CTTCTACAAT 180  
CATCAGTGCC TATGAACACA TNAAGTGNCC TAAGATCTGG TGGCACGTTT GGTTGGATGG 240  
ATTATNAGGG GAGCCAGTTT TTTNTTTCGG AAAGTCTGGT CTGGAAATAT GTNACCTNCG 300  
GGAAANTT 308

(2) INFORMATION FOR SEQ ID NO:1570:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 156 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1570:

GGCAGACCGG CACGAGGNN AACTGGGTGC TGGAAATGGA AACCTGCAGT NCCTNGACAC 60  
ATGCAGAAAG CCAGAGTGGA AACTAGCAGA GTTCTTCACA TCATGGNTTT NNAANGAGGG 120  
CAAAACTTC TAAATNCCAG TTATTACAGC TGGTAG 156

(2) INFORMATION FOR SEQ ID NO:1571:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 264 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1571:

CGCCAGACGG CCATGTCCGA AACCTACGAT TTTTNTTTA ATTCCTTGGT TATTGGAAAT 60



GCAGGANCTG GNCAAATTTN GCTTACTTCA TCANTTTATT GAAAAAAAT TCAAAGATGA	120
CTCAAATCAT ACAATAGGAG TGGGAATTTG GTTCAAAGAT AATNAAATGT NGGTGGTAAA	180
TATGTAAAGT TACAAATATG GGATACAGCA GGNCAAGACC GATTCAGGTC CGTGNNGGAG	240
NAAGTTATTA CCGAGGCGCG GCCG	264

(2) INFORMATION FOR SEQ ID NO:1572:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 335 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1572:

TATTTGGTCA AGATACTCAC TTGTAATTAT NCCAAAAANT TGGAGTCTGT TTCCNGTTAA	60
TTCNTTTTGT GGGGCAGCAG GAGCCTCTCA CCTTTTNGGT ATTTGGAGAT ATAACCAAGA	120
NCTAAAAGCT AAAGCACACA AATGAAAAGA NTTCTGATC ACCTGANCAA TCTAGATGTG	180
GACAAAACCA TTGGGGACCT AGTTTATTAT TTGGTTATTG ATAAAGCAAA GCTAACTGTN	240
TGTTTAGAAA GGCAGTGTNA ACTGGTAGCT AGTTCCTTGG ATTCCAATAG AAAAATGNCA	300
GCAAACTTT TAATAACAG TTCTCTNTAN CATGG	335

(2) INFORMATION FOR SEQ ID NO:1573:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 108 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1573:

TTTTTANCTT CGGGCTCTNA ATTTTNGCGA GTAAAANTGG CTAAGTGAAT ATGGTGGAAA	60
TGGTTTCGGA AGGACGTNTT AGAATGATGT TGAAACTAT NACCCATG	108

(2) INFORMATION FOR SEQ ID NO:1574:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 329 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1574:

GGNAGGAGGT GTCGACTCCC TCAAAGCCAT GACCAGGCGA ANCAATACGG ANAAGTTNCT	60
AATCTCCTTN AGGGTGTAAT GAATGTCCTG GAAGCACTTC CACAAGTATA TGGGGATTCC	120
CCAGATCCGG CAGCTTTCCG AAAGNNTGAA GGCTGCACAG ACTGANTTAG GACAGCAAAT	180
CCTGGCAGAT TTTGAAAGAA GCGTTTCCTT CCCAGGGGCA CCAAGNGNCC AGGTGGACCC	240
AGCAATGTTC TTACGAGATG CATGTTCTGG TTGCTAAATA TTCTGGATTCC CCAGGGTTCA	300
ANCNGGNATC CTTCAANAAG TTTNTTAAA	329

(2) INFORMATION FOR SEQ ID NO:1575:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 397 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1575:

AGCTGCCAAA AGGGCATCCT GGAAGCCCCA TGGAGGACGG AGTAANATGG ATCGGGAAAT	60
TTCCATTGTT GTNCTTAATT TTNAATGAAA ATANGTTTTG GTATTTGGAG GAAAATNTGG	120
CAACCCATGG NTCCCAGGAT CCAGGCAGTA TTAACCTACA GGATGAAACT TTCTTGGAGA	180
GCAATAAAAT GCATGCAATC AATGGGAAAA CTCTATGCCA ACCTTAGGGG TCTTACCATG	240
TACCAAGGTG AACGANTGGC CTGGTACATG CTGGCCATGG GCCAAGAATG TGGATCTACA	300
CACCNTCCAT TTTTCATGCAG AGAGTTTCCC TCTATCGGAA TGGCGGGGAA CTACCGGGGC	360
AGTTGTGGGT GGTTCNTTTC CCCNNGGANT TTNAAGG	397

(2) INFORMATION FOR SEQ ID NO:1576:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 328 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1576:

AGCCCAGGGN AGCCCAGCCA GACGCCTCCG GTAGTGTAAG TAAGGACAAT GCCTGCTGGC	60
CCACATGAAC GGGGGGATGT AGACGGCAGC GGCGCCAGTC GTNCCTGGCA CCATGGACGA	120
TGCCACANTC CTGAAGGAAG AAGGGTTACA TCGTAGGCAT CAATCTTGGC AAGGNTTCCT	180
ACGCAAAATT CAAATCTGCC TACTCTGAAG CGCCTCAAGT TCAATGTGGC TGTCAAGATC	240
ATCGACCGCA AGAAANCACC TACTGANTTT TTGGGAGAGA TTCCTTCCCT CGGGAGGATG	300

GGNCATCCTG GGCAACTNTN CAAACCAA

328

(2) INFORMATION FOR SEQ ID NO:1577:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 403 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1577:

AATAAAGATG CTTCANACTG CAAAGAATTT GTTGAAAGAG GAGAAATTGG TGCATAGCTA	60
TCCGTATGAC TGGAGGACCA AGAAACCTGT GGTATTTCGT GCCAGCAAGC AGTGGTTTAT	120
AAACATCACG GATATTAAGA CTGCAGCCAA GGAATTGTTA AAAAAGGTGA AATTTATTCC	180
TGGATCAGCA CTGAATGGCA TGGTTGAAAT NATGGACAGG CGGCCATATT GGTGTATATC	240
AAGGCAAAGA GTTTGGGGTG TTCCAATTCC TGTGTTTCAT CCATAAGACC AAGGATGGAA	300
TACTTTGATN CAACAGGTTG GTTGGNCCCT GATGCCTTGG GAATATGTGC CCAGGTCCAG	360
GTNATTTTTG GGACATCTGG GNTTTGNTAG GCGGGAACCT TCC	403

(2) INFORMATION FOR SEQ ID NO:1578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1578:

CGGCNTNTNT NTGCTCCGTC GCAGGACGCA GGGTTCGGGC CTAGGGTAGG CTCTCCTGAA	60
TCGACAGGCG CCGGACCTCT NACAATGCAG ATCTTCGTGA AAGACTCTGA ACTGGTAAGA	120
ACCATCACCC TCGAGGTTGA AGCCCAGTGA ACACCATCGA GAATGTCAAG GCAAAGATCC	180
AAGATAAAGG AAGGCATCCC TCCTGACCAG CAGAGGCTGA TCTTTGCTGG NNAAACAGCT	240
NGGNAAGATN GG	252

(2) INFORMATION FOR SEQ ID NO:1579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1579:

TNTNCCCATC TTCCACATCC CTGGNCGTAC CTTCCCTGTT GANATCCTCT TCAGCAAGAC	60
CCCACAGGAG GNTTACGTGG AGGCTGCAGT GAAAGCAGTC CTTGCAGGTG CCACCTNTGC	120
GGGGGCCCCCT GGGAGACATC CTTATCTTTC ATGCCTGGNC AAGAGGACAT TGAAGGTGAC	180
CTNAGACCAG ATTNTGGGAG CATCTGGNAG GGAAGTNGGA GAACGNGNCC TGCCCTNNGG	240
TGTGNTGGNC CATCTAATTT NNAGTTGNNT TTTGAANCTT CCAGGNCAAA ATTTTTCAG	300
AAGGGTTCCA ATTGGGGGTT CGGGAAGTTG CATGGTTGGC CAACNATATT GCCCCGNGAA	360
GGTTTTTTNA ATTGTTTGAN GGGATCAAGN T	391

(2) INFORMATION FOR SEQ ID NO:1580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1580:

GGCACGAGTA AAGTTAACCA TTAATATGAA CCCAAGCTTA TTATAGATCT TTCCAATTGG	60
AAAGAACAAA GCAAAGAAAA ATCTGATAAG AAAGGCAAAT CAAAATGTGA AAGGTAATGG	120
NTTGGTTAAA GCCCAGATAG CGCTAGAGGG AAGCATCACA GCAACTGGCT GGNAAAAGNA	180
AAGGGAAAAG NAATCAGGGA TTTGAATTTT GAATTCCTTT ATTGCAGGAA CTATTNCAGC	240
TTAGTTTCCC AGNCATGAGC CTAATGATGT TGTGATAAA ATTNAAATGG ACTTGGAATA	300
GCTCAGTGT CCCAACTNNG AATTTGAAAA GGTTTTGATA TCCAAGGTTT CGTAAGNCCA	360
GGGAAAAANCC GGG	373

(2) INFORMATION FOR SEQ ID NO:1581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1581:

GATTNAACAA CGCNTTACTG CTCGCTGGGT TCATCCCGCC NATGGNCGTG TCTATAACAT	60
TGGAATTCAA CCCTCCCAA NCTGTGGGGC ATTGGTGACC TGGACTNNGG GNGCCTCTGC	120
ATTGCAGC	128

(2) INFORMATION FOR SEQ ID NO:1582:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 394 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1582:

GGCAGAGCTC GTCCTNTTNC CCAGGGACAA GTGAGGTCGA TGAAATCTTT AAAATTTNCC	60
AAGTTTTAGG GACTCCCAAA AAAAGTGA CTGAGGAGG ATACCAGCTG GGCATCCTCT	120
ATGAANCTTC CGTTTTCCCC AGTGTGTTCC TATAANCTTA AAAACTCTTA TTCCCAATGC	180
CATAATGAGG CTATTCAGCT CATGACCGAA ATGTTGAATT GGGGTCCAAA GAAACGGACC	240
GACAGCAAAG CCCAGGCATT GAAACACCCT NTTTNCCAAG TTGGTNCAGG TTTAGGCCCC	300
TTGGTTCAAT CCATCTGGGA TNCAAAACAT CTTTAATTAA GCAGTNGCAA CCCTTAGATT	360
CAAAGCCCTC TTTAGTTTNG GGTTNGGNCT TAGG	394

(2) INFORMATION FOR SEQ ID NO:1583:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 380 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1583:

GGCACGAGTG GACTAGGACT GGCCCCGGCA AAAACAAGT NTTATAGCTG CCCAGTGTCC	60
TCTGAGTGGA TGCTGGTGAT TCTGGTATGG AGCCCAGATG TAAGGCAGCA GGTGGTCCAG	120
AAGGCACCAG AAGAGGTCTC CTGTCAAAGT CAGGGCCAGA GAAGAAGGCA CAGGGNNCCT	180
ACTGCACGAG AACTTTCACT TGCAACGAGC AACCCTATGAT GAGGAGGGAG GATTCTTGGG	240
GGCATTGAGT CCCCAGACA CAAGGACCCN GNACCTTCTT GCTTGGGAAA GTGGANTTCC	300
TTCAGAATTC CGAGATGATG CCATTTTNGG AGGAAGNTGA CATGAGGGAC CCAAAACTTT	360
NTTGCTTTGG AAAGTGNATT	380

(2) INFORMATION FOR SEQ ID NO:1584:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 336 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1584:

GAGCTCGTGC GGNTTNANTT AATTCTNCTG TTTCGTGAAC TGCGAGTGGA ACAGGAATCT	60
CTGTTGANAG CTTTNNGCTG TGGCCTGCAG TTTTNAGGCA ACATTNCCTC ACGGATTGAA	120
GATTCCCAGT CTATTGTTTG GGTGCATGCT TTCCCAGAAC TNTTTTGTGTC TTGCTTAAAT	180
CATCCGGACA AAAAAATTNT TGCCTACTNT NCAATGATTT TGTTTACATC CCTTAATCAT	240
GAAAGATTGA AAGANCTNGT GGAGGAACCT NAATATTGCA ATTNATGTCA TAGATGCTTA	300
CCAAAAACAT CCNGAATCAG ATGGCCGTTT CTTGAT	336

(2) INFORMATION FOR SEQ ID NO:1585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1585:

GGCACGAGCT TTGCACCNAG CCTGTGCTAA TGGACATACA GATGTTGTAC TTTTCCTAAT	60
TGAGCAACAA TGCAAAATAA ATGTCCGGGA TAGTGAAAAC AAATCCCCAT TGATTAAGGC	120
AGTACAGTGT CAAAATGAGG ATTGTGCTAC TATTCTTCTA AACTTTGGTG CAGACCCAGA	180
TCTGAGGGAT ATTCGTTATA ATACTGTNCT TCACTATGCT GTTTGTGGTC AAAGTTTGTC	240
ATTAGTTGAA AAAC TGCTTG AATACGGAAG CTGGATCTTG AAGCGGAAAA ATAAGGGATG	300
GGTATACTCC ACTATTAGTT GCCGTTTATT TAACATTATN CCAAATGGT AAAATTTCTT	360
CTNGNGGAAG GGGGNTGATG TGAATGCTTT CAGN	394

(2) INFORMATION FOR SEQ ID NO:1586:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1586:

GGCACGAGGG NCTCTTCAGC TCAGCCCTCC ACAAAGTGTG AGCCTGAAGG ACCACCCTGA	60
ATTGCCCTTG TAGGACCCAG AACAGCTACC AGCAGAATCA GATTCTNATG GACCAACTGG	120
TATTCAAAGA GACAATCTGG GAATGAATGC GTTCTGGCAG AACCCTGGG AACCAGGGAG	180

NCCTGGNCAG TGAATTATCT TATTCATCAC CGCTGTCTCTG CTTCTGAATC TTATTTGCCA	240
TCGTGTTTGG TTTACTCACT TCCACAGAAA AACTTTCAGT GTGNAAGCGG GTNAAAGAGG	300
AGTNAACCTG GACTTNGCTG GGGGACTGAG AN	332

(2) INFORMATION FOR SEQ ID NO:1587:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 403 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1587:

GGCAGAGCGG CACGAGAGAA CCAGAAGGCT GGGCTGGGCC CTCGCTTCTN GCCCATCACC	60
CCTCTCCAAC AAGCTGCTCC CGGAGTGGGT CCCCCCTTCA GCCAGGNCC AGCTCCCCAA	120
CTACCCCCAG GACCCCCTGG CGCCCCAAG CCACCACCTG CTTCCCAGCC CAGTCTGGTC	180
TCCACTGTGG CCCCTGGCTC CGGCCTGGTT CCCACGGCAC AGCNCGGGGC ACCGTTCCAT	240
GGCAGGCACT TTGGNCCCAG GAGGGGTGAG CGGCCCTTTC CCAGNCCAGT TGGAAGNCCC	300
CAGTCCTTGG GTTGGGGAAG CAATTNAATT TTTCCAATAA AGTTTTTTTG GNCTTGGGAG	360
CGGGGGTTNC TTGGANTTGG GNAAAGGGAA AACCCAAAAT TTG	403

(2) INFORMATION FOR SEQ ID NO:1588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1588:

GGCACGAGAA TGAGCTCGTC GGCTGAAAGG GAACATCCGA GTAATTGCTC GTGTCCGGNC	60
AGTNACCAAA GAGGATGGGG AAGGACCTGA GGCCACCAAT GCTGTAACTT TCGATGCCGA	120
CGACGACTCC ATCATCCACC TGCTGCACAA GGGNAAGCCT GTNTCCTTCG AGCTGGACAA	180
GGTCTTCTCC CCACAGGCCT CGCAGCAGGA CGTGTTCAG GAGGTGCAGG CCCTGGTCAC	240
CTCTTGCAAT GATGGCTTCA ATGTCTGCAT CTTTGCGTAC GGCCAGACGG GCGCCGGCAA	300
GACGTACANG ATGGAGGGGA CCNTGNNNAA CCCAGGTTTT CAACCAGNGG GCCNTGCAGT	360
NGTNTTATTC CGAGGTGNCA GGAGAAGGCG TTTTATTTGG GAGTTACACC TTCACCTTCA	420
GGNTTGNGGN GNTTTTACAT TGAGGTTTNT CAGGGACTTN TTAGGGGAAG AGCCNTCAGG	480

GAAAAATGGA GTTCGGTTNT GC

502

(2) INFORMATION FOR SEQ ID NO:1589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1589:

GGCAGAGCC CCGGTGTTCA CTCAGGAGGA GAGATACAAG ATGGTGCAGG CCATCAAATG	60
GGTGGACGAG GTGGTGCCAG CGGCTCCCTA CGTCACTACA CTAGAGACCC TGGACAAATA	120
CAACTGTGAA CTTCTGTGTT CACGGCAATG ACATCACCCT GACTGTAGAT GGCCGGGACA	180
CCTATGAGGA AGTAAAGCAG GCTGGGAGGT ACAGAGAATG CAAGCGCACG CAAGGGGTGT	240
CCACCACAGA CCTCGTGGGC CGCATGCTGC TGGTNAACCA AAGCCNTCA CAGCAGCCAG	300
GAGATGTCCT CTGAGTACCG GGAGTTTGGC AGACATTTTG GCAAGTGCCT GGTGGGCGGT	360
AACCCTGGGA CCGGGGNTT CCCATTNCTG NCAGACTTTT CAGNAGTNC TTCCATTGN	420
TTNTGGGGAA GGAGCCCCAG CCAGGGAGAC ATTCNNTATG TNGTTGGTGN CTTTGGACCT	480
TTTCCACNTG GGGCTGTGGA TTTC	504

(2) INFORMATION FOR SEQ ID NO:1590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1590:

GGCAGACCTG CACNCCTGAT CCATAATGCT NACGCCAAA AAAGCTCCTT GGGTCTNANA	60
GGCCTCCAAA GCCTACTCCA AGGTTTCACC NNTNTTTNCC TGAAGTNANC CTGCTTCGGN	120
AGNATAGACA GCTTATTCTN TGCCCCATG GACTTCCGGG GNTTCCNTGG GAAACTACCA	180
CAAAGAAGGA GAACCAGGAG CACCAGCTGG GGGAGCAACA CCCTCTCCAG CCACCTCCAG	240
ATCGACAAGA TGACCGACAA CAAGACAGGN GAGGTGCTGA TTTCCGNGAA ATGTGNGTGG	300
CATCCATTNC AACCAGCGGT GGGGGAGCTT TCGAGGGGTG ATTTTGAAAG GTACCCAGN	360
TTGG	364

(2) INFORMATION FOR SEQ ID NO:1591:



(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1591:

GGCAGAGTGA ACTTCTTCCT GTTGGTNTCC CCCC GCCGCT GTGGGGCCGT CGAGACCCGN	60
CTGGNCGCTG AGATCCTGTG CCAGGGCAAG AAGTTCTACT TTGTGCGCAC CAAGGTGGAC	120
GAGGACCTGG CGGCCANGGC AACCNCAGNG GCCGTCGGGC TTCAAAAAGG CCGCTGTTCC	180
TGCAGGAAAT CCGAGACCAC TGTGCCGAGC GGCTGCGAGA AGGCCGGCGT GGCTGACCCT	240
CGCATCTTCC TGGTGTCCAA CCTCTTNGCC GGTTCGNTA ACGACTTTCC CACGCTGGTG	300
TCCA ACTGGG AAGCATGACC TGNCTCCNA ACGGTGGCCA AGNTGGTCTG GT	352

(2) INFORMATION FOR SEQ ID NO:1592:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1592:

GGCAGAGGNT GGTTCATACC GACGGGGAAA GGCGACCTGT GGTGATGTCG ACGTGCTCAT	60
CACTCACCCA GATGGCCGGT CCCACCGGGT NATCTTCAGC CGCCTCCTTG ACAGTTTTTCG	120
GCAGGNAAGG GTTCCTCACA GATGANTTGG TGAGCCANNA GGAGAATGGT CAGCAACAGA	180
AGTACTTGGG GGTNTGCCGG CTCCCAGGGC CAGGGCGGCG GCACCGGCGC CTGGTACATC	240
ATCGTGGTGC CCTATAGCGA ATTTGCCTGT GCGCCTGCTT CTACTTGCAC CGGCTCTGCA	300
CACTTNCAAC CGNTCCATGC NNAGCCCTGG CAAAACCAA GGCATGANTT CTGTTCAGAA	360
CATGCCCTTC AGCAATGNTT GGGTTCCGGA AACAACCATG GGTGNAAAGT TGGGGCCTGG	420
NCNA	424

(2) INFORMATION FOR SEQ ID NO:1593:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1593:

GGCAGAGAGA ACTTCTGANC GTTGGTAGTN TGGGGATCCT GGCTTTNTNC TTCTTCACCC	60
ACCGTATCAG GATCGTCCAG GATACAGCAC CACCCCTCAA TTATTACTGG GTTCCTATAC	120
TGACGGTGAA TCGTTGGCTC CTACTTGNAT TGCACACGGT TTCTTCAGCG TCTATGGCAT	180
GTNTGTGGAC AGCTGTTTCT CTGCTTCTTG GAGGACCTGG AGAGGAATGA CGGCTCGGCC	240
AGAAGCTTTN ACTTGCATGT CTTCCACCCT CAAGAACTN TTGAAACAAG ACCAACAAGA	300
AGGNAGGGAG TTCCTGAAGG CCCCCTGNTC CCCAACTTTT CAAGGAGTTT TCATGNCGCA	360
GGTTGNTTCA	370

(2) INFORMATION FOR SEQ ID NO:1594:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1594:

GGCAGAGTGC CTGATCGAAG GCAGCNCGGC CAAGCTCACT TGCCGCATTT NGGCTTTCCC	60
GGACCCATTC ATCCGCTGGA GTAAGGNCGG CAAGGAGCTA CGTAACGGTC CCAAGTANCG	120
CTACGTNTTC AAGGACCCTG AACGTGGTGG CACTGGTGGT GCGCGAACGG CAAGCTGGCA	180
GACCTGGGCC AGTACAGCAT CAACGTTTAC CAACCCCTTC GGCCAGTGCT TCCGACTTCG	240
GNCGCGGCAT CCTCGTGGA AGTCCCCGAC GGAGGATTTC AAAAGGGGAC CCGACAACAC	300
TAAGGCGCGC AAAGGCACCA CCGTNAACGN TTGATTCGGG AGATTCTCTGG GGAGAGNCTG	360
CGCCCCGACG TAGGNTNGGA CCAAGGACGG GGGAGGGACA TTGAGG	406

(2) INFORMATION FOR SEQ ID NO:1595:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1595:

GGCACGAGCT GGGGTGCCTN ATGCNATCAT GCTGTGTGTG CGCCAAATCT GCGCTGTNAT	60
CCTGGAGTCC CCACCCANAG GAAGCCACTA TCCCCTACCA TCCNAGCCTC TCCCTAGGTA	120
CTGTTCTTCT CTCTGCCAAC CAGGGCTTCT NTGTCCAGGG TCAGTATGGG GCTGTGAACC	180

CCAGCTGAAG GTCACCAAGC TCCAGCAGCT CTGNAAGCNA TGCGGTTCCC CTTTGGGNAC	240
ACCCAGCGTG GTGCCAGGGA CTGNGATCCC GGCACACAGA CCAGCTTCAC AGGAGTTCCT	300
TGGGTTCCCA ACGATTGAA TTGGTTGTNT GGATTGCGGN CGGCCAGGG NAGCAAAGNT	360
TCAANGGAG	369

(2) INFORMATION FOR SEQ ID NO:1596:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 209 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1596:

ACAGAACGGC CACGNTTCA CCTGCCCAGG CACCTGCCCC AAACCATTCA AAAGAAGGTC	60
GGGGAGCCTG TGAAACCTTC TNATCCCTTT CCAGGGCAAG CCCCAGCCTC AGGTGAACCT	120
GGNACCAAAG AGGGGAGCC CCTGGNAGGT GAAGGTAGGT GNAGCATCCG CAACAGCCCC	180
ACAGANACCA TCCTGTTNCA TCCGGGTCG	209

(2) INFORMATION FOR SEQ ID NO:1597:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 318 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1597:

CCTTTGTCCG TNTGAATTAC CAGCACCGTA TGTCCCCTGA AATTGCCCGC CTTTGGACCC	60
CCCACATTTA CCAGGATCTG GAGAATCATC CATCTGTTCT TAAGTATGAG AAAGATTAAG	120
GCCAAGTNCA AATTCCTGCA GAGCTTTGGC AACTGGGAAT GAGAAGAAAAG CATAAGAATT	180
TCAGGGNATG AATTTTNATC TTTTNNAAA GCTTACGATT AAGAAAGTGC CACGTTTTC	240
AATTGCTCCC TNCTGGGGNT TCTTGGGACC ACTGNNCTTC CTTCCCCTTC TGCCAAGGAG	300
CCGNTTTGCT TGTGATTG	318

(2) INFORMATION FOR SEQ ID NO:1598:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 232 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1598:

CTAGTGNNTC CCCCGGGCCT GCAGGAATTC GGNAGAGCAC ACCTTTCNT NTCCTTTTGT	60
GTGATGAAGG GCCCATTAA GGCCTGCTG CGGTGGCCCT TNANCCAGAA GGTAACCTTA	120
ATNCTGCTCG ACCAGAATAA CCGGGAAGCA CGTAATTNAG NGCTTTCAGG CCCGAGGTGA	180
ACTTCATCCT GTTTTAAAAG GCCAGTTAAA CGNCATGTAA CATNGCAAGG NG	232

(2) INFORMATION FOR SEQ ID NO:1599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1599:

GGNAGAGGTG ACCCTCTGGA ACCTGCNAGG AGCCGGCTCT CCAGGCTGCC CGGCTNANAA	60
GTACCTAAAG CAGGTAGACT TCANCCGCTA TAACTTCTTC CTGTTGGTCT CCCCCGCGG	120
CTGTGGGGCC GTCAAAACCC GNCTGGGCGG NTGAGAATCC TGTGCCCAGG GCCAAGAAGT	180
TCTNACTTTG TGCGCACCAA GGTGGACGAG GACCTGGCGG CCACGGGCAC CTNGTGGNCC	240
GTGGGGGTTN NAAAAAGGCC G	261

(2) INFORMATION FOR SEQ ID NO:1600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1600:

CCCGGCTGCA GANTCGAGAG CCGGACACCG AGTCGAGNTT TTNAGGACAT GTTANTAGAC	60
ATCAAGGCTT CACCGNTTTC TGCACCAGGC CGTGGTGTAT TNACGCAGAA TGTNACGTGG	120
GATCCTGAGT CTTCCGAATG GGCGGACGAA AGACATGGTC ATCATGCCGG TACTGGTGAG	180
GGACGTCGGC CAAGTCTCAG GGGAGGGAAG TCGAATGGAG GGGGGAGTGT GGAGTCAGTG	240
CAGTGGAGTA CATGTNTTCA GGACAGGGAC GCAGGGATCT GCAGTGGTGG GCAGCAGAGC	300
GAGAGGTGTG TGGTGATGG CGAGGCAGAA GTGGATTCTG AAGCAGAGTC GAGCAGGAGT	360
CCGGGTCCT GTACATGNCG CCATGGCGAG ACGTGCGTGC CACAAGCCCA GCTGCCNTAG	420

CTCTCGTGGG GTGTGAAGGG GANTGGCGCA GGGTGTNCTG AGGCAGAAGC TGGTCTGAAG	480
GACCTGTCTG AGGCACAATT CGGTGTGTCT CAAGAGTCTC AAGGTNGNTT NGTT	534

(2) INFORMATION FOR SEQ ID NO:1601:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 219 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1601:

GGCACGAGCT CACCATNTCC ATNAACGTGN TCTACAACTA CCTGGAGGCC AACCCCAAGG	60
TGCCCTGGGA CGATCTCCGN TACCTTTTTG GTGAAATNAT GTATGGNGGC CACATCACAG	120
ATGACTGGGA ACCGTCGGCT GTGCAGGACC TACCTGGNTG AATACANCCG GACGGNGATG	180
CTGGAGGGAG ACGTNCTGNT GGCCCCGGC TTTGCAAAT	219

(2) INFORMATION FOR SEQ ID NO:1602:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 85 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1602:

ACCAAAGTCC AGCACANACC CTCGGGNCTC ATCANGGCCA GGTAAGCTGA TCCACCTTGN	60
GATCAAGCCG GCCATCCGGA ACCAG	85

(2) INFORMATION FOR SEQ ID NO:1603:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 314 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1603:

GGCAGAGGTG TGGCGAGGTG GTCCGGGACC ACATCATCAG GGCCCTGGGN CAGGCCTTCC	60
ACCCCTNCTN CTTACGTGT GTAACCTGCG CNNGGTGCAT TGGGGATGAG AGCTTTGCCC	120
TGGGCAGCCA GAACGAAGGT GTACTGCCTG GACGACTTCT ACAGGNTATT CGCCNCCGTT	180
TGCAGCATCT GTGAAAAATC CCATGCATCC CTCGGGGATG GGGAAAGATG CCTTCAAAAT	240

CGGAATGCAT GGGAAAGAAA CTTNCATGNA AAATTGCTNA CAGGTGTGAA GGNCTGCAAG 300  
ATCCTCCNGT CTGT 314

(2) INFORMATION FOR SEQ ID NO:1604:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1604:

GGCACGAGGG TACNCCATTG CGGCCATGTN TGTNATGCGG CCGGAGCAGA TCATGAAAGT 60  
CCATCATCCC AGTGGTCATG GCTGGNATCA GANNCCATCT ACGGCCTGGT GGTGGCAGTC 120  
CTCATCGCNA ACTACNCTGA ATGAACGTAC ATCAGCNTCT ACAAGAGCTT CCTCCAGCTG 180  
GGNGCCGGCC TGAAGCGTGG GCCTGAAGCG GCCTGGCAGC CGGCTTTGTC ATCGGCATNG 240  
TGGGGGAACG CTNGCGTGCG GGNGCACCNC CAG 273

(2) INFORMATION FOR SEQ ID NO:1605:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1605:

GGCACGAGAG GTCATCGGGA CCCTGGAGGA GGTCCACATG CCACAGAATG GGAATCAACC 60  
ACNCTGGCAT CACTGCCCTG GCCCAGGCTT TCGCTGTCAA CCCCCTGCTG CGGGTCATCA 120  
ACCTGAATGA CAACACCTTC ACTGAGAAGG GCGCCGTGGC CATGGCCGAG AACCTTGNA 180  
GACCTTGCGG CAGGTGGAGG TGATTAATTT TGGGGACTGC CTGGTTGCGC TCCAAGGGTG 240  
CAGTTGCCAT TGCAGATGCC ATCCGCGGCG GCCTTGCCCA AGTTAAAGGA GCTGAACTTG 300  
TCATTTCTGT GAAATCAAGA GGGTTGNTGC CCTGGNTGTT TGTGAGGCC ATGGCAGACA 360  
AAGTTNAGTT GGAGAAGTTG GACNTGAATT GGCAACANCC T 401

(2) INFORMATION FOR SEQ ID NO:1606:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1606:

GGCACGAGGT TTGATGAGGG CCGGCTGACA GATGGAAAAG GGAAGACCAT TGATTGCAAG	60
GACGCCATCT TCATCATGAC CTCCAATGTG GCCAGCGACG AGATCGCACA GCACGCGCTG	120
CAGCTGTAGG CAGGAAGCTT TGGAGATGAG CCGTAACCGT ATTGGCCGAA AACCTGNNGG	180
GATGTCCAGA TAAGTGACAA GATCACCATC TCAAAGAACT TCAAGNGAA TNTGATTTCG	240
CCTATCCTGG AAAGCTTCAC TTCCGGAAGG GATGAGTTTT TNGGGACGGG TNCAATGGAG	300
GTCGTCTNAC TTT	313

(2) INFORMATION FOR SEQ ID NO:1607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1607:

AACAACAGGC TGAACAACCG CGCCAGTTTC AAGGGCTGCA CGGCCTTGCA CTATGCTGTT	60
CTTGCTGATG ACTACCGCAC TGTCAAGGAG CTGCTTGATG GAGGAGCCAA CCCCTGCAG	120
AGGAATGAAN GNGGACACAC ACCCTTGGAT TATGCCCCGAG AAAGGGGNAA GTGATGAAGC	180
TTCTGAGGAC TTCTNAAGCC AAGTACCAAG AGAAGCAGCG GAAGNTGNAG GCTGAGGAGC	240
GGCGCCGCTT CCCCTGGAG CAGCGACTTA AAGNGCACA TCATTNGGCC AGGAGAGCGC	300
CATCGNCACA GTGGGTGCTT GCGNTTCCGG AGTAAGNGAG AATGGCT	347

(2) INFORMATION FOR SEQ ID NO:1608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1608:

GGCACGAGAG AAGATGCTGC GTATCCAGAA GGAGCACCGC GNCNAACTTC CCACGCTCCA	60
AGCACCTGAC AGGCGAGTGC AAGGACCTCA TCTACCACAT GCTGCAGCCN GACGTCAACC	120
GGCGGCTCCA CATCGACGAG ATCCTCAGCC ACTGCTGGNA TGCAGCCCAA GGCACGGGGA	180
TCTCCCTCTG TGGCCATCAA CAAGGAGGGG GAGAGTTCCC GGGGAATGGA ACCCTTGTGG	240

ACCCCCGAAC CTGGCTCTGA CAAGAAGTCT GCCACCAAGC TGGAGCCTGA GGGAGAGGCA 300  
CAGNNCCAGG CACAGTCTNA GNACAAAACC CGAGGGGACA GCAATGCAAA TN 352

(2) INFORMATION FOR SEQ ID NO:1609:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 146 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1609:

GGCAGAGCC AGGTGCGGGT TGCTGCCCAA GGGGTGCAGG GACAGATGAG GGAGGGCACT 60  
GCCTTCAGGN ACGACATATG GGGGCCACCA TCGCTTTGTT GGTGGGGACA GGGTCCCCCT 120  
TTTTTTTTTT TTNAANATGG GNTNTT 146

(2) INFORMATION FOR SEQ ID NO:1610:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 419 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1610:

GGCAGAGCTT TGATTAAGT CCGGGAGTTT GTCTCTGGGC TAAGTGCTGC ATGCCATGGG 60  
GACCTCACAG AGAAGCTCAA ACTCCTGTAC AAAATGCACG TCTTGCCTGA GCCATCCTCT 120  
GATCAAGATG AACCAGATTC TGCTTTTGAA AGCAACTCAG TACTTCTTTG AAGATATTAC 180  
CCCAGAATGT ACACATGTTG TTGGNATTGG ATAGCAGAAG CAAACAGGGT GCAGATGATG 240  
GCTGTGTTAC GGTGAGCCTA AAGCCAGACA AAGGGAAGAG AGCAATTCCC ANGAAANTCG 300  
TAATTATTTG NACTGTGGA CTCCAGAAAA TAATCTAAGT CAAGNTGCAA AGGTTTACCC 360  
AANTAAATTC AGGGCATTTC ATTGNACCTT GTTAAGACAT GGTATANCNG GTTCAGCGA 419

(2) INFORMATION FOR SEQ ID NO:1611:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 280 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1611:



GGCANGAGGT GACCTCCGTG GGCTGGTCTG AGCGGGGGAA CCTNGTGGCG GTGGGCACAC	60
ACAAGGGCTT CGTGCAGATC TGGGACGCAN CCGCAGGNAA GAAGCTGTCC ATGTTGGAGG	120
GCCACACGGC AGCGTCGGGG CGCTGGCCTG GGAATGCTGA GCAGCTNTCG TCCGGGAAGC	180
CGCGACCGCA TGATCCTGCA NAGGGACATC CGNACCCCGN CACTGCAGTC GGAGCGGCGG	240
CTTCANGGCC ACCGNCAGGA TGTGTGCGGG CTCAAGTGGT	280

(2) INFORMATION FOR SEQ ID NO:1612:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 380 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1612:

NTGGTTNCCC CGGGCTGCAG TANTGGGCAG AGTGAAAGGT GCCTGNGGNG CAGCAGCACC	60
TGCTTTTCCG TGGCCAGCTC CTGGAGGATG ACAAGCACCT CTNTGACTAC TGCATTGGGC	120
CCAATGCCTC TATCAATGTC ATCATGCAGC CCTTGGNGAA GATGGCGCTA AAGGAGGCCC	180
ACCAGCCGCA GACCCAGCCC CTGTGGCACC AGCTGGGACT GGTCCCTAGCT AAACACTTTG	240
AACCACAGGA TGCCAAGGCC GTGCTGCAGC TGCTAAGGCA GGAGCACGAG GAGCGCCTGC	300
AGAAGNTTAA GCCTGGAGCA CCTGGAGCAG CTGGNCCCAG TACCTNCTGG CAGAGGAGCC	360
TCACGTGGGA GCCCANTTNG	380

(2) INFORMATION FOR SEQ ID NO:1613:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 301 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1613:

GGCACGAGGG GTTCTGCAAA GCGGGNCTGT CTGGGGAGTT TNGACCCCGG CACATGGTCA	60
GCTCCATCGT GGGGCACCTG GAAATTCCAG GNTCCCTCAG CAGAGGCCCA ACCAGAAGAA	120
GTACTTTNTG GGGGAGGAGG CCCTGTACAA GCAGGAGGCC CTGCAGCTGC ACTCCCCTTT	180
CGAGCGTGGC CTGATCACAG GGTGGGATGA CGTGGAGAGA CTNTGGAAGC ACCTNTTTGA	240
GTGGGAGCTA AGGCGTGAAN CCAGCGACCA GNCCCTGNNT TGCAACGGAG CCCTCCCTGG	300
G	301

(2) INFORMATION FOR SEQ ID NO:1614:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 221 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1614:

GGCACGAGCG GCGGCTGCAC GCTGTGGCCC GGCNCCAGCG CTGTAGGCCT GTGGCAAGAC	60
CTTCCGCTAC CGCTCCAACC TGCTGGAGCA CCAGGAACTG CACCTGGGCG AGCGCGCCTA	120
CCGCTGTGAA GCACTGCGGG CAAGGGCTTC TTCTACCTGA GCTCCGTGCT GCGCCACCAG	180
CGCGCCCATG AAGCCGCCGN GGNCCGAGCT NNCGNTGCCC C	221

(2) INFORMATION FOR SEQ ID NO:1615:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 213 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1615:

GGCACGAGGG AAACCTGCAC GACAACCTGT NGGACCTNCG TGCCCAGGTG GCAGCCAACC	60
AGAAGGGCAT CCAGCTGGTG GGGGAGCTCA TTGGGCAGTA CGGCCTGGAA CGTGGTGCAG	120
GCCTGACATG GGCCATATTC AGGNAAACGC TGCAGCTGGA CCGTGCGNAG ACATGTTGCG	180
TGCCTTTTGT AACCTTCCCG GCAGGNCCG NGG	213

(2) INFORMATION FOR SEQ ID NO:1616:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 313 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1616:

GGCACGAGGT CAATCTCACG GGGTTGAAGA AGCGGGACCG CTGCGNAAGG CCTGGCCTTT	60
GCGGAGGAGG TGATGGATGA CATCCTGGAC TCCGCGGACC AACCCTTGAC GGGCCGAAAG	120
TGGTGGATGG GCGCGGAGGA ACTCTGGCAG ACGCTGGCCT GCTGTATGGA GGTGGCGAAC	180
GCTGTGGGCG CCTCCAACCC TGAGCGCCTA TGTCTCCAC CTCCCCGTCC ATCAGGAGNC	240

TTCTTGCAAC GGCCTGCAGC ATTATGCTGT NCTNGGCCGC GGACANTGGG GCGCCGNCT 300  
CCGTTCAACC TGG 313

(2) INFORMATION FOR SEQ ID NO:1617:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1617:

GGCACGAGGN AAGAGTGTA GGCCTGCCTG AACAGACCT GCATGNAGTN CTACG 55

(2) INFORMATION FOR SEQ ID NO:1618:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 321 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1618:

AACGGCCTNC ACNGACGGNA TCGGNTTNGC CATCGCCCCG NGTTTGGCCC AGGACAGGGC 60  
CCACGTGGTC GTNAGCAGCC GGAAGCAGCA GAATNTGGAC CAGGCGGTGG CCACGCTGCA 120  
GGGGGAGGGG CTGAGCGTGA ACGGGCACTG TTTCATNNTG GGAAGGCGG AGGNACCGGG 180  
AAGCGGCTNG TGGCCATGGC TGTGAAAGTT TCATGGAGGT ATCGATATCC TAGTCTCCAA 240  
TGCTGCTGTG CAACCCTTTT TTTGGAAGNC TAATGGGATG TNNACCGNAG GAGGTNTTGG 300  
GGACAAGATT TTTGGGACAT T 321

(2) INFORMATION FOR SEQ ID NO:1619:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 445 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1619:

AGGTACACAG ACACACGTTA TTACATATGT GCACATGCAT GCATATGCAA ATATGCACAG 60  
TACACAGACT GCACAGAGCT CCACAGACAT AACTTGCAC CTTGGGGTTT AAGCCCTGAG 120  
CAAATTGACA TCCCGTGTCT TGTCTCCAC AGTGTCTCCA GTGCCAAGCA TGGGGCTGGG 180

TGTGGTAAAT GTTTNTNGAG TCAGTGAATG CATGGNTGGC TCGAACCGTG TCTTGACTCA	240
GCAACACCGG GNCCAGTGGG GTCTGGAGGT GAGGTTTCAGG AGACAGTCAG CCCTCTGCTT	300
TTGCTGGAGA CTGGGGAACA CCTTTAGGGA CATTTTCAGAG GAAGGACAGT TGCAGGNACA	360
ACTTTGGTCT AGCAAATCAC AAGNCTGGGT TGAGGNCTCA GGATTTTCCTT GTACCGTGTT	420
NCTTTTCCAA TTTGCCCAGA GNTAG	445

(2) INFORMATION FOR SEQ ID NO:1620:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1620:

GGCAGGAGCC AAGGGTGAGC GCCATGGCTC AGCAGCCGAA CGACTTCTGG CAGCTCAGAA	60
CCCGCTCTCC CAGGCTGATC GCCCTCATCA GCTGTTTGCA GATGCACCTC CTCCACCCTC	120
TGCTCCCAAT CCTGTGGTAT CATCATTGGG GTCTGGGCTT CCTCCACCAG GCATGCCTCC	180
TCCTGGCTCC TTCCCACCCC CAGTGCCACC TNCTGGAGCC CTCCCACCTG GGNATACCCN	240
CAGCCATGNC CCCAACAACT ATGGCTNCTG GGGCTGNAGG ACATGGCCCC CCATNGGCAG	300
GNACCCAGG GTAGGACATT CTGGTNANTG GGCATTNANA ANTTNAACNA TTTNCAACGG	360
GTGGGATNNC CCCNTTCAGG GGTNTTTTAA ATGGAAATTT GAAAAAATG GGGCTTTAAG	420
GTTTTGGGGA ATNCCAAGGT TGGGACCCCA GTTTTGGGGG GNNAATNAAT GGTC	474

(2) INFORMATION FOR SEQ ID NO:1621:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1621:

AAGCTGGGCT TACAGGATGG AAAAGAATAT TTATTCCAGG CCAAGGATGA GGCAGAGATG	60
AGCTCGTGGC TACGGGTGGT GAATGCAGCC ATTGCCACAG CGTCTTCTGC CTCTGGAGAG	120
CCTGAAGAGC CGGTGGTGCC CAGCACNCGN NGGGTCATGA CCCGGGNCAT GACCATGCCN	180
NCAGTGTAC CCCTCGGGGC TGAGGGGGCCT GTTGTGCTCC GCAGCAAAGA CGGCAGAGAA	240
CGAGAGCGAG AAAAACGCTT CAGCTTCTT TAAGGAAGAA CAATAGTTNG GGGCAAGTTC	300

CAGGNCAATT CCTTCCTTNN GTTCAGGAAA NTT

333

(2) INFORMATION FOR SEQ ID NO:1622:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1622:

GCTGCGCTCC TCCGAACCTG CCTGCACGCA GCCTGGGTTC CAGGATCTGG AGGTCGTGCC	60
CCCAAAACCA CAGCCGAGGC CTACCACGNG GGCATGTGCA GCCGGGAACG GTCGGGTAC	120
AGCGAAGCCT TCATGCAGGG CCAGTTGCGG GTGGTGGTGG CCACGGTGGC CTTTNGGATG	180
GGGCTGGACC GGTCAGATGT GCGGGGTGTN CTGCATCTGG GGGTTGCCCC CAAGNTTCGA	240
GAGCTACGTN CANGCCGTGG GCGTGACCG	269

(2) INFORMATION FOR SEQ ID NO:1623:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1623:

CATGCCCTCC CCGNTATGA GCGGGCCGT GCTGGAGACC AAACAGAGCC TTGAGGCTGC	60
GGGGCACACG TGGTTCCCTT CTTGCCAAGC AACATACCCC ATGCTCTGGA GACCCTGTCA	120
ACAGTGGGCT CTTCACTGAA TGGTGGCCAC ACTTGCTTAC AGAACTTCAA AGGTGATTTC	180
GTGGACCCCT GCCTGGGGGN ACCTGGTCTC AATTCTGNAA GCTTCCCCAA GGCTTAAAGG	240
TATGCTGGCC TTCCTGGTTG AAGCTNCTGC TGCCANGGCT GTCCAGTTTN NCTCAGCAAC	300
AT	302

(2) INFORMATION FOR SEQ ID NO:1624:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1624:

GGCANAGGGA GGCTCAGTCT GTAAGTGAAG CAGGGCGNTC TCCCCGATAT CTGCATCGGA	60
CGCGCCCTCT AGTGGAACC GAGAGTNAAG CGGCCTGGAT TCCGCGATGA ACAGATTCTT	120
TTGTGTCGCT GGGAACACTG GAGGGTTGTC GTTAATGTCC TTCACCTCCA CGTCCACATG	180
GGAAAACCTG CAGCGGCCCTT TCCACGATCA CCTCCAGGNG GATGCTGCAC TCCGCGCTCC	240
GCCCGCACAG CTCCTCGCGG TCGATCCGAG AATTCACAAA CAAAATGCCA TTCTGGCAGA	300
TTTACCTCCA GAAGGTCCCC GGGGNCCTTT GGGATTCCAA TTGGAACAGN GNNGGGCANC	360
A	361

(2) INFORMATION FOR SEQ ID NO:1625:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 495 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1625:

GGCACGAGGA AGGAACTCAC TCTGGGGGCC TCACAGGCCA CCACGGACGA GGTAGCTGCC	60
TTCTTCGTGG CTGANCTGGG TGCCATAGTG AGGAAGCACT TTNCTTTCT NAAGTGCCTG	120
CCACGAGTCC GGCCCTTTNA TGCTGTCAAG TGCAACAGCA GCCCAGGTGT GCTGAAGGTT	180
CTGGCCCAGC TGGGGCTGGG CTTTAGCTGT GCCAACAAGA TTGCTTCCGT NATCAACTCA	240
GCCTTGGAAC TGTACTTCCC ANAAGGGCTG TGGGCGTGGG ACATCTTTGG CTTGAGCTTG	300
GGGCGGTTAC TNACGTGNAC CTNGGCCTNT NACTGGTGGG CAGTTCAGCA TTCATTGCCA	360
AAGAAAGGGA GGTTCCTGNT TAGACCAGGN CTNGGNAGGG GAGGAGGAAA ATGGTTCCAN	420
CTTCCAAAGA CCATCGTTGT ACCACCTTGG ATGGAGGGGC GTGTATTNGG ATCTTTCAAA	480
CTTCNAGTCC CTGGT	495

(2) INFORMATION FOR SEQ ID NO:1626:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 375 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1626:

GGCACGAGGC CAGCAGTGGC TGGAAGCCAC TGGCGTACTC TGACACCGAC GAATTTNACC	60
CAGTTGCAGG AGGCACAATG AGCCAGCATT TACCTTTGGT CGCCGCACAG CCCGGCATCT	120

GGATGGCAGA AAAACTGTCA GAATTACCCT CCGCCTGGAG CGTGGCGCAT TACGTTGAGT	180
TAACCGGAGA GGTTGATTCTG CCATTACTGG CCCGCGCGGT GGTGCGCGGA CTAGCGCAAC	240
AGATACGCTG CGGATGCGTT TTAACGGAAG GATTAACGGC GAAGTCTTGG CAGTGGGTCTG	300
ATGATGCGCT GNACGTTNCG AACTNGCCAG AAATTNATCG ACCTACGGAA CCAACATTTG	360
ATCCGCACGG TACTN	375

(2) INFORMATION FOR SEQ ID NO:1627:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1627:

GGCAGAGAA AGAGATGACC CCAGGGAACA TCCTGACCAG GCCGGNTTCC TGGATGGCTG	60
TNTTCAATGC CATGCCCACC ATCTGCTTCG GAATTTNAGT GCCACGTCAG CAGTGTGCCC	120
GTNTTCAACA GCATGGCAGC AGCCTGAAGT GAAGACCTGG GGTGGTAGTG GTGACAGCTG	180
CCATGGTCAT AGCCCTCGCT GTCTACATGG GGTGCAGGCA TCTTTGNGGT TCCTGACCTT	240
TGGNAGCTGC TGTGGGTCCT GACGTGGCTC CTGGTGCTAT CCCTCGGAGG TACATGGNCG	300
TGGCCGTTGC CCGAGNCTTT CAGCATCCTG AGCGTNGCTC ANCTCNT	347

(2) INFORMATION FOR SEQ ID NO:1628:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1628:

GGCAGAGGC GCCGGTAAAA TCGACCACAA AGGCGATAGT ACCGTCAGGC TGGCGAATCA	60
GGTTCGACTG CTTACATCC CCCGTTGAAC GACGCGTTN TTGCACCCAT GCGTTATCTG	120
GCGCATGCAG TTTGTTTTCA TCACGGCTGA AGGTGATGGT GTATTTAAAG TTCATCTCTT	180
TACCCGGCTC CGGCAGCTGA TCCGGCGTCC AGTAAGCGAC GATGTTATCG TTGGTTTCAT	240
CGTTGGTTGG AATTTCACC AGCTCAACGC TGCCTTTACC CCACTCCCCT TTCGGAGTCA	300
CCCATGCGGT TGGGACGGAG NATCGTAAAC GATCATCGAG ATCTTTCAAA GCGGGAGAAA	360
ATCACGACCC GNGTTGCAAC AGACCCAAAG NCTTGNGGGG TTTTNNCCAT GGGAGNAAGT	420

TGTTT

425

(2) INFORMATION FOR SEQ ID NO:1629:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1629:

GGCACGAGCT TTGCTCCCAC CCCACCCCCA ACCCACAACC CCTGCCTCTG CCCATCAGCC	60
TGGCCTTGAT GAGGAGCGGG AAGGCCTCCT GCACCCTGGA GACCGTGTGG GAAGACAAGC	120
ACAAGTATGA GGAGGCCGAG CGGCGCTTCT ACGAACACGA GGCCACACAG GCGGCCGCCT	180
CCGCCCAGCA GCTGCCAGCC GAGGGGCCAG CCATGAATGG GCCCAGCCAG GACGACCCTN	240
AGGACGCTGA TGAGGCGGAA GCCCCTNACG GCGGCAGCAG GCGTNGATCC CAGGAAGAGC	300
CAGGACAGCA GGAAGCCCCT NCAGAAAAAG NAGGAAGCGT TCCCCAAGA GCGGGTTNGG	360
CCCCGNGGGA CCTGGCCTTN TTGGCTTTTT GGCCGAA	397

(2) INFORMATION FOR SEQ ID NO:1630:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1630:

GGCACGAGGC GGCTGTCGCT NAGCCCACTG CGGGGCGGGG AGGCCGGGCC ANACGCCTCA	60
CCCACAGTNA CCACACCCAC GGTGACCACG CCCTCACTAC CCGCAGAGGT GGGCTTCCCG	120
CACTCGACCG AGGTGGACGA GTCCCTGTNG GTNTCCTTTN AGCAGGTNNT GCCGCCATCC	180
GCCCCACCA GTAAAGCTGG GCTGAGCCTC CNGCTGCNTG GCCCCGGGC GCGGCGNTCG	240
GTTCCCCAC ACGATGTGGA CCTNTGCCTG GTGTNACCCT GTNAATTTNA AGCATCGCAA	300
GGTGGTGCCA ATGGCACGNC AACCTGNITT CCCCCGNAG CTTGNAATG AANAGCANTN	360
CCCGGTTTAC AGGAACGGGG CAGGTGGGCT GGGGGCCGAG NAGACGCCAC CCACATTCGG	420
TTCAGCAATT CCCTGCCCAA CCTGTTTGAN TTGGATCCNG TTGCCCTNGN CCCGGTTGCG	480
GNANANTTAG ACGGAGACAA A	501

(2) INFORMATION FOR SEQ ID NO:1631:



(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1631:

```
GGGGCAAGAG TATNCCCTCA TGGGGNCAAA TTGGCACCCC TTTGGGTTGG NCTTNCAAAG      60
GGTTTCCAGG GGCCCAGGGT CCCTATTTAC TNTGGGTGTG GGGAGCANAC AGAGGCTTTG      120
GGCAAGGGGN CCATCGTGGG AGGGCCCCTT TAACCGGGGC CTNCTTTTTT ATNTNTNGGG      180
TTCAAAANTT GGGGGGGGGC TAATTTCCGG GGGT                                     214
```

(2) INFORMATION FOR SEQ ID NO:1632:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1632:

```
GGCAGAGNCA TACCAAGAAG ACGGTGATGA TCAAAACCAT CGAGAACACG GGATGGGGAG      60
GTCGTNAGTN AAGGCCACAC AGCAGCAGCA TGAAGTCTCC TAAAGACAGA AACCTCTGCG      120
NACCAGAAAC CGTTCCTCAC CCCTGTTCTT CACTGGCTCC CTGAAGCCAG CNTTCTTCCA      180
TCCCAGGGAC ACCACACCCA GCCTTCANTC CTCCCCTNAN AGCCTCTGAA CCCCTCTNA      240
TTGGGCCATC CCTNGTGGTC CCCAACAGCG ACATAGCCCA TCCTTGNTTG GTTCACGGGG      300
CATGGTCCCG GNCACCTTTG NGGGNNCCTA GTTGTTAAGC TTTTGGGTGT TTGGGA        356
```

(2) INFORMATION FOR SEQ ID NO:1633:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1633:

```
GGCAGAGGGA ACAACTCCAT GTTTTTNTAA AGGCCTAGAG AACATATATC CAGTGCCTTT      60
CCTTTTTGCC TTTGTATTCA TCATTTTGGC AAATTACTGG AAGATGACGG TTCTGGCCAA      120
AAGGCTGGTT TTNTTTTGGG GTCACATTTT CTTGCTTCTC TCGTTAGAA ATCTTGGATT      180
```

AGATGATGGA CATGGTGAAG ATCTCAGCAA CCTCATTAC TAGAAGATCA TGTGGATTGG	240
GANTCATACA ATGGGGGAAC AAATGGAAAA GAGTACTTTT GNAAATAGTG GCTGGGNGAC	300
CACTGTGGAC CACAGANTGT TCAAGACACG TGCTGCCCNT AACTGTTTAC TN	352

(2) INFORMATION FOR SEQ ID NO:1634:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1634:

GGCACGAGCT GGCCCCGTGT TCAAGGGCGT CTGTAAGCAG TTCTCACGCT CACAGGGCCA	60
TGGCTTCATC ACCCCCCGAGA ACGGGTCCGA GGACATCTTC GTACATGTTT NTGACATCGA	120
GGGGGAGTAC GTGCCANTGG AGGGCGACGA GGTGACCTAC AAGATGTGCC CTATCCCTCC	180
CAAGAACCAG AAGTTCCAGG CCGTGGAGGT GGTGCTCANT CAGCTGGCCC CCCACACTCC	240
CCACGNAGAC GTGGTTCTGG CCAGGTCGTG GGCTCCTAGG CTGAGTGGTT CACAGGCCAG	300
CTGGCCGNGG GTTGGGNGAG CCACACAGGG TGAACGGNCA GCAGCCGGCT CCATGCCCCA	360
CTGCCTNGNT GATGAGT	377

(2) INFORMATION FOR SEQ ID NO:1635:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1635:

GGCACGAGGN AGAATCTTGC CTAGAGCTTG CGGAGTCCAG CNAGGCCCTT NCTGAAGGGC	60
CCCAAACCAC CGGCCACTTC TCCCCGTCC ATCTAACCAG CTGGGCCCCCT GCGCCACCT	120
GGCCTCCACG TTCCCTCTCC TCTAACCAC ACCCCTGGCC ATGGCTAACT ACTATAAAGT	180
GCTGGGNGTG CAGGCCAGCG CTTCCCCGGA GGACATCAAG AAAGCCTACC GCAAGCTGGC	240
CCTTCGTTGG CACCCCGACA AGAACCTGA CAATAAGGAG GAGGCGGAGG AAGAAGTTCA	300
AGCTTGGTGT TTTGAGGCCT ATTAAGGTTT CTGTTNTGGA CTTCCAAGGA AACGNTTCCT	360
TGTTATGACC GTGTTGGGTT GTAAACAGTT GGGGGGTTTG TTTGGCGGGG GCCAGGAANG	420
GTNTTACCAA AGGCCCTTTT GGGAAACGGG TTANAANTTT CGTAAACCTT TNNGGG	476

(2) INFORMATION FOR SEQ ID NO:1636:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1636:

TGCCTACTCT AAGCGCCTCA AGTTCAATGT GGCTGTNAAG ATCATCGACC GCAAGAAAAC	60
ACCTACTGAC TTTNTGGAGA GATTCCTTCC TCGGGAGATG GACATCCTGG CAACTNTCAA	120
CCACGGCTCC ATCATCAAGA CTTACGAGAA TCTTTGAGAA CCTCTGAACG GACGGATCTA	180
CATCATCATG GAGCTTGGCG TCCAGGGCGA CCTCCTCGAG TTCATCAAGT GCCAGGGAAG	240
CCCTGCATGA GGACGTGGCA CGCAAGATGT TCCGACAGCT CTCCTCCGNC GTTCAAGTAC	300
TGNCACGACC TGGGACATTG TTCACCGGGG ACCTTCAAGT TGCNAGAAC CTTTTTCTTG	360
GACAAGGANT TTCAACNTCA AGTTGTCTGA CTTTGGGTTT TTCCAGGGGT TGCCTNGGGG	420
ACAGAATTGG GGGTNT	436

(2) INFORMATION FOR SEQ ID NO:1637:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1637:

CGCACTGTCA AGGAGCTGCT TGATGGAGGA GCCAACCCCC TGCAGAGGAA TGAAATGTGA	60
CACACACCCT TGGATTATNC CCGANAAGGG GAAGTNATGA AGCTTCTAAG GACTTCTGAA	120
GCCAAGTACC AAGAGAAGCA GCGGAAGTTN GAGGCTGAGG AGCGGCGCCG CTCCCCCTG	180
GAGCAGCGAC TAAAGGAGCA CATCATTTGGC CAGGAGAGCG CCATCGCCAC ANTGGGTGCT	240
GCGATCCGGA GGAAGGAGAA TGGCTGGTAC GATGGAAGGA ACACCCTCTG GTCTTTCCTC	300
TTTCTTTGGG GATTCATTCT GGAATTAGGG AAAAACCAGA GCTGGGCCAA GCCAGACAGC	360
CAATTNTTTN GCACAAGGNT GCTTAAAAAG GGNTTTNATT CAGGTTGG	408

(2) INFORMATION FOR SEQ ID NO:1638:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1638:

ATAATGTNAC GTCAGCCGTA GAAGGCATCA ACAGAATGAC CAGAGCTCTC ATGGACTCGC	60
TTGGGCCTGA GTGGCGCCTG AAGCTGCCCT CAATCCCCTT GGTGCCTGTT TCAGCTCAGA	120
AGAGGTGGAA TTCCTTGCCT TCGGAGAACC ACAAAGAGAT GGCTAAAAGC AAATCCAAAG	180
AAACCACAGC TACAAAGAAC AGAGTGCCTT CTGCTGGGGA TGTGGAGAAA GCCAGAGTTC	240
TGAAGGAAGG AAGGCAATGA GCTTGTAAG AAGGGAAACC ATAAGAAAGC TATTGAGGAA	300
GTACAGTGGA AAGCCTCTTG TGTAGTTAAC CTGGGATTCT TGCCACGTTA CAGGCAACAG	360
AGGCACTTTG TTATTTTGGT CCCTGAAGGC AGTAACACAG AAGNCAGTGA NGGACTGCAC	420
ANAGGCCCTG AAGGTNGGNT TGGAAAGACC TTTAAGGG	458

(2) INFORMATION FOR SEQ ID NO:1639:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 332 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1639:

CCCGAGGNAT TATTCGATAA AGATAAGCTT ACATTATGAA GAGCAGCATA TTACAGCCGT	60
ATGGTCTACT TGCNCAGTAA AATTTGAAGA GCATTGGAAG CCTGTTGATG TAGAGGTCGA	120
GTTTAGATGC AAGTTC AAG GAGCGAAAGG TGGATGGGTA GGTTATATAG GGATATAGCA	180
CAGAGATATA TAGCAAAGAG ATACTTTTGA GCCAATGTTT GTGGAAGCGG TATTCGCAAT	240
ATTTTAAGTA GCTCGTTACA GTCCGGTGCG TTTTGGTTT TTTGNAAATG CCNNTTCCA	300
AAGCCTTTTG GGTTTTCCAA AGGNTTTTNG GT	332

(2) INFORMATION FOR SEQ ID NO:1640:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 260 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1640:

CAACCCTTGG ACGTNAGCNC TGAAGGCTAC AACANCTGGN TCTTCATGTC CACCCACTTC	60
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TGGAATGAAA ACCCACAGGG CGTGTGGTAC CCTGGGCCTA GAGAACAAGG GCTTACTATT	120
TNAACACGGG GACGTTGTAC CGCTAACACG CTGCTGCTCC TATGGGAACG GCCGAGGACA	180
TGANAGCGCC GGCCTTACAG GCCCCCAGG TGAACCAGCA NCGGTNNTTT GCAACGGGAC	240
ACAGAGGGGC TTNTCCCAGG	260

(2) INFORMATION FOR SEQ ID NO:1641:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 445 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1641:

TCCTCACCAA TMTAACNNTT NTCCANTTGC TGCAACACCG TGCCCCGGTA ACCAGAGCAC	60
CGCCCCACC TGAGCCCTAA GGNTGAAGTA GAGCCCCAGC NACAACCAGA GCCCACACCA	120
NTTAAGGGAG GAAATAAAGC CACCACCGNC ACCACTGCTT CCTNACCCCG NTAACCTCCTC	180
CTCCTAAGAT TGGTGTCTGT GAGCCCCGGA AGCTGACTGT GGGCATCANT GGTTTTGGAA	240
CGCATCGNTC GCCTGGTTCC TGNGAGGTTG CNTGGNGGAA GGGTGTTAAG GTGGTGGTTG	300
TGAAATGATT CCTTTCATTG GACCCGATT ACNGGTGTAC NGTTTAAGTT TGGTTTCCAC	360
CCAGGGCCGT TACAAGGGAG TTTGGGATTT CAGGATTGGN CAATTGGTTN TGGGCAACCT	420
GGGTTTTTTT TTTCCNTGN AANGG	445

(2) INFORMATION FOR SEQ ID NO:1642:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 502 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1642:

GGCAGAGTGT AAAACCAGAA AATATANTAA TAAAGGATGT CCTGAAATTA GGGGACTTTG	60
GCTCCTGCCG GAGTGTCTAT TCCAAGCAGC CGTACACGGG AATACATCTC CACCCGCTGG	120
TACCGGGCCC CGAGTGTCTC CTTACTGAAT GGGTTCTACA CGTACAAGAT GGACCTGTGG	180
AGCGCCGGCT GTGTGTTCTA CGAGATCGCC AGTNTGCAGC CCCTCTTTCC TGGAGTNAAA	240
TGAAACTGGA CCAAATCTGC AAAAATCCAC GATGTNCATC GGCACACCCG NTTCAGAAGA	300
TCCTGCACCA AGTTCCAAAC AGTTCGAGGA GCTATGGAAT TTTGGATTTT TCCTTTTGAA	360

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 345 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1659:

GGCACGAGCC AGTTTTCTGT TGCCCTTACC AATTCTGGAG CTGTTTATAC CTGGGGCAAA	60
GGCGATTATC ACAGGTTGGG CCATGGATCA GATGACCATG TTCGAAGGCC TCGGCAGGTC	120
CAAGGGTTGC AGGGGAAGAA AGTNATCGCC ATCGCCAATG GCTCCCTGCA CTGTGTGTGN	180
TGCACAGAGG ATGGTGNGGT TTATACATGG GGCACAAATG AATGAGGGAC AANTGGGAGG	240
ACGGAACCAC CATTGCCATA CAGAAGGCCT CGGTTGGTAG CTGCCCTTNC AGGGTNAAGA	300
AAGGTNAAAC CGTGTGGNCC TGTGGGTTCA GCACATNACC CTTTCG	345

(2) INFORMATION FOR SEQ ID NO:1660:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1660:

ANGCAACGGA CAGGCCCCTG GAACGAAAGG CATNCCCGNG CCAAGGTGGC TCCCCTAGAG	60
GTNACAAGTC TTAGGCATTN CGGTCGGGAA ACGCTACCTG CCTGGAGNTC ACT	113

(2) INFORMATION FOR SEQ ID NO:1661:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 134 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1661:

CCCNGNGGAT CCCCCGCCCC TGCAGGANTT CGGCANAGTT CTGGTTGGTA CAAACCCACG	60
GTTTTTGAGG CACCACTGTT TAATGCTAGG NTTCGAAAGA CCTNGCTNGC ATAATGGNCT	120
TAAAATTGGG CCTT	134

(2) INFORMATION FOR SEQ ID NO:1662:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1662:

GGAAGCCCCA GCGCATTNCT TTCNTCCTG CTA CTCTGGT TCCCAGATAT AACTGGNGAA	60
ATAGTGATGA CGCATNGCA GTCACCCTGT CTGTTTCGCT AGGTGAAAGA GTCACCCTCT	120
CCTGCGGGGC CAGTGAAGAG TATTAGCACT AACTTAGCCT GGTACCAGCA GGAAACCTGG	180
CCAGGCTCCC CGANCTCCTG CATCTATGCT GCATCCACCA GGGNNCACTG GNCATCCCAG	240
CCAGGTTNCA GTGGCAGTGG GTTTTGGGGA CAANTTGCAC TCTTCACCAG CAGCAGCCTG	300
CAGTTTNGAA GNTTTGGGGG GTCTNATTAC TGT	333

(2) INFORMATION FOR SEQ ID NO:1663:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1663:

TCCCAGATCC AGGANTTTAA GGGAGGGTTT NAACATGNTT AACCAGTNAC CTTGATGGTT	60
TCATTAANAA GGGGGGACCT GGGACGGAAA ATGTTGGCTT CGTNGGGGT AAGAACCCCC	120
	120

(2) INFORMATION FOR SEQ ID NO:1664:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1664:

CATGGGGTTT TNCCTTTGGC CACATATATG CGAATTTTTT ANGAGAAGGT GATATTTTGG	60
ACATCANGGG AANTGGTTAC TTTCCAAAA GGGTTTGCCC CACANTTTTT ACC	113

(2) INFORMATION FOR SEQ ID NO:1665:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1665:

GGCANAGCCG NCGGTTCCNA GGATGCCAGC GCCATGCTGA GGCGCTTCCT GGGCCGTGAA	60
CCCCAAGCAG GACGCCTTCC TCCTGAGCAA GGGGCTGCAG GTCGGGGGCT GCAAGCCGNA	120
GNCCGCAGTN TGNCTGAGGC CTGGTNACTG CGAACTGCCC AGTNTGGCCT GCGCTCCCCG	180
CGCCCTGGTG CCTTAGCCCC CGGNACAGGT ATGGGGTNAG GCTNTGGGCA CATGNCTGGA	240
GAAGTGGCA	249

(2) INFORMATION FOR SEQ ID NO:1666:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1666:

AAGAGGCCAA NGTACAGTGG TNGGTGGATA ACGACCTGCA NTCGGGNAAC TCCAAGGAGT	60
GTCACAGGCA GACACAAGCC AGCACCNACA GACTCAGTAA CA	102

(2) INFORMATION FOR SEQ ID NO:1667:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 335 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1667:

NGGGGGTNGG TGACCCNCGG CTGCTGCAGG GAATCTGCNG ANCTTGCAGN CCATGGGGGC	60
GCACCTGGTC CGGCGCTACC TGGGCGAATG CCTCGGTGGA GCCCGACCCC CTGCAGATGC	120
CAACCTTCCC GTTCAGACTT ACGGCTTCCC CGAACGGCAA GGAGCGCGAG ATGGTGGCCA	180
CACAGGCAGG AGGATGATGG ACGTGCCATT NAGGGCTCCA GCTGGGGGGA CTAATTGCGG	240
CCCACCACCT TCATTCCGGN TGCTTCAAGT GGCAAGTTTT GGACAGTTTT TCCCCAAATT	300
TNCTTGGGCC TTGNAAAACA NGGAGCNGGG CAGGA	335

(2) INFORMATION FOR SEQ ID NO:1668:

(i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 441 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1668:

GGCAGAGNCA CAGATGTCTC AGACGGCCTG TCCATCCGCC TCGGGNCAGC CCTGAAAATC	60
TACGAGCACC ACATCAAGGT GCTTCAGCAA GGCCACTTTG AAGGATGAAT GACCCCNATG	120
GCTTCTTAAG GCTGAGCGCC CAGCCTGCAC CCCTGCCCCA GCCCATTCCG GCCCCATCT	180
NCACCCAAGA ATCCCCCAGA GTCCAGGAGC TGGACGNGGA CACCCTNCAG CCCTCATGAA	240
CAGAATTCCA AGGAGAGGGC ACCCTCTTGT GCCTTATCTT TGGCCCTTGT GTCTGTTTCA	300
CACACATNTG CTTCCCTCAG CACGTCGGTG TGGGGAGGGG ATTGCTTCNT AAAACCCAG	360
TGGNTGNACC TTCCCCACCC ATTCCAGGAC ATTTAGGAAA AAAAAATGNA ATTTGGGGGG	420
TTTANTTTC CCAGTTCTTT T	441

(2) INFORMATION FOR SEQ ID NO:1669:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1669:

GGCAGAGGCG GGTGCAGGTC CAGCCCTTGG AGCTGCCCAT GGTCAACCACC ATCCAGGTGA	60
TGGTGTCCAG CCAGTTGAGT GGCCGGAGGT GTTGGTCACT GGATTTCCCTG CCAGCCTCAG	120
GCTNAGCTGN AGGTGGAAGC TGCTGGNACA AGCTCAGAGA ATCTNCTTTG GNCAAGACTA	180
GGNAACGGTG GTNGNCGGAT GTGGNACGTT CCGGGAAGCT AACTGCCAGG GAAGTNTTCA	240
TGCTGGGGTT TGCTAGGGAA TGGAGTGGGC TCANCGTCTG TNCCCAAATC GGCCAGTTTC	300
ACAGTGCCCA CTGGGGTGGG GCAGCAATTC CCTCTGAAGA GTTTTNTCCG TATGTGAAAT	360
GGGGAGTTCC AAAAGGNTGA GTTCAGTTGN AACCATTTCC CGTTCGGTNA NTGGTG	416

(2) INFORMATION FOR SEQ ID NO:1670:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1670:

NAGCCGCATC CTCAGGGCAG GGGGNAAAAT CCTAACTTTC AACCAGGTGG CCCTGGNACT	60
CCCCTGAAGG CCTGTGGCAC TGTCCTGTTC TGCCGGTGCT CGCGAAGGCG CGCAAAGCCT	120
GTGANCGGGC ATTTGGGNNA AGGCCCCCAG GAAGCCCCGG CACAGCCACA CCAAACCTTA	180
NCGTCNG	187

(2) INFORMATION FOR SEQ ID NO:1671:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1671:

GGCAGAGTAT GATGATGTNA AGAGTATGGA GACCAAGGTT CAGTTCTTAA AGAATTTAAA	60
CCTGGGAAGG AGCCATGATC TGGTCTATTG ACATGGATGA CTTCACTGGC AAATCCTGCA	120
ACCAGGGANC CTTACCCTCT TGTCCAAGCA GTCAAGAGAA GCCTTGGCTC CCTGTGAAAG	180
GATTAACCTTA CAGAGAAGCA GGCAAGATGA CCTTGCTGCC TGGGGCCTGC TCTCTNCCCA	240
GGNAATTCTN CATGTGGGAT TCCCCTTGGC CAGGCCGGCC TTTGGGATCT TCTCTNCCA	300
AGCCTTTTCCT GGAATTCCCT TTAGATTCAT AGATTGGGAC CGGTTTTGGT TTTNCTGNCA	360
GTGTTGGANT NGTTGNCCTG GAGTTACATT AAAAAAATT CATTTTGNTC CAAAAAATA	420
AAAAAATAATT CGGGGGGGGG CCCGTAACCA ANTGGGCC	458

(2) INFORMATION FOR SEQ ID NO:1672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1672:

GGCANAGGNA CAAGCCCAGC AACACCAAGG TGGNACAAGA AAGTTGAGCC CAAATNTTGT	60
GAACAAACT CACACATGCC CACCGTGCCC CAGCACCTGA ANCTCCTGGG GGGAACCGTG	120
NAGTTTTCTT GTTCCCCCA AAACCAAGG ACACCCTCAT GAATCTCNNG GNACCCCTGA	180
GGTCACATGC NTGGTGGTGG ACGTGAGCCA GATGGACCCT GAGGTCAAGT TCAACTGGTA	240
CGTGGNACGG CGTGGTAGGT GCATTAATGC CAAGTACAAA GNCGCGGNGA GGGGGNGTNT	300

300

(2) INFORMATION FOR SEQ ID NO:1673:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 376 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1673:

GGCAGAGGTT CGCTGCACCG ACCGNCCCTC AAGGACCTGC TCTNAGGTTT AAAAGCAAAC	60
CTAACGTGNC AACTGACCG GCCTGAAAAA TGCCTCAGGT GTNACCTTCA CCTGGAACGC	120
CCTTCAAGTG GGAAAGAGCG CTGTTCAAGG ACCACCTGAA GNCNTGAACC TCTNTGNGCT	180
GCTAACAGCN TGTGCCAGTG TNCCTGCCGG GGCTGTGCCG NAGCCATGGG AACCATGGGA	240
AAGACCTTGN ANTTGCACTG CTGCCTTACC CCGAANTCCA AGAACCCCGN TAAACCGNCA	300
CCCTTTTCAA AATTCCGGAA ACACATTTCC GGGCCCGAGG TTCCAATTG TTGNGCGTCG	360
NCGTTNGGAG GGAGTT	376

(2) INFORMATION FOR SEQ ID NO:1674:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 322 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1674:

GGCANGAGCC CTGGCGCACA CGNCGNCGTN AAGGGTGAGC ATCCCGCTGT CGATCCTGGA	60
GGCCCCGCAC CGGTACCACA TCCACCGGCG NAAAGAGCTT TGACGCCTCT NAACACACTG	120
GGCCCTGCCC CGGCACTGCC TGCTGGGCTG GGAACATTTT TCCTCCGAAG TNTGAGAAAA	180
GCTCAGCCCC CAGGAACCTG GACCTCTGGT CTNCTGTTTT CCGCTGAGGG CCCAGCAACA	240
GAAAGNTGTC CGGCAACANC AAGCCTTTTT AAACCGGGCT TNAACAATTG ANATTGTTNC	300
CCCCGAACCC GACTTGTTAA TT	322

(2) INFORMATION FOR SEQ ID NO:1675:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 257 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1675:

GGCAGAGCNA AGGTGGACAA GAAAGTTAAG CCCAAATNTT GTAACAAAAC TAACACATGC	60
CCACCGTGGC CAGCACCTNA AACTCCTGGG GGGAACCGTA AGTATTCCTC TTCCCCC	120
AACCAAGGG ACACCCTGCA TGAATCTCCC GGNACCCCTG AAGAGTTCAC ATGCGNGGTG	180
GTGGGACGTG AAGCCACGGT GTACCCTGTG GTCAAGTTCC AACTNGGTNA CGTGGGACGG	240
CGTGGTGGTG CNTNAAT	257

(2) INFORMATION FOR SEQ ID NO:1676:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1676:

GGCANAGTGC ATCACCAAGT TGGAGACCTT TATCCAGGAG CACCTGAGGG TCATTGGGGC	60
TGTGGGGATC GGCATTGCCT GTNTGCAGTN CTTTGGCATG ATCTTCACGT GNCTGCCTGT	120
ACGGAAGTCT CAAGCTGGAG CACTACTGAA CCCTGCCTTG GGCCTTNGCT GCTGCTGCAC	180
CCAACTACTG AGCTGTAGAA CCACTGTAGT NACCAGGNGG TCTGGGNCTT CCCTGAATNG	240
	240

(2) INFORMATION FOR SEQ ID NO:1677:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1677:

CCTAGCACCT NGTGGATCCC CCGGGCCTGC AGGANTTCGG CAGAGNATTT GGTGACCTTA	60
AGTNTACAGA NCACTGATTC CCCATCCTAT CCAGAGATTA GTTTTAGTTG CAGCATGGAA	120
CAATTACAGG ACTTGGTGGG GAAACTTAAA GATGCTTCGG AAAAGCCTGG NAAAGAGCAA	180
CTNCANTTGT AAACCTGGGG NAAGTTAAAN NATCCGCCCG AGTGCCAGAG GGAAAACCAG	240
AAAGNCCTTG CCTTCAGCTG GAACCACCGT TTGTGCGNAG CTGGGATGTN CCTTTTCAGT	300
AGGAAAAGAA TTTTCCCTTT TGANTTTATA ACCATTCATC AATTTTGAAC ATTTNAAAAA	360

GNGTGAAAAG GGTTAAGAGG GGAAAGATTA TTGCCAGTT TTTTGNATTC GTTTTAGTGG 420  
TAAAATGTNC CATTN 435

(2) INFORMATION FOR SEQ ID NO:1678:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 146 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1678:

GGCACAGTGA AATACATTTT GGAAGANAGT TTTTNATCTT AGAGATTGGT GAACAAGTGT 60  
AAGGGTGTNA GAAACTCACA GGAATACAAA TTTNCCTGTA TGTTTTGTGG GTTTTTTTTTT 120  
TNCCCCNTCA AGATGTTTNC TATTTC 146

(2) INFORMATION FOR SEQ ID NO:1679:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 450 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1679:

GGCAGAGGTG CCTGATACGA CTACCAGGCA GCCGACGACA CANAGATCTC CTTTAACCCC 60  
GAGAACCTCA TCACGGGCAT CGAGGTGATC GACGAAGGCT GGTGGCGTGG CTATGGGCCG 120  
GATGGCATT TGGCATGTNC CCTGCCAACT ACGTGGAGCT CATTGAGTGA AGGCTGAAGG 180  
GCACATCTTG CCCTTGCCCC TCTNCAGACA TGGCTTCCTT ATTGCTGGAA GAGGAGGCCT 240  
GGGAAGTTGA CATTACGAC TCTTCCAGGA ATAGGACCCC CANTGAAGGA TGAGGCCTCA 300  
GGGCTCCCTC CGGNTTTGGN AGATTCAGCC TGTNAACCC AAATGCAGCA ATTGGCCTGG 360  
TGATTTCCCA NAATTTTCNTT CCTGGNAACC CCCGAACCTT TCCCCAAAAA TTTTGGTTTTT 420  
NGCCCCTTAA NAGGTTTTTTT GGGCCCAAGC 450

(2) INFORMATION FOR SEQ ID NO:1680:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 157 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1680:

ANTCTGGGCC ACGGGANAGA CAAGCTGGAA CCTGCATTTG NAACCCTNGC TTCAGNGAAT	60
ACCACCATTG TTTGCAACTG CATTGGACGG CAGCAACTGG GGGGCAAGTA ACAACGGGNA	120
GATTNACCNT TGNTTGCACT CCCANGGTTT AAAGGTC	157

(2) INFORMATION FOR SEQ ID NO:1681:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1681:

GGCACGAGCA CCAGCNACTC TNCCAGCTCA AGGNACCCAC CTGCNAGTAC AGGGCAGCCC	60
AATCTGGTCC CTCTNAACGG CCAGGACCTC CGCAGAGGGC CCTGCTGGCA CGAGGCACTA	120
AGTCTCAGGG GCCAGCCAAG CCCCCACCCC CAAGGAAGCC ACTGCNTGCN GACCCCCAGG	180
GCCGGTGCCC ATCGGGTGAC CTGCCCCGCC CAGGGGCTGG AATCCCGCCC CTAGTGGTAC	240
CCTCCANACC AGCGTCACCG NCTCCAACAG TGTTCCTCGC TCTTACCTCT GAACCTCTTC	300
CGGGAGGTTT CCGGTTGCCT TCCAAAGCCG GGACTTTAGG GGTTTCAAAG AAGGCGGGGT	360
GTGCCCCTTT TGGGNAGTCC CCCTAACCAT TGANTTAAAG GGGGNCAAAA AANTTGGGGG	420
TTGTTTTNAA GATTCGGGG AAACGCCAAG GGGTTTTT	458

(2) INFORMATION FOR SEQ ID NO:1682:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1682:

GGCACGAGCA CAGGGGAGCT GCTGGGCGAG TACAAGGGCC ATAAGAACCA GGAATACAAG	60
CTGGACTGCT GCCTGANCAA GCNTAACACA CATGTGGTCA GCTGTTCTAA GGACGGGAAG	120
GTGTTCTTCT GGGACCTGGT GGAGGGTGCG CTGGCTCTGG CCCTGCCTGT GGGTTCCGGT	180
GTGGTGCACT CGCTGGCCTA CCACCCAACA NAGCCCTGCC TGCTGACCGC CATGGGAAGG	240
CAGCGTCCAG TGCTGGCGAG NGGAGGCCTA TGAAGGCAGA GGATGGAGCA GGCTGAAGCC	300
AAGGGACCCA CCAACAGGAC CAAGGACCGA GACACAGACA TGGAAGGACT TCAGTTACCN	360

CTTATTTTTA GAGACGTAGT TGACCCAAAA ATTAGGGGNG GGGGTTNGGT TTNCAAATT	420
NATTAATTAG AGGGGGGGGT AAGACCTTCC TGGGNCCCCA AA	462

(2) INFORMATION FOR SEQ ID NO:1683:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 492 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1683:

GGCACGAGGA ATCCTGACAG GGACAGGCAG GCACAAGGCA CAAAACCTGG GAAATCTNAG	60
CCACAGAGAA TGCTGTTTTG CTGCGGCAAA GCGCCTCGT NAGTCCTGGG GCCTGTTTGC	120
TCTTGCCCCG GGNCCAGGG CCAGTTTCTG GCACCCCTAG GAGAATGAAT AGGGCTCAGT	180
GTGGTGGCTC CGCTGAAGCT TCAGAGCCCC CTTTNTGCCT GCCTGGGAGT GNGCCGTTAA	240
GGAGTGCAGAA CCAAGGACCT GCCGGTGNGG TGGGCTGTCC CTGCAGGAGC TCTTTNAGTT	300
TGCACTGGGA GGGGCANGTT CANCCCCAGC CCCATGGTTC CCTGTTCTTG NAACAACCCC	360
GAGTGGTTTT TCCTTGNCCT CCAGGCTTTN GGTTTAAGGT TGGGCTTCAA AACCATTGGG	420
GAATTCANT TTTNGCCCTT NCCCGGCTTA AGGTTTTTTA AACTCCTTTT GGGATNCCTT	480
AAAGGTTGGG TT	492

(2) INFORMATION FOR SEQ ID NO:1684:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 156 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1684:

CAGCACANCC TGTGGCAGGC CCGTAAGTTT TCCTNTTCCC CGAAAACCA AAGGACACCC	60
TCATAATCTC CCGGGACCCT TAAGGTAACG TNANNGGTGG TGGACGTAAG CCAGAAAAAC	120
CCCAAGGTNC AGTTCAACTG GTCACGTGGN CGGCGT	156

(2) INFORMATION FOR SEQ ID NO:1685:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 58 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1685:

GGCANAGGGC CAAGGNGAAG NTCCCGCGCT ACTACANGAA CATCGGNCTG GGCTTCAA 58

(2) INFORMATION FOR SEQ ID NO:1686:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1686:

GGCAGGAGCC CAAATTCAAC ACATTCCACT CATAAGTGTT CTGTACTCTT CAAAAATATT 60  
CATTAAAGTC AAAGAGAGGC TGAGGAACTA TTTCAAATC AGGAGACTTG GAAACTAAAT 120  
GCAGTGTGTG ATCTTGGATT GGATTTTAGA TTAGTAGGAA ACATGACTGT AAAAAAGTGN 180  
CTGAAAAATA NCTGGTATTA TTGGGACATC AATGTAAAT TTCATGAATT TAATATATAT 240  
TGGTTATGTA AGTTAAATGT NCTGTNCTG AGCTGNAAAT TAAGTTTGAN CCTATTAGGG 300  
GGGCAAAGCT GTCTAAANCT CCCCAAATAG TTCCTGCAAA ANGTTTTTCC AGTGGGGGTN 360  
ACCACACATT GGGAGAGGNG 380

(2) INFORMATION FOR SEQ ID NO:1687:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1687:

GACGCCTTCA GGCCCGACGT GACTTCATCC TCTTTTCAGA GGCCAGTCAA CGACATGAAC 60  
ATCGCAAGCG GCTGCCCCCT CTTCTGCCCC GTNTCCAAGA TGGAGGCAAA GAATTCCTAC 120  
GTGCGGGACG ATGCCATCTT CATCAAGGCC ATTNTGGACC TGACAGGGCT CTAAGTGCTC 180  
CCTACTGGTG TTTGGGGGTT GGGGGCAGCC AGGCACAGCC GGCTCACGGA GGGGCCACCA 240  
CGCTGGGCCA GGGTCTCACT GTACAAGTGG GCAGGGGGCCG CGCTTGGGCG CTTGGGAAGG 300  
GTNTCGGCCT GCAGCCAAGT TCACTGTCCA CGGGGGGAAG GAGCCACCAG CCAGTTCCTC 360  
AGATTTTACA GACTNCGGAG GGGTTTNGGC AGACGGTTTT AGNCAAGGGG TTTTGTGGCA 420  
TTNGCCGAGG GTTTTTCGGG GTGNTTTCCTA G 451



(2) INFORMATION FOR SEQ ID NO:1688:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 192 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1688:

TTNTTTCCTC ACCNTCCACC AAGGCCCAT NGNTTTTCCG CCTGGGGCCC TGTTTCCAGA	60
AGCACCTCCA ANAGTGACAG GGCCCTGGG CTGCTTGGTC AAGGACTACT TCCCCGGAAC	120
CGNTNACGTT TCGTGGAAC TAAGGCGATC TGAACCAAAG GTNTGCACAT TTNCGGGTTG	180
TCCTANAGTA CT	192

(2) INFORMATION FOR SEQ ID NO:1689:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 311 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1689:

GGNAGAAAGG NGCGCACGCC CNATGGCCAG TACATCTNCA GGCTGGAGCC GAACGTGGAG	60
GAACCTNGCC CGCTTCCTTA ACCTGCCTGC CCGAAAGCCC CTNACCTACC AAACGNANNC	120
AGCTCATCGC CCGNAAAAAT CCGAGGTGGA GNAAGATGCG GCGGGCGGAG GTTTCTCCCC	180
GGGNTAGAGG AACAGCCCCC AGGTGGGATG GGAAGCCCCC CAGGGCTCGA AGAGGGTNTG	240
CTTGGGNGGG GCATTGGGGG AGAAAGGGGG TGCACCGACC TNCCCCACGC AACCTTGNGG	300
CANCGGTTGG G	311

(2) INFORMATION FOR SEQ ID NO:1690:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 321 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1690:

CAGCCCCGAN ACCACAGGT NTATACCCTG CCCCCATCCG GGAATGACCT GACCAAGANC	60
CAGGTNAGCT TGACCTGCTT GGTCAAAGGT TTCTNTCCNA NCAACATCGC CGTGGAAGTG	120

GGAAGANCAA TGGGCCAGCC GGAGANCAAC TACAAGACCA CGCTTCCGGT GCCTGGANTC	180
CGAACGGCTN CTTCTTCCTN TNACAGCAAG CTNCACCGTG GGACAAGAGC AGGTGGGCAG	240
CAGGGGNAAC GTTTTCTAAA TGNTTCCGTG AATGGCATGA GGGTNTTTTG CACAACCAAT	300
TACAAGGCNG AAGAAGCCTN T	321

(2) INFORMATION FOR SEQ ID NO:1691:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 219 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1691:

GGCACGAGCA AGATCACGTC TCCCGTGCTC ATNATCCACG GCACGGAGGA CGAGGTGATC	60
GANTTCTCGC ACNGGNTGGC GCTCTACGAG NTCGNCCCCA AGGCGGTGGA GCCCTGTGNG	120
GTGGAGNGCG CCGGGCACAA CGACATCNAG CTCTACAGCC AGTACCTGGA GCGCCTGNTT	180
CGCTTTNATC TTCCCAGGAG CTNGCCCAGC CAGCGCCGC	219

(2) INFORMATION FOR SEQ ID NO:1692:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 325 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1692:

TCCCCGGCNG CCCCTACTGG AAAGTAAGGA GCCCCTCTGC NTGGCCAGCC GCCCGTCCG	60
GAAGGNCGGT GGGGGGGTCA GCCCCNCCC GNCCAGCNGC CCNATCTGGA AGGTNAGGGG	120
CACTTNTNCC GGGCCGCCCC TACTGGNAAA GTGAAGGAGC CCTTNTGCCC GGCCAGGACC	180
CCGTTTGGA GGTGTGCCCA GCGGNTCATT GGGGATGGGG CATGATGACA ATGGCGGTTT	240
TTGGAATAGA AAGNGGGGAA GGGTGGGGAA AAAATTNAGG AATNGGGTGG TTTNTTGCTT	300
TTTTTTGATA GAAGTAGACN TGGGA	325

(2) INFORMATION FOR SEQ ID NO:1693:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 264 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1693:

ACCCCAAATG TCCTCATCAT CCCGTAAAN CTGAGGTACT TCGTAAAGGA TGTCTNNGC	60
TGTTTCTGTT TAAACCCTGG GCGCCTTACC AAAGGGCAGG TGGGAAGGNA CCTTCGCCCCG	120
ANTNTACCTT AGGAAGGCCG GCAGCGGACG GGNGCAGAAA GGCAGAGCCC ATGCATTGCT	180
GTGCAGGTCG TNAGGTATCT GAGGGCTTCT TTTNCTCTGC TGTTCTCTGC TGTTTGGGNN	240
CCTTAAAAGT NTTTAGNCCA AGAG	264

(2) INFORMATION FOR SEQ ID NO:1694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1694:

GCCTGTTGGA GGAGGAGAGA GCTTTNTGGC ATGANCCACA GTTCTTGAT GGNGGGCATC	60
AACCTTTGGT GAGGGTTNTN TTGGGCCTGA AATTGTTGGC CATGGTGGGT GGGTTTAAGG	120
TGGCTNTGCT GATAAGGGCC TCCGTTTCTG GGTAAAGTGA NAAGAGAAAA AAGGAGTTAT	180
TGAAGTNGAC GTTGATAATA GGTTTAANGT GAATCATGAA TGNAGGAATT GGAGNATTTG	240
TGGTTGGAAG AGGGGAAGGT TTTTNCGGTA ATG	273

(2) INFORMATION FOR SEQ ID NO:1695:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1695:

ANACTACGTG GGCAGCCCCA TCACCTGCAC CTGCTTCACC CGGGATGGGC AGTGCACCCT	60
GGTGTCCAGC CTGGACTCCA CATTGCGGCT CCTGGACAAA GACACAGGGG AGCTGCTGGG	120
CGAGTACAAG GGCCATAAGA ACCAGGAATA CAAGCTGGAC TGCTGCCTGG ACCNAGCNTG	180
ACACACATGT GGTCAGCTGT TCTAAGGACG GGAAGGTGTT CTTCTGGGAC CTGGTGGAGG	240
GTGCGCTGGC TTCTGGNCCT GNCTGTGGGT TTCCGGTGTG GNTGCAATNG NTGGAC	296

(2) INFORMATION FOR SEQ ID NO:1696:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 391 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1696:

TCCCGGGGGN CAAGGNAGGN CAGTTCACG CGAAACCGNA NGAACCAGGA AGGTCACGCT	60
GGAAATGCTC TTCCTAGCC GGACTACGTG GGTGTACTCC ATCAACAACG TTCTCATGTN	120
TCTTTCAGGA AAGACCCCCC ACCTGTATTC TCATAGCATC CTTGGCCTGC TGGAACGGAA	180
AGAGACCAGT GCAGGAAACC CCATCGCTCA CATTAGCCCC CACCGCCTAC TGGCAAGGAA	240
GAACATGGTT TCCACCAAGA TCCAGGACAC CAAAGGCTGC CGGGCGTGCT TGTGTGGCGG	300
AGGGTGCGAG TTCTNGGGGN CCGTTNCTGT NCGGTGCATT TGAGACGTCC GTTGTCTGT	360
TNAGTGGTAC CAGCCATGAA CAATTCTTGT T	391

(2) INFORMATION FOR SEQ ID NO:1697:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 103 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1697:

AAGCCACCT TTTTNGCTGT TCGGGTCCNT GACTCCATAG AANCGGTAGG TGCCGCAGGA	60
TTAATGGNCC TGNTCCAGAA TCTTGTTGCT ACCGGCAATT AAC	103

(2) INFORMATION FOR SEQ ID NO:1698:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 340 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1698:

GGCAGAGNCA AGGGCTCTTT NCCCGTGCCC CTGTACGATT ACCAGGCAGC CNACGACACA	60
AAGATCTCCT TTAACCCCGA GAACCTCATC ACGGGCATCG AGGTGATCGA NGAGGCTGGA	120
ACACGTGGNT ATGGGCCGGA TGGCATTATT GGNATGTTCC CTGCCAACTA CGTGGATGCT	180
CATTNANTGA GGCTGAAGGG CACATNTTGC CCTTCCCCTC TAANACATGG TTTCCTTATT	240

GCTGGAAGAG GAGGCCTGGG AAGTTGACAT TTCAGCACTC TTCCAGGAAT AGGNCCCCCA 300  
GGAAGGTTNA GGNCTCAGGG GTTCCCNCCG GGTTTGNAAG 340

(2) INFORMATION FOR SEQ ID NO:1699:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 82 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1699:

GGCAGGAGCC AGGATCACGC CATTNCACTC CAGCCTGGGT GATTNANTNA GACTCTGTTT 60  
CAAAAAAAAA AAAAAAAAAA CC 82

(2) INFORMATION FOR SEQ ID NO:1700:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 191 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1700:

ANAGNCAACA GTTCCNAGTT NAGTGCTCAC CGGCGCATCC AACTGGGGA GAGCCCATAC 60  
AAGTNTGCAG TGTGTGAAA AATCTTCAAC AATAGCTCCC ACTTNAGTGC CCACCGAAAA 120  
ACCCACACTG GTGAAAAGCC TTANAGGTGT TCTNACTGTG AAGAGAAGGC TTCACTTAGA 180  
ANCTCTGNCC T 191

(2) INFORMATION FOR SEQ ID NO:1701:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 334 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1701:

GGCAGAGCAC GCGTGGNTGG TATNTGTTTG TGGCTGCTCC CATTCCTATA ACCTCCGAGA 60  
CCTTCACTCC TAGGAATGTC CCAAGGCCAA TTCCCTTGGC AGCAATGAGA AGAAATGCCC 120  
TTTTCCAAAT AGCGACTTCT GCAAAACCCG CTGTTGTTTG TGGGTGAGCA CTGCAGTNCC 180  
CACCGCATGC CACAGCCAGC CTCCCTCCTG GCTCCTCTGC CACGGTGGCC TTCCCCAGCC 240

CTCACCCAGG CCCCGACTTT CCTCTNANAG GTTTCAGTT TCCTGGGGGC CTNGGAACTT	300
TTCCTGAGTT CCTTTCNAA NCCAACAGGT CCAG	334

(2) INFORMATION FOR SEQ ID NO:1702:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 363 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1702:

GGCAGAGCGG TGACAGCGNC TCCAGGGCCG AAGCCGCNGG GCNCCACTCG GGGGCTGNGN	60
CTGCGCGTTG GNAGACCGTG CTCCTNAGTC TGCGGTTCCC GANTNATCAG CNGCTGNTCC	120
CGGAAGTGGG GCCAGTGCTG CGAACCTCTC TATATGGATG TGCAAGCTAC AACTCCTNTG	180
GACCCCCGGG TGCTTGATGC CATGGTCCCT TACCTAAATC AACTACTATG GGAACCCACA	240
NTCCCGGACA CATGCTTATG GCTGGGAAGA GTGAGGNAGC CATGGAACGT GCTTGTTNAG	300
CAAGTTAGCA TCTNTGATTG GGAGTTGATC CTCGTGAGAT TCANTTTTAA TNAGTGGGTG	360
TTA	363

(2) INFORMATION FOR SEQ ID NO:1703:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 340 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1703:

CCTCCCCAGG CCCCAAAGCA CCCCAAGGCT GGTATTCCTT GAGTNATAGG TATTAATAAT	60
AAAAGCCTCA ATGCAGCTTC TCCATGTAGT TCCTCTCCTA CAAGCCAGGT GGATTCTGGT	120
CCTAACTAAA GAGATGGGAG TTCACCTGAG GGCAAGAAGT ACCCAGGATG CCCAAACAGC	180
CGCACAGGTG TCCTGTGCTT CCTGTGAGAC TTCCTGGGGG AAATATACAA ACTTAATATA	240
TTTTTAAATG TTTACGTCAT TTACACTGCT GCTTTTCTAA TANTCTGNNT TTNATTACTT	300
GTAGTNAATC ATTTGTTTGG GGTTC AAGC ACTGTCTTCC	340

(2) INFORMATION FOR SEQ ID NO:1704:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 147 base pairs
  - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1704:

GGCAGAGCNA ACGTTGGTGA GGACTNTCCA GTATTCAATG GCCTGTTTAA GTTCTGTNAG	60
TTGTNTACTG GTGGTTCTGT GGCAAGTGCT GTGAAANTGN AATAAGCAGC AGACGGGACA	120
TGGNTGTGAA ATTGGGCTGG GGGCCTG	147

(2) INFORMATION FOR SEQ ID NO:1705:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 101 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1705:

AGGCCCCCTG AAGCTGCAGC CCCCCGAGA ANCTGGCCTG GAACTATGGC CGCCCCCTNAN	60
CTTCCCTCCA CCCC GNATCC GGAAGAAGNC ATCCAGGAAA G	101

(2) INFORMATION FOR SEQ ID NO:1706:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 261 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1706:

GGCAGAGGGN ATGGAGGATC TCAACTGTNA ATCCACACTG TTCTCCAGGC CAGGGAAAGC	60
CTGGGAAGGT AAGCCTGGGA AGAGGCCCAA GCCCACAGTG GGTAATTGGC CCCATGGGCT	120
NCCAGACTGT NNACTNCCCC AGGTTGAATC ACTGTGGTGC TCCAGCCTGG CTGTGATCTA	180
GTNAAGGGTG TTGTGGGGGG CATCTNTGGG CCTTCAGGGG CCCCAGGTNA CTTCTGGGT	240
ATAACTTGNG TNACACGTGT T	261

(2) INFORMATION FOR SEQ ID NO:1707:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 256 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1707:

GGCACGAGCG GAGATTGACC TGGGAGGCCA CGCCCCGTTT GATTCATGAC GGTGTGGCTG	60
CGGCCATCAT GAACAGCGAC TGCCTTGTTT TCGACACAGC CATAGCACAT CTTTTGNCA	120
GATAATGGGA ACCTTGGGAA TCAATGTTAC TATTTCTACA TGTGTCCAT GNATGTGAAC	180
TTTCGTAAAC CTTCAAAATT ATTTGGGCAT AGTGCTCTAT GTTGAATNA AAGGTTTTTA	240
TAGATGTTTT ATTCCA	256

(2) INFORMATION FOR SEQ ID NO:1708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1708:

TGTATTAAGT CTGCGCTAAC TAGGTTCCCA GGGCTTCTGT CCCTGGGACG TGGGGTCCCC	60
ACAGACCTGG AAATTCTCCG GCGTCTTCCT TTGCCAGAG CAAATTGAGA CATCCCCGTG	120
AAGAGCCCGA GGGTCGCTTC CTTTTGGGTT TAAAGTCGTC CTGAGGCTGG TCTCGTCCCC	180
GGTCTTTCTG CTATAGGTCA ATGTATACAC TTTCTGTTGA GTANTTTTCC TGCTGTAAAA	240
CCTTGTTCTG AT	252

(2) INFORMATION FOR SEQ ID NO:1709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1709:

GGNAGAGGNT AAGACGCCTC CNTNCTGCTT GTGNAACGTC CTAAGCGTAC CCNCTCTTCC	60
CAGCACCCAG GCCAGTATTA AAATCAATTC TNTCTATGAA AGGGAATCGA CTTCAATACC	120
TGCCATTAAAC CCGTGCCCCG AATTGAAAG AACTGAAATG NTGGACCTGT TCCCGTGGGA	180
ACCCTGGAAC CCAGTAGAGA AAAGCCCTTG GAGAATGCCA AANTGGGGCA AGTGNANAGA	240
TTTCATGATA TTGCNCCTGG GTTGGTGGTT NTTACTGG	278

(2) INFORMATION FOR SEQ ID NO:1710:

(i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1710:

CAGAAGAGTT AGTTTCCAGG CATCCATTTC CAGGTCCTGG CCTGGNAATC AAAGTAATAT	60
GTGCCTGAAG AACCTTATAT CTGTAANGNN CTTTCCTGAA AACCAACAAT ATTTTAAAAA	120
TAGTAGCTGA TTTTTCCTGC CANT	144

(2) INFORMATION FOR SEQ ID NO:1711:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1711:

GTGCGNCATC CTAAGCACCA TCNATCGGGA AGCTGCTCAA GCCCAACGCC TCATTGGCCC	60
TCCACAAGCA CAGCAATGCA CTGGTGGACG TGCCTGCCCC CCGAAAGCCG ACAGCAGCAT	120
CATGAATGCT NCACCTTCAA ACCAGAAGCC AGATGTNAAT GTACGCGGAC ATCGNGGGG	180
ATGGGACATC CAGAAGCAGG TAGGTGCGGG AAGGCCGTGG AAGCTTCCCG CTCACGCNA	240
TTTGAAGCT TTACAAGCAG ATTNNGANAT TGTTTTCNNC CCCGAGGG	288

(2) INFORMATION FOR SEQ ID NO:1712:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1712:

ATCTCCCNCG AGAAAGCTTT CTTTCTNAAA ATGGTGGTGG ATGCNGTAAT GATGCTCGAN	60
GATTTCTGN AGTTTAAAAT GATTGGAATC AGGAGGGTAC AGGGTGGNGC CTTGAGGGTT	120
TCTA	124

(2) INFORMATION FOR SEQ ID NO:1713:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1713:

GNAAGACCAA GGCTCATGGA ATCCTCNAGC AAATGTGGGG AGCTTNCCTC CTCTATGTTT	60
CCATGANGAT GGGAAAGNAC TGNNGGAAAA AGCCTTAACC AGCCCTNTAA GGTGAANAGC	120
TGTGGAAGGG GCCATTTTCC CGAATAA	147

(2) INFORMATION FOR SEQ ID NO:1714:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1714:

CTAAAGGACC TGCNCGTNTG GACCAGCCAG CTGAAGAGCA CCATCCAAAC GGCCGAGGCG	60
CTGCGGCTGC CCTACNAGCA GTGGAAGGCN CTCAATNANA TCAACGCGGG CNTNTGNAAG	120
GAGCTGACCT ACGAGGAGAT CAGGGACACC TACCCTAAGG AGTATGCCCT GCGGGAGCNG	180
NNCAAGTNCT ATTACCGNTA CCCCACCGGG AAGTCCT	217

(2) INFORMATION FOR SEQ ID NO:1715:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 298 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1715:

GGCAGAGCTT AATGGCAGAA GCTCTGGAAA AGCTCTTNTT GCAAAAAATA AATGGGCTAC	60
CCACAGAAGA AACCGAGATC ATGATAGTCC AGGCAAAAGG AAGAGGACGT GGGAGGNAAG	120
AAACAGGGAC AGCAAAACCT GGCGTTTCCA CGGTACCAAA CACAACCTNAA GCATCGANTC	180
CTCCGCAGAC CCAGACCCCT CAGCCGAATC CTCCTCCTGT GCCAGGCCAC GGNTTCACCC	240
CTTCCCTGCG GTNNACCCCG GACCTNATCG TNCAGACCCC TGTTAATGAC ATGGGTGC	298

(2) INFORMATION FOR SEQ ID NO:1716:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 base pairs  
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1716:

GGAAGAGTGA CCGGCTGGTG GAGGTGCAGT GGGAACAGCA GGAGGCCCGA AGCCTCTGGT	60
ACCTGCCCCA AGGNCANAAA ACCTAANAGC AGCACANNCA TGGTA	105

(2) INFORMATION FOR SEQ ID NO:1717:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 217 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1717:

CGCGGNTACT ACAACCAGAG CAAGGCCGGT TNTAANACCA TCCAAATGAT GTATGGNTGC	60
AACGTGGGGT CGGACGGGAG NCTTCCTCCG CGGGTACCGT AGGNCGCCTT ACGAACGGCA	120
AGGTTTACAT CGCCCTGAAG AGGACCTGCG NTTCTTNGAC CGNGGNGGAA CATGGGCAGT	180
TTCAAACCAC CAAGCACAAG TGGGAAGGNG GGCCCCCT	217

(2) INFORMATION FOR SEQ ID NO:1718:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 71 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1718:

GNAAGACCAC CAAGGCCTCA AAATTAACCT AAAGACCCAC TCCTTNCAAG TGGTGGTAAT	60
CTCCAANATC T	71

(2) INFORMATION FOR SEQ ID NO:1719:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 258 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1719:

CGGGCAACCC TGAAGGCTGG TGGTGCCGGC AACCCAGTNC GGCTCCNTGA ATTGGGAAAA	60
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GGCGGGTNTA ANATCAANGA GAATCCGCAA AAGTACGGGG GCGCNGTCCA GGTGGCGGGG	120
GAATATGCTG CCCATTCCAC CGAGGGGGCC ATCACCATCG CTGGNGTGCC GCANTTTGTA	180
ACCGAGTGTTCACGNATTT CCCTGGTCAT GCTGGAGACG GTCTCCCGTT TTCGAAAGGA	240
AGNGTCATGN CCTTCCGT	258

(2) INFORMATION FOR SEQ ID NO:1720:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1720:

GGNAGANCNA GGTTACNAGG GCTGGCTGGC CGGCTACCAA ATGAATTTNA AAAGTGCAAA	60
ATCCCGAGTG AACCCAAAGC AACTTTCCAG TTGGCTACAA NACTGNATGA ATTCCAGCTT	120
CANACTGAAT GTGAAATGAA GGGGANCAAA GTTTGGGGGC TCCATTTACC AGAAAGTGAA	180
ACAAGAAGTT GGGAGACCGC TGTGNAATTC TTGCCCTGGG NCAGCAGGGN AACAGTTAAC	240
ACGGGCTTTG GGAAATAGCC AGCCCAAGTT ATCAGAATTG NACCCTGAAC GGCTGTTTTT	300
TGNGGGTTTA ANGTGNAACA AATT	324

(2) INFORMATION FOR SEQ ID NO:1721:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1721:

AGATCAAGCA CTTTGGNATG CTTGCGCGCT GGGAAATGANA GCCAAAANTA CCTGTNAAAA	60
CAACGTCCAC CTGGTGTTCA AGGAGACAGC CAATTACCTG GTCATTTGGT GCATTGNCCT	120
AGAGGTGGAG GAGAAATGTG CCACTCATGG AGCAGGTGGC CCACCAGAAC AATCGTTAAT	180
GCAATTTAAT CCTGGGAGCT GGCCAAGAGC CTTAAGGGTG GGACCCCCGG GNNCTGNTTC	240
CGGNAGTTTT TCCACTAAGN TTAG	265

(2) INFORMATION FOR SEQ ID NO:1722:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1722:

GGNANANACG GAGATTAACC TGGGAAGGCC ACGCCCCGTT CCAATTNATG ACGGTGTGGC	60
TGCGGCCATG NATGAAACAG CAACTGCCTT GTTTTCAANA CAGCCATAGC ACATCTTTTT	120
GCCAGATNAA TGGGAAACCT TGGGAATGCA ATGTTAACTN ATTTCTANCA TGTNGTCCCA	180
TGAATGTGAA CTTTGCGTGA AACCTTNCAA AAATTATTTG GGCCATAGTG CTNCTTATGT	240
TTAANAAAGG TTTTANTAG ATGTTTTNTT CCCATATGTT CTCA	285

(2) INFORMATION FOR SEQ ID NO:1723:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1723:

GGAACAGGCC ATCTCCTTGG CNAAAAATTT CTGGCCGGA NATNCGACCG CCGNNATCTC	60
CAAGAAGGGC CGTGGCTCCA ATCGAGCCGG GTAAAGCTGC TGTGC	105

(2) INFORMATION FOR SEQ ID NO:1724:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1724:

GGNANAGGNA GNAAGAAGGA GCTGAAGGCC CCCC GGCTCG GANCCAGCCC AAACAAGGAC	60
AAGGACGAAC CTTTTCCCC CAAAGCAGAA GGCCGAGCGG NAGAAAGGAG CGCCCGGGTG	120
GCCAATTAAC GCCCGGGAGA GANTGNGNAG TNCCGTGAAA ATTCAAGAGG CCTTTAAGG	179

(2) INFORMATION FOR SEQ ID NO:1725:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1725:

AACGACACCC TNAGGAAGAT CCTGGACCTA AAATTTTAAG GGGGCCCCC CAGGGCTAGC	60
NAGCCCTCTG GCCGCCTGCA GGCTNAACCA GTCCCTAAAC AGGATGGACA ACAGCCAGCA	120
CCCCCAGCCT GCTGANAGCG NACAGAACTG GGCTCTCAAA GGCTCTGGCC CAGAACCCTC	180
CCACCACCCA CGGTTGCTGG TGAAAGNAAT TCTNTGAACC TGCAACTNTG GCCAGGAGGC	240
TGTGCTGNTT CACTGTCCGT NAGGAGGGCC CCAACCGGG CGG	283

(2) INFORMATION FOR SEQ ID NO:1726:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1726:

GGCACGAGGG AACAATGCCT TTCCTGAGCC GGGCAGGGTG CCATTTCCCG TGCCTAANAA	60
AGTGCTGTGG CCGCAGCTGT GTAAGGCGCT CAANATGAAA TTNAAGGCCG AAGTGCAGAG	120
CAACCGGGGC CTGAACCAAG GAGAAACCTC GTGTTCTTGG CGCAGAACT NTTCAACAAC	180
AGCAGCAGCC ACCTGGAAGG TATGACAGTG GCCTGTTCCG TNTCCTGGTC CCAGTTCCAA	240
CAGGGNGGNA CTTGCCGGGC TGGNAATTAN ACCTTTTGGN CAGTGGTTTG AGGGGGTGAT	300
GGAGGTGTTG AAGANGCACC ANAAGCCCCA TGGAATGATT GGGGCCTTCT AGGTTTTTTG	360
AATTAGCCAA CAGGCCCAGA ACTGNTNCTT AAACAAGTCC GGGGNACTTT TTGTTTGGCT	420
TTAAGTGANT TCGAAATTTG GGGGGN	446

(2) INFORMATION FOR SEQ ID NO:1727:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1727:

GGCACGAGGG AACTGCCCCT AAAACATCCT GCCCTCTTNA AGGCAATTGG TGTNAAGCCT	60
CCTAGAGGAA TCCTGCTTTA CGGACCTCCT GGAACAGTAA AGACCCTGAA TTGCTCGAGC	120
TGTAGCAAAT GAAAACTGGA GCCTTCTTCT TCTTGAATCA ATGGTCCTGA AGAATCATGA	180
AGNCAAATTG GCTGGTGAGT CTAAGAAGCA ACCTTCGTGA AAGCCTTTGA NGGAGGCTGA	240

GAAAGGAATG CTCCTGCCCC TGCATCTTGC ATTGAATGAA GNTTAGATGC CATCGTNCCC 300  
 AAAAGAGGAG NAAAANTCAT GGTGNGGTGG AGCGGTGCAT TGT 343

(2) INFORMATION FOR SEQ ID NO:1728:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 107 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1728:

GCAGAGACCC CGACATCANG ATCTTTGGGA AGTGGAGCCC CGATGATGTG CAGATCNTGA 60  
 CTTTCCCTGA NGGATTNCTT GAAGTGAGGA NAGTTTGCCA GTCCCTG 107

(2) INFORMATION FOR SEQ ID NO:1729:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 314 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1729:

GGCANAGATG AAAGTTCCAC CAGTNTGTGC GGCTATNACG CTCCGAGAAA TAACCGCACC 60  
 ATCTCCTTNA TCCCACCCNA CGGCGAAGTT CNAGCTCATG TCCTACCGTN TNAACACCCA 120  
 CGTAAAGCCT TTGAANATGG GATCGANTCG GTGAATCGAN AAAGCACTCC CACAGCCGCA 180  
 TCGAGTACAT GAATCAAGGG CGGCAAGGGA GTTACCTGAA TGCGGGCCCA CTTNGGCCTG 240  
 NCTAAGTGTG GGAGGCCGAA GACAAGGGGG GGCAAGCCCC CGATTCAGTG TCCAGTTTCG 300  
 AGATNCCTTN ATTN 314

(2) INFORMATION FOR SEQ ID NO:1730:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 167 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1730:

GGCAGAGTNT ATACCAAAAA GCAGCTCTTG GATAGNATGT GTATGAACTT TAGGTGGTCA 60  
 AGTCTCTAAA GAAATCTNCT TTGAAGAAT TACAAGTGGT GCTCAAAATG AACTTGAGAA 120

AAAGTNAACT NCAAGTGCC ATATGCCCCA AATTNTTCCA GTTTGGN

167

(2) INFORMATION FOR SEQ ID NO:1731:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1731:

CTGGGAGGTG AATCAGTAAT GACCATGGNA TCAACCCAC CGGAACCTAC NACGGGGAAC	60
AGNGAACCTG NAGCTGGNCC GATTCTTTTT TTACTANAAT GAAGGCCACA GGTGGNAAAT	120
TTNTNCCTGG TGCCNATCCT GGTGGATTCT NGAAACCTGG GAACCATGGC CTTTTTTCGC	180
TCAAGGTCCT TTTGGCCA	198

(2) INFORMATION FOR SEQ ID NO:1732:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1732:

GGNACGAGGG AAGGTGTCTN AAAACTGGAG ACTGGGGCGC TGCCGAAAGG GGATTCTCCT	60
GAAGTGGAGA TGCAGTCAAA TGCCCTGGAA TGCAGCTAGA GGATGATTCT TTGTNCATAA	120
TCCCAGGCTA ATTNNAATCC TGGCCTACCA GTTCCGTCCA AATGGTGCCA GCTTGAATTC	180
GTCGGCCTCT GGGAGTCTTT NNTGGGGCAT GATNAGGACG TTTGCNACTT TNTCCTGGCC	240
AATTCG	246

(2) INFORMATION FOR SEQ ID NO:1733:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1733:

GGCACAGTGG TGGCTCATGC CTGCAGTCCC AGCCACTCAG GAGGCTTAGG CAGGAGAACC	60
ACCTAACCGG GAGGTGGNAG GCCGCGGTGA GTCGAGACCG GAAAACACTC TAGCCTGGGA	120



AAACAAGAGC GAAACTCCGC TCAAAAAAAAAA AAAAAAAAAA AAAAAANNTNG GGGGGGNCCC 180  
CNT 183

(2) INFORMATION FOR SEQ ID NO:1734:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 362 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1734:

GGTAGTATTC CNGGCGTACA GGTGCGCAGC TCGCGGCTCC AGTNATAACC AAAGCCCAGC 60  
ATTTTAAGCT GGTTTTNAAT ATACGCAATG TTGTCGTACG TCCACGGTGC CGGAGCGGTG 120  
TTGTTTTTAA CCGCCGCGCC TTCCGCAGGC AGACCAAACG NGTCCNAGCC GATCGGCTGC 180  
AGGACGTTTT TCCCCAGCAT ACGCTGGTAG CGGGCAATCA CGTNACCNAT GGTGTAGTTA 240  
CGTACGTGGC CCATGTNTAG TCGACCAGAA GGNTTAGGGA NAGCATAGAC AGGCAGTAAT 300  
AATTCTNTTT GATCTTCGTC TTCGGTTAAC TTNAAATGTG CGGTTTTAAT NCCCATGAAA 360  
GT 362

(2) INFORMATION FOR SEQ ID NO:1735:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 180 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1735:

CACTTTATNA NCCGGGAAAT AATGCGGGCA ACGGTGTTTA ATTATNTCGA TTGTNATTNC 60  
AATCGGTGGC GGCGGCACAG TTGGTGTGGC GGCTCAGTC CGGAACANTT TGAAANCAAG 120  
ACCCTCGCTT AGGCCTGTNT TCCATATTAN GTGGGTAGGT TCAAAATGCC GTTTNTGGTG 180  
180

(2) INFORMATION FOR SEQ ID NO:1736:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 351 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1736:

GGCANAGGNA GAGAGAGAGA GAACTAGTCT CGAGCGGGAG TCCGGCGGGT TACAGCGGAG	60
GCCTAGGTGG CAGACAGGGG GCCCGGGCCG CTGCGTGTG TCCACCCAAA ATGGAGTTCC	120
TCCTGGGGAA CCGTTNCAGC ACACCANTGG GGCAGTGCCT CGAAAAGGCA ACAAATGGCT	180
CCCTGCAAAG TGAAGGNTTG GACGTTGAAA TATGGAGATC TGTGAACATC ATCCAATGAG	240
AACGGAGGNA AGGGCCAAAG GATGCCATTC GAGCCCTGNA AGAAGCGGCT TCAACGGGGA	300
ACCGATACTT ACAGAGAAGG TTGATGCTGG NATTTAANCA GTGNCTGGNA G	351

(2) INFORMATION FOR SEQ ID NO:1737:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1737:

AGCACGAGGT GGA CTCACAA TTCCAAATAT TACCAGAAAG GGAGCCATGT NAGACAGGAC	60
AGCATGGAGC CCAGCGACGC TCTGGGAATG AATGTGTCTA ACTGTTCGGTG TGGGGACAGG	120
CTGAAGACCC TAGAGCAGAG GGC GCGGTAG CAGNCACGCA GAGC NCTGNG NNACATTGCA	180
CTGGTGGGGA CTCCAAACTA CATNGCACCC NAGGTCTNCC TCCGCAAAGG GTACACTCAA	240
CTTTNTGACT GGTGGAGTNT TGGAGTGATT CTTTTCGAGA TGCTGGTGGG GGCA	294

(2) INFORMATION FOR SEQ ID NO:1738:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1738:

GGCACGAGGG ANCANNCTCA ATAAGGTTGT NACACGACAC CCTNATCTNA AAGACTGCAT	60
GGTTTTGGCA NTGNCACATG TCGCAGCATG GTGGCCGTGA ANGGCATAGC GAACACCACA	120
GGGCAAGCTG G	131

(2) INFORMATION FOR SEQ ID NO:1739:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1739:

GGCAGAGCCA ATNAGGGNTA TTTTNATNAT TCCCACAAAT CCACCACCAA CATTCAGAAA	60
GCCAGANCTT TGGTCCGATG ATTCACCGA TTTTTTTAAA AAGTGTGTTGG TGAAGAATCC	120
TGAGCAGAGA GCTACTGNAA CACAACCTTT ACAGCATCCT TTTATCANGG NTGCCCCAAC	180
CTGTATCAAT ATTAAGAGAC CTGATCACAG AAGCTATGGN GATCAAAGCT AAAAGNNCAT	240
GNGGAACCAG CAACGGGANT TGGAAGGAGG AAG	273

(2) INFORMATION FOR SEQ ID NO:1740:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 155 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1740:

GGCAGAGGGC GACCANAGGC ACTTTTCCCC ACAGACCGGC GGCAGTANGG CAAAGGCTGT	60
GGGCAGCNGT TCGCTGGGAA GAAGTGCCTN CTGTGGTGGG CCANGCGCTG CTCGGAAGGG	120
CCTGTNTGCC CNCTGCTTTG GCCATTGCTT GGGGT	155

(2) INFORMATION FOR SEQ ID NO:1741:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 383 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1741:

GGCACAGGGN TCATCGGTGC AGGGGAGTTT GGAGAAGTGT ACAAGGGGCG TTTGAAACTN	60
CCNGGCAAGA GGGAAATCTA CGTGGCCATC AAGACCCTGA AGGCAGGGTN CTCGGAGAAG	120
CAGCGTCGGG ACTTTNTGAA GTNAAGGCGA GCATCATGGG CCAGTTCGAC CATCCTAANA	180
TCATTGCGCT GGNNGGTGTG GTCACCAAGA GTCGGCCTGT NCATGATCAT CACAGAGTTC	240
ATGGAGAATG GTGCATTGGG ATTCTTTCCT CAGGCAAAAT GACGGGCAGT TCACCGTGAT	300
CCAGCTTG TG GGTATGCTCA NGGGCATCGC TGCTGGCATG GAAGTACCTG GCTGNNTGA	360
ATTANGTGCA TCNNGGACCT GGG	383

(2) INFORMATION FOR SEQ ID NO:1742:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 279 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1742:

GGTANAGGTT GTNCCGAGGT GACACAGTGT TGCTGAANGN AAAGAAGAGA CGAGAAGCTG	60
TTTGCATCGT CCTTNCTAAT GATACTTGTN CTGATGAGAA GTATTCGGNA TGNAATAGAA	120
GTTGTTCCGG GAATAACCTT CGTGGACGCC TGAGGGGGTG TNATCAGCAT CCAGCCATGC	180
CCTGATGTGA AAGTACGGGA AACGTNATCC AGTGNTNGCC ATTGGTGACA CATTTGGGAGG	240
GCATTACTNG GTAATCTCTT CGAGGGTATA CCTNAAAGG	279

(2) INFORMATION FOR SEQ ID NO:1743:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1743:

GNAAGACCNA AGGCCAAGAC CATAATCGTG GCGGGCNTGG TGTNCCTGTT GGCCGGCCTT	60
ATGGTGATAG TGCCCGGTTT CCTGGAACGG CCCANAAAAT CATCCAAAAT TTCTANAATC	120
CGNTGGTGGC CTCCGGGCCA GAAGCGGGAA ATGGGTGCTT CGTTCTACGT GGGNTGGGCC	180
GNTTCCGACC TT	192

(2) INFORMATION FOR SEQ ID NO:1744:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 120 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1744:

TNGGGNTGCA GGAATTGGGN AGAGCGTGGG CAGCAAGGGT GGGTAAAGGA TCCAAANATG	60
GCTGGGCGAA AAATTGCTCT AAAAGAATT NATTGGGTAG CTTTTCAGN GATAATANNC	120
	120

(2) INFORMATION FOR SEQ ID NO:1745:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 59 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1745:

GGCANAGGCG CGCCCGAAAN CCCGNGNTGA TCCGCCGCCG CTGCCTTGAG TCGACTCTG 59

(2) INFORMATION FOR SEQ ID NO:1746:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 489 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1746:

GGCAGAGCCC GGGGTGGAGG AGCTGCTGAA CAAGGGGCAG GACCCTCTGG CAGACAGGGG 60  
TGAGAAGGAC ACAGCTAAGA GCCTCCAGCC CTTGGCGCCC CGGAACAAGA CCCGTGTGGT 120  
CAGCTACCGG TGCCCCACAA CGCTGCGGTG CAGTNTACGA CTACCGANAG AAGCGAGCCC 180  
GCNTGGTCTT CGGGCCTNAG CTGGTGTGCG TGGGTCCTGA GGAGCAGTTC ACAGTGTGTG 240  
CCCTCTNAGC TGGGCGGCCC AAGCNTCCCC ATGCCCGCCG TGGGCTTCTG CCTGCTTGCT 300  
GGGGCCTGAC TTCTTCACAG ACGTNATCAC CATCGAAACG GNGGATCATG CCAGGNTGCA 360  
ATTGCATTGG NTTACAATTG GNATTTAAGG TGAATTAACC GNAGGACCCC CAAGAGACGG 420  
CCAAGTTTTT TTAANTGCCA ATTTTATAGN ATGCTNAAAA CCNTGNATCC CGGTNGGGGG 480  
NCCTGGGTT 489

(2) INFORMATION FOR SEQ ID NO:1747:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1747:

GGCAGAGTTT AATCATCCAG CGCACATTTA TTGAGCCTGG CTTTCAGCCT TCGTGTGGT 60  
GCAGTGTGAG CCCCCGGCTT GAGTTCACCT CCTTGGCCCT GCACTCTNAG TGGCGGCTCG 120

TGGCCTTCGG CACCAGCCAT GGCTTTGGCC TCTTTGAACC ACCAGCAGCG GCGGCAGGTC	180
TTTGTTAAGT GCACACTGCA CCCCAGTNAC CAGCTGGCCT TGGAGGGCCC ACTCTCCCGC	240
GTCAAGTCCC TCAAGAAGTC CTTGCGTCAT NATTCGCGG GATGCGTCGG NGCCGGGTGT	300
CCAGCCGGAA GCGGCACCCG TTGGCCCCC AGNAGAGGCA CAGNAGGGGA NTGCCAAGGT	360
TNAGCGGCCA GGCTTCCAGA ACATGGGAGT TTGNNGGCTTT	400

(2) INFORMATION FOR SEQ ID NO:1748:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1748:

GGAAGACCTG ACGGGCATTG TAAGCTGGGN ANATGCCTGT GNGGCCCCGAA ANAGGCCTGG	60
NGTGTACATN CTGGCCTCCA GCTATGCCTC CTGGAATCCA AAGCAAGGTG AACAAANCTC	120
CAGCCTCGTN TGGTGCCCCA AACCCAGGGG TCCCAGCCCG AAAGAAACCT TTTTGGCAGC	180
CACCTGGCCT TAAAGNTNTG CCCAGCCCCA GGGNTTNNTG AGGCCCATCC TTTTCCTG	238

(2) INFORMATION FOR SEQ ID NO:1749:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1749:

GGCAGAGNCA GCAGGCACAG TCTCGCCATC TGCATCCATC TTGTTTGGGC TCCCTACCCT	60
TAAAAAGTGC CTCAAATAAT ACCCTGGTGG CCATGGACTT CTCTGGCCAT GCTGGGCGTG	120
TNATTGAAGA AACCCCCGGG AAGGCTCTGA AGTGTGGCCC TGGAGGAGGC CCAGGCCTGG	180
NAGGNAAGAA GACAAACCAC CGCCTTCAGC CTGCCCCATGC CAGCCTCCGG NAAGAGCCTC	240
AGTGGCAGCC ATCCACCGNA CCCAACTTTG GTTCCACGGG GCGGCATTTT CCGTGAAGGA	300
GAGCCAGGGT TNATTTGGGA CAGCAGGGTT TNGTTAGACG GNCTGTTCCCT GGTNCGGGAA	360
GAGTCANGGG AACCCCCAGG GTTTTGTCC	389

(2) INFORMATION FOR SEQ ID NO:1750:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1750:

GGNAGAGCCN AGTCTTAAGT TTTTNTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTNAAA 60  
AAAACCCCTT TTTTTTTN 79

(2) INFORMATION FOR SEQ ID NO:1751:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1751:

CAACGNGNGN GGNCCAAGTA AGCAAGGGCG GGCAACTCCG GAGATNCAAC GGGGAGCTGT 60  
ACGCCCCGCT GCAGCATGTG AAGCCCCGTG CTGCCCCGGG GGGCGGCCGA ATCGGGCCCCG 120  
GNNTGCGCAA GGGGGACCGC ATCCTGGAAG GTGAACCACG TGAATTTTGA GGGGGCGACA 180  
CACAAGCAGG TGGTGGGACC TNATTCGAGC AGGCGNNNAA GGAATTGAAT CCTTGAACAG 240  
TTTTATCTGT ACCTCCTCAT GAGGCAGATT AACCTTAGAT CCCAGTGAAC GGATTCGTTN 300  
NGGGACAATT NATTTTAATG NTTTTACAAC AGAAAAGCNA AGG 343

(2) INFORMATION FOR SEQ ID NO:1752:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1752:

GGCANAGCTC GAGTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT 60  
TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTNNNC N 101

(2) INFORMATION FOR SEQ ID NO:1753:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1753:

GGAAGANCCC TCTCCCAGTN TCCGAAAGGA AGAGTAATGA CCATTCCGTA CCAGCCCATG	60
CNGGCNAG	68

(2) INFORMATION FOR SEQ ID NO:1754:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1754:

GGCAGAGACT GGGAAGGAAA GAACATGGCC TGTGTGCAGC GGACGCTTAT GAAATCTGGG	60
TGGGCTGGCA GTAGCCCGAA ATGATGGGCT CTTCTCTGGG GTATCCCAAC TGGTTCCCTA	120
AGAAATCCAA GGTAGAATCC TCGGNAACTT CTCGGATAAC CAGCTGCANG AGGGTCAAGA	180
ACGTGAATCG GGTTACAGAT GGGCACCAAC CGCGGGGCGT CTTCAGGCAG GCATGNACTG	240
GNCTTACGGG AATGCCACGN CAGATCCTTT GAATCCCACC CCAGGCCTTN GCCCCTGNC	299

(2) INFORMATION FOR SEQ ID NO:1755:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1755:

GGCANAGGTT TCCCGAAGTA AGTNCCCANAG GAGCTGGCTG TGGAACGTTG AAGGACTTGA	60
AANAGCCACC GAAAAATGGG AATCTNTACG AAGGCTCATG AAATATATTT TTAAAAGACT	120
CCATCACCAC GTGGGAAGAA TTCTGNGCTG TGANGCATGT NGGACAAGA AAGGGAATCT	180
NTNTGGCAAA CCCCTTCAAG GTTCACAGTT ATG	213

(2) INFORMATION FOR SEQ ID NO:1756:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1756:

GGCAGAGTGA AAGTCACTGT GGATCGAGCT CACAGGGGGC ACCCATGCCT GTTGTNAACA	60
GAGTCTNAAG CAGTCAGGGT GTTGAATTC CTCTGTTGTT GTNATCAATT CCTGCTGAGG	120
GGTTTCTGGG GTTTTNTTTT TAATAAATGA ACTCCTTTGT AGCCTTTGTN ACATAATCTT	180
CACTTTGGTT GTTGGTACCA AACAGAGCTC CCAGCCATCT CCTCCCTGTT CCTGAAAGAC	240
TAAAAATCCA CTTNCGGACT CTCCCTTCCT TCCTTCTTNA GCCCTCGAGG GTGCATATTA	300
GCTAATTAAG CAGGNCCAGA GNCAGAGAGG GGGGGTTCCA AAATGAANTC GGNTTTAAGG	360
GGCAAGTGNC CATTNATTGG GTTGAATTA ACGGTTATCC TTCATGGNCC GTAAATCCCA	420
GCATTTTGG GGGGCCNNG CANGTGGGTC CCNAGGTTGG GGGTTCGGGA CCAACNGGGC	480
CAAC	484

(2) INFORMATION FOR SEQ ID NO:1757:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1757:

GGCAGAGCTT TGGAGAGAAG GGAACAGAAG GTGACATCGG CTTCCCTGGG AATAACAGGC	60
GTAANTGGAG TCCACGGCCC TCCAGGGTCG CAGGGAGAGC TGGGGCGAAT TGGAAGTGCC	120
TGGTGGCAAA GGAAGATGAT GGCTGGCCGG GAAGCTCCGG GNTTNACCAG GTTTTCCGGG	180
NACTCCGTGG GAATCCGCGG NNTTACACGG ATT	213

(2) INFORMATION FOR SEQ ID NO:1758:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1758:

TTTTTTTTTT TTTTTTTTTT TTTTTTNAAA GGGGGGGGGG GGGGGNAATT TT	52
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(2) INFORMATION FOR SEQ ID NO:1759:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1759:

TCCGGNATGT GCCAAAGCTG GTTTTCCTGG GGAACGAACG CTCCCGAAGN NGANGTTTCC	60
TTCCATCGTC GGGNGCCCCA AACACCAGGG CCGTGCATGG TGGGTCATGG TNCCAGTAAG	120
GACTCCTGAC G	131

(2) INFORMATION FOR SEQ ID NO:1760:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 420 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1760:

GGCAGAGGNA ACCATATACA AGTTCTGCCC GACCATTGTA ACGCAAGGTT GGAAAGTCCT	60
AAATTCAATC ACAATCTTCT GCCAAGTGNA ACTGGNACAT AAACCTGGAC TTGTCTTCAA	120
AAACTCCAC TTCTCCAAAA ACTCTTGTA AAATCGCACA GTTTGGGCAC AGCCTNCCTG	180
AGTTTGAACA GTGGAGTTGA AACTTTCTCT ATCCCATGCA GAGGAAGCCT AAATNATGCA	240
AATAAATAAT TATCCAGCAC AGTGCCTNAA AGCTATTTCC TGTGAAGTCC CTTTCAGCTG	300
TGGGAAGAGG GATGGAAGGA TGGAAGATGG GTNCATAACT GTGGGTGGGC CACAANCCCG	360
AGGGNATNNT TTAACAGCAA TGGGGGGCGT GCTGAGTTCC CTAGGAAACT GGTGTTTAGT	420
	420

(2) INFORMATION FOR SEQ ID NO:1761:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 180 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1761:

GGCANAGTAA GAACAGGGTG ATTTTNAATC AGAGAACTC TGGGAACGGG TAACTCGAGC	60
CATAAATGCC AAAGACCAA CTGAAGCTAC CCAAGAGAAG TATGTTTTGG ANGAAGCTCA	120
AAGACAAGCT GCCACGGATC GGAANACANA AANTGTNAGA GTGGTCTTTC AAATTATTTG	180
	180

(2) INFORMATION FOR SEQ ID NO:1762:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 292 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1762:

GGCAGAGAGN ATGCTTCCTT TAAATACCAA TATTCGACTT GCGTACTCAA ATGGAAAAGA	60
TGATGAACAG AACTTCATTC AAAATCTCAG TTTGTTTCTC TGCACCTTTC TTAAGGAACA	120
TGNTCAACTT GATGAGGAAA AAAGGTAAA TCTCAGGGAA ACTCTTATGG GAGGCCCTTN	180
CATTATATGT TGTGGGTAT CTGGAAGTGA GNAAGAACT GGAAAATTCT TTGAAAATTT	240
GTNCTTGGA TGACTGGNAA TCCATNTAGG GCTGGCTGGA ACNCTATAGG AG	292

(2) INFORMATION FOR SEQ ID NO:1763:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 414 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1763:

GGCAGAGNAG AAGTTTAAGA TCAAGCTCAT GAGTNANTTG GTCAGCAATG GCGTCCAGAT	60
ATACCANTTC CCAACGGATG ATGACACTAT TGCNANGGTC AACGCTGCAA TGAAATGGNA	120
CAGTTGCCGT TTGCTGTTGT GGGAAGTATG GTTGAGGTAA AAGTCGGAAA CAANTGGTCA	180
AAGCTCGCCA GTTACCCTTG GGGTGTGTA CAAGTGAAA ATGAAAACCA CTGTGAACTT	240
TGTAAAAGCT GCGGGAAATG CTCCATTTGT ACAAATATGG NGGTNCCTGC GNGAGNAANC	300
CCATACCAGG CACTATGAGG TTTTACAGGC GCTGCAANCT GGAGGAAATG GGGTTTTACA	360
GTGTGGGCCC AGNAAANCAA GCCATTCATT TTTCAGGGGA CNTTGNGGCC AAAG	414

(2) INFORMATION FOR SEQ ID NO:1764:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 137 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1764:

AATGGCGGNA AATTNTTGAT TACAAGGNTA TTNAGCTTAG TTGGAAAGCA AGAAATTTCA	60
ACTTTTTTATT GTTTAGAGCN TCATAAAGTT TTGTGAAAGA GNGAAGNATT TTTGGTTCCA	120
AGNTTATATG GTTNGGG	137

(2) INFORMATION FOR SEQ ID NO:1765:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1765:

GGCAGANAAG TNTAAATGCA CATNANTGGC AGCTTATAGA GAACCACCTT GTAACCAGTA	60
TACAGGTACA ACTACAGCTC TTCAGAAATT GGAAGGTTTT GCTAGCCGGT TATTTCATAG	120
ACACTCTAAA GGTACTGCNA CATGAATCAG AAAACAGCTC TGGNAAAATG AACAGCCTTT	180
CATTTCTTTG AAACATACTG CCTTTATGGG AACAGATTCA ATGNAAAGAN TTTCTAGCCA	240
AAGCCAAAGA AGGACTTTTT GAAAAAATG GGGNGATTCC AACTCNGAAG TTAATGCCGG	300
ACTTGNAAG	309

(2) INFORMATION FOR SEQ ID NO:1766:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1766:

GGCAGAGGGC ANCATCCACA ATAAAGAGAA GCCATTTAAG TNTCACTTAT GTAATAGGTG	60
TTTTGGTCAA CAAACCANTT TAGACAGNCA CCTAAAGAAA CATGAGAATG GGAAACATGT	120
TCCGGTACAG CAACANCGTC GACTCATTCT AAACNGTAA AGTACAGGTG NGAATTCTGG	180
TTGTACAAAG ATGAATGNNT ACTTTACAG AAATTCCGAA ATTTTCATTGG GNAACANCA	240
CCATGGGCAG CCAATCTCCC AGGTATTNTG GGTGGAGAGN ATGA	284

(2) INFORMATION FOR SEQ ID NO:1767:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1767:

GGCAGAGCTC GTCNTNNGNN ATCAAAAGAA ATTTGGTTGC CACCCCCACA GTTCTACGAA	60
GGAGNAAGAC TTGCAAACCTT TGCCTCTCTC TCTGACTTGC ACAAATTTTG TTTGGGTCGT	120
GCATTAGAAG GACTGGTAAA GGTGGCTGCC GATCATCTNG TTAAGTCTG ATGGGATGGT	180
CCATCTTTTA CCAGGTGATG AGCTATATTT AGAAGATTCA NACTTTTTTG AAAATCTTAT	240
GTCTACTGAA AAAAAGACTG AGGAAATCAT GAAGGAAGGC AAGCAGTTTC ACCGGGNTAG	300
TGACATACCA TCGNCACCTT TATGGATATC CCCGNGGACT GTTCCAGCCA AAGTTTTAAA	360
CCAGGTTTTT CCNCANGAAC	380